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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:39:42 / Search time 3691.2 Seconds
(without alignments)
16303.117 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank1:
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2: gb_hcg:*
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41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	621.4	42.2	1856	8	AF005096
2	559.4	38.0	1684	6	AR076814
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4	559.4	38.0	1684	6	BD062571
5	559.4	38.0	1684	6	BD070919
6	559.4	38.0	1685	6	AR020904
7	559.4	38.0	1685	6	AR200408
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12	551.4	37.5	1478	8	AY055117
13	538.2	36.6	1347	8	AY131238
14	529.4	36.0	1341	8	AR406816
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34	377.8	25.7	1702	6	AR200409
35	359.6	24.4	96312	2	AP005554
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ALIGNMENTS

RESULT 1
AF005096
LOCUS
DEFINITION Ricinus communis desaturase/cytochrome b5 protein mRNA, complete
ACCESSION AF005096
VERSION AF005096.1 GI:4101625
KEYWORDS
SOURCE
ORGANISM Ricinus communis (castor bean)
Bukariyotai; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Euphorbiales; Ricinus.
REFERENCE
1 (bases 1 to 1856)
Sayanova,O., Smith,M.A., Lapinskae,P., Stobart,A.K., Dobson,G.,

TITLE Sunflower albumin 5' regulatory region for the modification of
 JOURNAL plant seed lipid composition
 Patent: US 5959175-A 1 28-SEP-1999;
 FEATURES Location/Qualifiers
 source 1..1684
 BASE COUNT 430 a 277 c 358 g 619 t
 ORIGIN

Query Match 38.0%; Score 559.4; DB 6; Length 1684;
 Best Local Similarity 62.8%; Pred. No. 4.7e-148;
 Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;

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 358 TATGACAAAAAGCATATATATGTTTGACATTTGTCTTATAGCAATGCTGTTTGT 417
 420 CTGAGGTTTACGAGGTTCTACTGCAAGAGACCTGGGCTCATCTTGTCTGTG 479
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 480 CTATAGGTATGCTATGCTCCAGAGTGTGGTGGGCGCATGATCTTGTCTACTACCA 539
 478 TTGATGGGGTTTCTTGTGATCAGAGTGTGATTTGACATGATGCTGGGATTAAG 537
 540 GTTATGCTTACCCGTAAGCTTATGCTCTTTTCAATCATTTGCAAGAAATGTGCT 599
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 600 GGTGTTAGTTGTCATGAGTGAAGTTGACCAATACACCATCATCTTGTCTATATAC 659
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RESULT 3
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 DEFINITION Sequence 1 from patent US 5977436.
 ACCESSION AR084177
 VERSION AR084177.1 GI:10010948
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1684)
 AUTHORS Thomas, T.L. and Li, Z.
 TITLE Oleosin 5' regulatory region for the modification of plant seed
 JOURNAL lipid composition
 Patent: US 5977436-A 1 02-NOV-1999;
 FEATURES Location/Qualifiers
 source 1..1684
 BASE COUNT 430 a 277 c 358 g 619 t
 ORIGIN

Query Match 38.0%; Score 559.4; DB 6; Length 1684;
 Best Local Similarity 62.8%; Pred. No. 4.7e-148;
 Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;

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 A sunflower albumin 5' regulatory region for the modification of
 plant seed lipid composition.
 ACCESSION
 BD062571
 VERSION
 BD062571.1 GI:22608174
 KEYWORDS
 JP 2001518795-A/1
 SOURCE
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 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 Thomas, T.L., Beremand, P.D. and Nunberg, A.N.
 1 (bases 1 to 1684)
 A sunflower albumin 5' regulatory region for the modification of
 plant seed lipid composition
 Patent: JP 2001518795-A 1 16-OCT-2001;
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 PN JP 2001518795-A/1
 PD 16-OCT-2001
 PR 09-APR-1998 JP 1998543140
 PR 09-APR-1997 US 08/831570
 PI TERRY L THOMAS, PHILLIP D BEREMAND, ANDREW N NUNBERG PC
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 Best Local Similarity 62.8%; Pred. No. 4,7e-148;
 Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;
 QY 60 AAGAACACATTTGCGACAGACCTTGCAGAAAGCATTAACCAACAGAGATTATGATC 119
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RESULT 5
BD070919
LOCUS
DEFINITION
An oleosin 5' regulatory region for the modification of plant seed
ACCESSION
BD070919
VERSION
JP 2001519668-A/1.
KEYWORDS
unidentified
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 1684)
AUTHORS
Thomas, T.L. and Li, Z.
TITLE
An oleosin 5' regulatory region for the modification of plant seed
JOURNAL
Patent: JP 2001519668-A 1 23-OCT-2001;
COMMENT
Rhone-Poulenc AGRO
OS
Unidentified
PN
JP 2001519668-A/1
PD
23-OCT-2001
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09-APR-1998 JP 1998543141
PR
09-APR-1997 US 08/831575
PI
TERRY L. THOMAS, ZHONGSEN LI
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C12N15/62, C12N15/29, C12N15/53, A01H5/00, A01H5/10 CC
Strandness: Double;
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Topology: Linear;
CC
An oleosin 5' regulatory region for the modification of plant
seed lipid
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composition
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key
FT
CDS
Location/Qualifiers
1..1684
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BASE COUNT
430 a 277 c 358 g 619 t
ORIGIN

Query Match 38.0%; Score 559.4; DB 6; Length 1684;
Best Local Similarity 62.8%; Pred. No. 4.7e-148;
Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;

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 Db 1015 GTTCACTCTCTCTGTAACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1074
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 Db 1075 AATTGCTTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 1134
 Qy 1140 TGGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1199
 Db 1135 TGGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1194
 Qy 1200 TGGCATTTCAGAAATCTCACCATTGTAACAACTTGGCAGAAAGCATTAATTGCTC 1259
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 Db 1375 CACACTCATGTTAAATTAACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCT 1434
 Qy 1440 TCCCAATGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 1469
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RESULT 6
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LOCUS AR020904 1685 bp DNA linear PAT 05-DEC-1998
 DEFINITION Sequence 4 from patent US 5789220.
 ACCESSION AR020904
 VERSION AR020904.1 GI:3975519
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1685)
 AUTHORS Thomas,T.L., Reddy,A.S., Nuccio,M., Nunberg,A.N. and Freyestine,G.L.
 TITLE Production of gamma.-linolenic acid by a DELTA-6-desaturase
 JOURNAL Patent: US 5789220-A 4 04-AUG-1998;
 FEATURES
 source 1..1685
 location/Qualifiers
 BASE COUNT 431 a 277 c 357 g 620 t
 ORIGIN

Query Match 38.0%; Score 559.4; DB 6; Length 1685;
 Best Local Similarity 62.8%; Pred. No. 4,7e-148;
 Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;
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QY	1080	GATTGGTTTCCACGACAGAACAAAGGGACCGTCAACATTAACAGCTTCTGCTTGTGGGAT	1139		
Db	1076	AATTGGTTTGAAACAAACGGAATGGGACACTTGACATTTCTGTCTCTTGGATGAT	1135		
QY	1140	TGTTTTCATGCTGGCCCTGCACTTTTCAGATTGAGCATCATCTGTTTCCAAAGATGCTAAG	1199		
Db	1136	TGTTTTATGTGTGATTTGCAATTTCCAAATTTGACATCATTTGTTTCCAAAGTGTCTAGA	1195		
QY	1200	TGCCATTTGAGAAATATCTCAACCAATTTGGAACAACTTTCACGAAGACATTAATTTGTCC	1259		
Db	1196	TGCAACCTTTAGAAATATCTCGCCCTACAGTGTATGATGCAAGAAACATTAATTTGCTT	1255		
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Db	1256	TACAATTAATGATCTTTTCTCCAAAGGCCATTAATTAATGACACTCAGAACATTAAGAACACA	1315		
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Db	1316	GCATTTGACAGCTTAGGATATTAACCAAGCCGCTCCGAAAGAAATTTGTATGGGAAGCTT	1375		
QY	1380	AACACTTTGGGGTGAACCTTATMAAACATCAAGTGTCTTTCCTCCGTAAGAAGCTTCCAG	1439		
Db	1376	CACACTCATGTTTAAATTAACCTTATGTCAATGTAATTAATTTGAGATTATGATCTCCTA	1435		
QY	1440	TCCCAATGTTCTTTTTTTTTTTTTTTTTTT	1469		
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RESULT 7	AR200408	1685 bp	DNA	linear	PAT 19-APR-2002
LOCUS	AR200408	1685 bp	DNA	linear	PAT 19-APR-2002
DEFINITION	Sequence 4 from patent US 6355861.				
ACCESSION	AR200408				
VERSION	AR200408.1	GI:20250482			
KEYWORDS	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1685)				
AUTHORS	Thomas,T.L.				
TITLE	Production of gamma linolenic acid by a DELTA-6-desaturase				
JOURNAL	Patent: US 6355861-A 4 12-MAR-2002;				
FEATURES	Location/Qualifiers				
SOURCE	1..1685				
BASE COUNT	431 a 277 c 357 g 620 t				
ORIGIN	1..1685				
Query Match	38.0%; Score 559.4; DB 6; Length 1685;				
Best Local Similarity	62.8%; Pred. No. 4.7e-148;				
Matches	885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;				
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Qy	120	TCATACAGGGAAAAGTTTACGATATCTCCAGTGGACTTAAGACATCCCGGTGGTAG	179
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Qy	240	GGCACTGCTTGGCAATACCTTGACAGGTTCTTTTACTGGTACTACGTTCAAGATTACTCT	299
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Qy	300	GTCCTGAGATGTCACAGACCTACAGAAAGCCGCTCTGAGATTTTGAAGTGGATTGG	359
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Qy	360	TTCAAGACACCAAGCAAGGGGTCTACTGCTCATCTTTTTCGTCTGTGTTGGT	419
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Db	479	TTGATGGGGTTTTCTTTGGATTCAAGAGTGGTGGATGGAATGATGCTGGGCATTTATG	538
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Db	539	GTAGTGCTCATATTCAGAGCTTAATTAAGTTTATGGGTTTATTTGTCGCAAAATGTCTTCA	598
Qy	600	GGATGTTAGTGGCATGGTGGAAAGTTGAGCATTAACCCATCACTTGGCTGTAAATAGC	659
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Qy	660	GCCAAATCGATCCTGATATTTCAGCACCTTCTCATTAATGCGATATGCCCAAAATTTTC	719
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Db	719	GGTTCACCTCACCTCTCATTTCTATGAGAAAAGGTGACTTTTGACTTTTATCAAGATTC	778
Qy	780	TTTTGTAGCTTTAGGACCTGGACATTTTATTCGCAATGTTAAGCGTTAAGCTCTATCTT	839
Db	779	TTTGTAAATGTAACAATGGACATTTTACCTTATATATGTGTGCTGAGGCTCAATATG	838
Qy	840	TTTATTTCTGCTTTTAAAGTGTGTGTTTTCCAAACAAGAGGTATACAAGAGAATCAG	899
Db	839	TATGTACAACTCTCATATATGTTGTTGACCAAGAGAAAT---GTGTCTATCGAGCTCAG	895
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Db	896	GAACTCTTGGGATGGCTAGTGTCTCGATTTGGTACCCGTGCTGTGTTCTTGTTCGCT	955
Qy	960	AATTTGGCTTAAAGGCTCATGATTTTACAGTCCGTGTTTACAGATGCGCGGTTTCCAAAT	1019
Db	956	AATTTGGGTAAGAAATATATGTTGTTATTTGCAAGTTTATTCAGAGTGTGAATGCCAACAA	1015
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Qy	1200	TGCGATTTCAGGAAATATCTACGCCATTGTGAAACAACTTTGCGAAGACATATTTGTGC	1259
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Qy	1260	TATGAAATCTGTACCATGTGGGAGGCCATTAATAATGTATATCTCACCCCTGGTGTGTG	1319
Db	1256	TACAAATTATGTCATCTTTCTCCMAAGGCCATTAATAATGACACTCAGAAACATTGAGAACACA	1315
Qy	1320	GCTATGGAAGCTAAGATGTTAACCAAGCAGTTCCCAAGAACATGATCTGGGAAGCATG	1379
Db	1316	GCATTGCAAGCTAAGGATATTAACCAAGCCGTCGCCGAAGATTTGGTATGGGAAGCTCTT	1375
Qy	1380	AACACTTTGGGGTAAACCTTATNNAAACATCAAGTGTCTCTTTCCCGTAAAGCTTCCAG	1439
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DEFINITION	Sequence	4 from patent US 5614393.	linear		PAT 13-MAY-1997
ACCESSION	138430				
VERSION	138430.1	GI:2084484			

SOURCE	Unknown.
ORGANISM	Unknown.

REFERENCE AUTHORS	
1 (bases 1 to 1685)	
Thomas, T. L., Reddy, A. S., Nuccio, M., Nunberg, A. N. and	

TITLE Production of gamma-linolenic acid by a DELTA-6-desaturase
JOURNAL Patent: US 5614393-A 4 25-MAR-1997;

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BASE COUNT	431 a	277 c	357 g	620 t
ORIGIN				

Query Match	38.0%	Score 559.4	DB 6	Length 1685
Best Local Similarity	62.8%	Pred. No. 4.7e-148		
Matches 885, Conservative	0	Mismatches 522,	Indels 3,	Gaps 1.

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QY 180 CTCCCATTTGTAAGTTTTGCCGGCCAGATGCACTGATGCGTTCATTGCCTAACGCTT 239

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QY 240 GGCACGTGTTGGCAATACCTTGACAGGTTCTTTACTGCGGTACTACGTTCAAGATTACT 299

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Db	479	TTGATGGGGGTTTCTTGGATTCAGAGGTGTGGATGGACATGATGCTGGGCATTATATG	538
Qy	540	GTTATGGCTTAACCGTAAAGCTTAATCGTCTTTTCAATTCATTTGACGAAATGATTTGCT	599
Db	539	GTAATGCTGATTTCAAGCTTAAATAGTTATGGGTATTTTGTGCAAAATTTGCTTTCA	598
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Qy	780	TTGTGTAGCTTTGACGACGTGACATTTTATCTGTCATTTGTAACGTTAGGCTCTATCTT	839
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Qy	960	AATGGCCCTGAAGAGGTCAATGTATTTACACGTCTTTAGAGTGGCGGGTTCCACAT	1019
Db	956	AATGGGGGTGAAGAAATTAATGTTGTATATGTCAGAAATATCAGTACTGGAAATCAACAA	1015
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Db	1016	GTTCAAGTTCTCTTGAACACTTCTCTTCAAGTGTATATGTTGAAGCTTAAGGGGAT	1075
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Db	1376	CACACTATGGTAAATTAATCCCTTAATTCATGTAATTAATTTGAGATTATGATATCTCCTA	1435
Qy	1440	TCCCAATGTTCTTTTTTTTTTTTTTTTTTTT 1469	
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RESULT 9
AF007561

LOCUS AF007561 1685 bp mRNA linear PLN 05-JAN-1999
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 ACCESSION AF007561
 VERSION AF007561.1 GI:4102020
 KEYWORDS
 SOURCE Borago officinalis
 ORGANISM Borago officinalis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; Lamiales; Boraginaceae; Borago.
 REFERENCE 1 (bases 1 to 1685)
 AUTHORS Numberg,A.N., Beremand,P.D. and Thomas,T.L.
 TITLE Engineering of Plant Seed Oils to Produce Gamma Linolenic Acid (GLA)
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1685)
 AUTHORS Numberg,A.N., Beremand,P.D. and Thomas,T.L.
 TITLE Direct Submission
 JOURNAL Submitted (09-JUN-1997) Biology, Texas A&M University, College Station, TX 77843, USA
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 BASE COUNT 431 a 277 c 357 g 620 t
 ORIGIN
 Query Match 38.0%; Score 559.4; DB 8; Length 1685;
 Best Local Similarity 62.8%; Pred. No. 4,7e-148;
 Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;

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Db 1436 TGTTCGTCCTGCTGTTCTACTTGT 1465

RESULT 10
BOU79010 1687 bp mRNA linear PLN 02-MAY-1997
DEFINITION Borage officinalis delta 6 desaturase mRNA, complete cds.
ACCESSION U79010
VERSION U79010.1 GI:2062402
KEYWORDS
SOURCE Borage officinalis
ORGANISM Borage officinalis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiales; Boraginaceae; Borage.
1 (bases 1 to 1687)
2 (bases 1 to 1687)
Sayanova, O., Smith, M.A., Lapinskas, P., Stobart, A.K., Dobson, G., Christie, M.W., Shewry, P.R. and Napier, J.A.
Expression of a borage desaturase cDNA containing an N-terminal cytochrome b5 domain results in the accumulation of high levels of delta6-desaturated fatty acids in transgenic tobacco
Proc. Natl. Acad. Sci. U.S.A. 94 (8), 4211-4216 (1997)
97268723
JOURNAL MEDLINE
PUBMED 9108131
REFERENCE 2 (bases 1 to 1687)
Sayanova, O., Smith, M.A., Shewry, P.R. and Napier, J.A.
Direct Submission
Submitted (20-NOV-1996) Cell Biology, IACR-Long Ashton Research Station, Long Ashton, Bristol BS18 9AF, UK
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BASE COUNT 441 a 276 c 356 g 614 t

ORIGIN

Query Match 37.8%; Score 556.2; DB 8; Length 1687;
Best Local Similarity 62.6%; Pred. No. 3.8e-147;
Matches 883; Conservative 0; Mismatches 524; Indels 3; Gaps 1;

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DB 117 TCGATTCAGAGGAAACCTATGATGTTTCGATTTGGGTGAAGAACATCCAGGTGGAGC 176
QY 180 CTCCTATGTTAGTTTGGCGGCAAGATGTCACTGATGCGTTCATGCTTACATCTT 239
DB 177 TTTCCCTTGAAGAGTCTGCTGTCAGAGATCAAGTCAATGCTATGTCATTCATCT 236
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DB 894 GAACCTTGGGATGCTTATGATGTTTCTGATTTGATGACCTGTTGTTTCTGTTGCTT 953
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DEFINITION	AY055118	1450 bp	DNA
ACCESSION	Echium pitardii var. pitardii delta-6-desaturase (D6DES) gene,		linear
VERSION	complete cds.		PLN 01-DEC-2001
KEYWORDS	AY055118		
SOURCE	AY055118.1	GI:17223796	
ORGANISM	Echium pitardii var. pitardii		
	Echium pitardii var. pitardii		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	Asteridae; Jamids; Boraginaceae; Echium.		
REFERENCE	1 (bases 1 to 1450)		
AUTHORS	Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R.		
TITLE	Cloning and Molecular Characterization of the D6-Desaturase from		
JOURNAL	Echium: Functional Expression in Yeast and Tobacco		
REFERENCE	2 (bases 1 to 1450)		
AUTHORS	Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-SEP-2001) Biochemistry, Universidad de Almeria,		
FEATURES	Campus Universitario, la Canada s.n., Almeria 04120, Spain		
SOURCE	Location/Qualifiers		
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Query Match	37.6%	Score 553	DB 8	Length 1450
Best Local Similarity	63.9%	Pred. No. 3,1e-146		
Matches 854	Conservative	0	Mismatches 480	Indels 3
				Gaps 1

Qy 60 AAGAAAGCATTTCGACAGCACTTGCATAAGCATTAAGAACGAGGATTTATGATC 119
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Db 23 AAGAAGTACATTACTCGCAGAAGAGCTGAAGAAGCATGTATAAAGAGGGGATCTCTGGATC 82
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Qy 120 TCTATCAAGGAAAAGTTACGATATCTCCAAGTSGACTAAAGAGCATCCCGGTGGTAG 179
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 DEFINITION Echium gentianoides delta-6-desaturase (D6DES) gene, complete cds.
 ACCESSION AY055117
 VERSION AY055117.1 GI:17223794
 KEYWORDS
 SOURCE Echium gentianoides
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; Lamiales; Boraginaceae; Echium.
 1 (bases 1 to 1478)
 Ruiz,J.R., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and
 Marco,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and
 2 (bases 1 to 1478)
 Marco,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and
 Unpublished
 Echium: Functional Expression in Yeast and Tobacco
 Cloning and Molecular Characterization of the D6-Desaturase from
 JOURNAL Submitted (10-SEP-2001) Biochemistry, Universidad de Almeria,
 REFERENCE Campus Universitario, La Canada s.n., Almeria 04120, Spain
 AUTHORS Ruiz,J.R.
 TITLE Direct Submission
 JOURNAL
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 Best Local Similarity 63.8%; Pred. No. 8.6e-146;
 Matches 853; Conservative 0; Mismatches 481; Indels 3; Gaps 1;
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ACCESSION	AY131238		
VERSION	AY131238.1	GI:22296825	
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ORGANISM	Argania spinosa		
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REFERENCE	1 (bases 1 to 1347)		
AUTHORS	El Filali, A., Anderson, M. and Abbas, K.		
TITLE	Characterization and cloning of delta-6-desaturase in Argania spinosa fruit		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1347)		
AUTHORS	El Filali, A., Anderson, M. and Abbas, K.		
TITLE	Direct Submision		
JOURNAL	Submitted (12-JUL-2002) Biologie Moleculaire, Faculte des Sciences, Ibn Batoua, Rabat, Rabat 1014, Morocco		
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Db	76	TGATTTCTTGGAAAGCCTATAGTATGTTTGGATTGGTGACAGACATTCAGGTGGCAGC	135

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 DEFINITION mRNA, complete cds.
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 VERSION AF406816.1 GI:22652110
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 SOURCE Aquilegia vulgaris
 ORGANISM Aquilegia vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
 Ranunculaceae; Aquilegia.
 1 (bases 1 to 1341)
 Longman, A.J., Michaelson, L.V. and Napier, J.A.
 Isolation and characterization of a cDNA encoding a delta 8
 sphingolipid desaturase from Aquilegia vulgaris
 Unpublished
 2 (bases 1 to 1341)
 Longman, A.J., Michaelson, L.V. and Napier, J.A.
 Direct Submission
 Submitted (07-ANG-2001) Cell Biology, IACR-Long Ashton Research
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 DEFINITION desaturase (sld1 gene).
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 VERSION X87143.1 GI:1040728
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 SOURCE Helianthus annuus (common sunflower)
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
 Heliantheae; Helianthus.

REFERENCE
 1 Sperling, P., Schmidt, H. and Heinz, E.
 A cytochrome-b5-containing fusion protein similar to plant acyl
 lipid desaturases
 Eur. J. Biochem. 232 (3), 798-805 (1995)
 MEDLINE 56028121
 PUBMED 7588718

REFERENCE
 2 Sperling, P., Blume, A., Zahring, U. and Heinz, E.
 Further characterization of Delta(8)-sphingolipid desaturases from
 higher plants
 Biochem. Soc. Trans. 28 (6), 638-641 (2000)
 MEDLINE 21116801
 PUBMED 11171153

REFERENCE
 3 (bases 1 to 1591)
 Sperling, P.
 Direct Submission
 Submitted (10-MAY-1995) P. Sperling, Univ Hamburg, Inst. fuer
 Allgemeine Botanik, Ohnhorststr. 18, 22609 Hamburg, FRG
 Related sequences: AJ224160, AJ224161, AF133728.
 Location/Qualifiers

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 Matches 805; Conservative 0; Mismatches 552; Indels 3; Gaps 1;

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Search completed: December 31, 2003, 21:04:19
Job time : 3697.2 secs

XX MPI: 2000-412336/35.
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 XX
 PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries
 XX
 PS Claim 2; Page 39; 57pp; English.
 XX
 CC The present sequence is a cDNA encoding delta-6 fatty acid desaturase
 CC from clone pps-pk0011.ds; this isolated from Florida bluebush developing
 CC seed cDNA library, pps. The delta-6 desaturase enzyme catalyzes the
 CC formation of linoleic acid, a fatty acid that has a triple bond at the
 CC delta-6 carbon. The present sequence is useful for producing
 CC transgenic plants having altered levels of delta-6 desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is also useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 KM lipid metabolism; delta-6 desaturase; transgenic plant; ds.
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 OS Borage officinalis.
 XX
 FH Key Location/Qualifiers
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XX (RHON ) RHONE-POULENC AGROCHIMIE.
XX Beremand PD, Nunberg AN, Thomas TL;
XX MPI; 1998-583201/49.
XX P-PSDB; AAW67471.
XX
XX New sunflower albumin 5' regulatory region - useful for directing
XX altered lipid metabolism in plant seeds
XX
XX Example 2; Fig 1; 38pp; English.
XX
XX This sequence is the gene encoding the borage (Borago officinalis)
XX delta-6 desaturase enzyme. The lipid metabolism gene is an example
XX of a heterologous gene which can be expressed at high levels in a
XX seed-specific manner in transgenic plants, when placed under control
XX of the sunflower albumin gene 5' regulatory region (AAV34397).
XX
SQ Sequence 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 other;
Query Match 38.0%; Score 559.4; DB 19; Length 1684;
Best Local Similarity 62.8%; Pred. No. 3.2e-158;
Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;
QY 60 AAGAACCATTTTCCGACAGACCTTGCAGACATACAGCAACGAGATTATGATC 119
DB 58 AAGAAATACATTACCTCAGATGAACTCAAGAACGATTAACCCGAGATCTATGATC 117
QY 120 TCTATCAGGAAAGATTACGATATCTCAAGTGAATAAGAGCATCCGGTGTAG 179
DB 118 TCGATTCAAGGGAAGACCTATGATGTTGGATTGGTGAAGACATCCAGGTGACG 177
QY 180 CTCCTCATTTGATGTTTGGCGGCAAGATGTCATGATGCTTCAATTCATACCT 239
DB 178 TTTCCTTGAAAGCTGTGTGCTGCAAGATGATGATGATTTGATTCATCTCT 237
QY 240 GGCACCTGCTTGGCAATACCTTGACAGGCTTTTACTGGGATCACTTCAAGTTACT 299
DB 238 GGCCTACATGGAAGATCTTGATTAAGTTTTCACGCGGATATATCTTAAAGATTA 297
QY 300 GTCCTGAGATGCAAGGACTACAGAGGCTGCTGAGTTTCTAAGATGGGTTG 359
DB 298 GTTTCGAGGTTTCTAAAGTTATAGAGAGCTGTGTGAGTTTCTAAAGATGGGTTG 357
QY 360 TTCAAGACACAGGCAAGGAGTCTACTGCTCAATCTTTTCTGTCTGTGTGCT 419
DB 358 TATGACAAAAGAGTCATATTAATGTTTGAACCTTTGCTTATACAGATGCTTGTCT 417
QY 420 CTGAGTGTTCAGGTTTCTTCTACTGCAAGAGCACTGGGCTCATCTTGTGTTG 479
DB 418 ATGAGGTGTTATGGGTTTGTGTTGAGGGTGTGTTGTAATGTTTCTGAGTGT 477
QY 480 CTAATGGGTATGCTATGGCTCCAGAGTGTGGGTGGGGATATCTTGTCACTACAA 539
DB 478 TTGATGGGTTTCTTGTGATTCAGAGTGTGGATTTGACATGATGCTTATATAG 537
QY 540 GTTATGCTTAACCGTATGCTTAATGCTTTTCAATCACTTGCAGAAATGATGCT 599
DB 538 GTAGTGTGATTCAGAGGCTTAATAGTTTATGGGATTTTGTCTCAAAATGTCTTCA 597

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QY 600 GGTTTAAAGTTGACATGAGGAGTTGAGCAACCATACCATCACTTGCCTATATAC 659
DB 598 GGAATATAGTATGTTGGTGGAAATGAAACCTAATGACATCACTTGCCTATATAC 657
QY 660 GCCAATCTGATCTGATATTCAGACCTTCTATATTTGCCATATCCCAAAATTTTTC 719
DB 658 CTGAAATATGACCTGATTTACAAATATATACCATTTCTGTGTGTCTCAAGTTTTC 717
QY 720 AACTCCCTTACATCATCTATACAACTGCAAAATGACCTATGATCGGCTGCCGTTT 779
DB 718 GGTTCACCTCACCTTCATTTCTATGAGAAAGGTTGACTTTTATCAAGATTTC 777
QY 780 TTGTTAGCTTTCAGACATGACATTTTATCTGATGTTTAAAGGTTATGCTATCTT 839
DB 778 TTGTTAGTTATCAACATTTGACATTTTACCTTATATGTCGCTGCTGCTCATATAG 837
QY 840 TTTATTCCTCTTTTAAAGGTGTTTTCACAAACAAAGGATATACAAAGAAATCAG 899
DB 838 TATGTACATCTCTCATATGTTTGTGACCAAGAAAT--GTGTCTATGAGCTCAG 894
QY 900 GAAATTTAGGCTATGACGCTTTCTTGACTGTGATTTCTACTCTTCTTGCCTACCC 959
DB 895 GAACCTTGGGATGCTATGTTCTCGATTTGTAACCCGTTGCTTGTGTTGCTT 954
QY 960 AATGGCCGTAAGGCTATGATTTTCAAGTCTGTTTACAGTGGCGGTTCCAAACAT 1019
DB 955 AATGGGCTGTAAGGATTTATGTTTGTATGCAAGTTTATGATGCTGGAATGCAACA 1014
QY 1020 TGGCAGTTTCACTGATATCACTTCTTATGTTTACACTGTGTTTGGCTTACGCTAT 1079
DB 1015 GTTCAGTTCTCTTGAACACTTCTTCAAGTGTATGTTGAAAGCTTAAAGGAAAT 1074
QY 1080 GATTGTTTACACAGACAAAGGCAAGGCTCAACATPAACGCTTGTGTTGGGAT 1139
DB 1075 AATTGTTTGAAGAAACAAAGGATGGAACACTTGACATTTCTGTCTCTTGATGAT 1134
QY 1140 TGGTTTCAAGTGGCTGACCTTCAATGATGATGATGATGATGATGATGATGATG 1199
DB 1135 TGGTTTCAAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1194
QY 1200 TGGCATTTCAGGAAATCTCAACCATTTGTGAACAACTTGGCAGAGCATATTTGCC 1259
DB 1195 TGCACCTTGAAGAAATCTCGGCTTACGATGATGATGATGATGATGATGATGATG 1254
QY 1260 TATGAACTGCTTACATGATGAGGCAATTAATGATTAATCAACCTGCTGTG 1319
DB 1255 TACAATTTATGATCTTCTCCAAAGGCAATGAATGACACTGAGAACTTGAGAAACA 1314
QY 1320 GCTATGGAAGCTTAAGATGTTTACCAAGCAGTTCCTCCAGAAATGCTGGGAACATG 1379
DB 1315 GATTGCAAGCTTAAGGATTAATTAACCAAGCGCTCCGAAATTTGTGTAAGCTCTT 1374
QY 1380 AACACTTTCGGGTGAACCTTATTAACATCAAGTCTGCTTCCGTAAGGCTTCCAG 1439
DB 1375 CACACTCATGTTAAATTAATCCCTTATGATGATTAATTAATTAATTAATTAAT 1434
QY 1440 TCCCAATGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 1469
DB 1435 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1464

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RESULT 3
AAK24917
ID AAK24917 standard; cDNA; 1684 BP.
XX
XX AAK24917;
AC
XX 21-JUN-1999 (first entry)
DT
XX Borage delta-6 desaturase cDNA.
DE
XX Delta-6 desaturase; borage; oleosin; At521; promoter;
KW

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transgenic plant; seed; lipid; fatty acid; oilseed; vegetable oil;
 gamma-linolenic acid; octadecatrienoic acid; ds.
 Borage officinalis.
 Key Location/Qualifiers
 CDS 43..1389
 /*tag= a
 MO9845461-A1.
 15-OCT-1998.
 09-APR-1998; 98MO-US07179.
 09-APR-1997; 97US-0831575.
 (RHON) RHONE-POULENC AGROCHIMIE.
 L1 Z, Thomas TL;
 WPI; 1999-180333/15.
 P-PSDB; AAM98130.
 Nucleic acid containing oleosin 5'-regulatory region - useful for
 modulating fatty acid synthesis and lipid metabolism in plants,
 particularly to increase content of gamma-linolenic acid
 Example 2; Page 59-61; 101pp; English.
 The present sequence encodes borage delta-6 desaturase (see
 AAM98130), an enzyme that catalyses the conversion of linoleic acid
 to gamma-linolenic acid (GLA). Delta-6 desaturase cDNA was
 isolated from a borage membrane-bound polysomal cDNA library
 using a partial clone, obtained from an EST database search, as
 probe. The borage delta-6 desaturase nucleic acid can be
 operably linked to the seed-specific 5' regulatory region (see
 AX24916) of the Arabidopsis thaliana oleosin At521 gene in claimed
 expression cassettes of the invention. Transgenic plants, e.g.
 sunflower, soybean, maize, tobacco, cotton, peanut, oilseed
 rape or Arabidopsis are obtained that show increased levels of
 GLA or octadecatrienoic acid. The levels of desirable fatty
 acids in oilseed crops can be manipulated to provide seed
 oils of use in human health and industrial applications.
 Sequence 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 other;
 Query Match 38.0%; Score 559.4; DB 20; Length 1684;
 Best Local Similarity 62.8%; Pred. No. 3.2e-158;
 Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;

358 TATGACAAAAAGTCATATTATGTTGCACTTTGCTTTAAAGCAATGCTTTGCT 417
 QY CTGAGTTTAAAGGTTCTCTACTGCAAGAGACCGGAGCTGCTGCTGGTTG 479
 DB ATGAGTTTATGGGGTTTGTGTTGAGGGTTTGGTACATTTGTTTCTGGGCT 477
 QY CTAATGGGATATGCTATGCTCCAGAGTGTGGGGGAGATGTTCTTGCTACACAA 539
 DB TTGATGGGGTTTCTTTGGAATGAGATGGTTGGAATTGACATGCTGGGCAATTATG 537
 QY GTTATGCTTACCGTATGCTTAATGCTTTTCAATCATTCGAGAAATGATGCT 559
 DB GTAGTCTGATTCAGAGGCTTAATTAAGTTATGGTATTTTGTCTCAAAATGCTTCA 597
 QY GGTTAGTTGTCATGAGTGAAGTTGAGCCATTAACCCATCTTGCTGTAAATGAC 659
 DB GGATATGATTTGTTGGTGGAAATGAAACATTAATGACATACATGCTGTAATAGC 657
 QY GCCAATCTGATCTGATATTGACACCTTCTATTAATGCAATATCCCAAAATTTTTC 719
 DB CTGGAATATGACCTGATTTACATATATACCATTCCTGTTGTGTCTTCAAGTTTTC 717
 QY AACTCCCTTACATCATATATCAAACTGCAAAATGACCTATGATGCGCTGACGTT 779
 DB GTTCACTACACCTCTCATTTCTATGAAAAAGTTGACTTTGACTCTTTATCAAGATT 777
 QY TTGTTAGCTTACGACCTGACATTTTATCCGATGTTTAAAGCTTAAAGCTCTATCT 839
 DB TTGTATGATTAATCAATTTGACATTTGACATTTTACCTTATATGTTGCTCTTACGCT 837
 QY TTTATTCGTCTTTTAAAGTGTGTTTTCACACAAAGGATATACAGAAAGTTCAG 899
 DB TATGTAATCTCTCAATATGTTGTAACCAAGAAAT--GTGCTATGACGCTCAG 894
 QY GAAATTTAGGCTATGACAGCTTTCTGACTGTGATTTCTTACTCTTTCTGCGCTAC 959
 DB GAACCTTTGGAGGCTGATGTTCTGATTTGTTGCTGCTGCTTTCTTTCTTTGCT 954
 QY AATTGCGTGAAGGCTCATGATTTTCAAGTCTGTTTGAAGCTGCGGGTTCACAAAT 1019
 DB AATTGGGGTGAAGAAATTAATGTTTGAATGCAAGTTTATCACTGCTGGAATGACAA 1014
 QY TGGCAGTTTACGCTTGAATCATTTGCTTAAATGTTTACAGCTGTTTGGCTAAGCT 1079
 DB GTTCAATTTCTCTTGAACCACTTCTTCAAGTTTATGTTGGAAGCTTAAGGAAT 1074
 QY GATTGTTTACCGACAGACAAAGGCGCTCAACATTAACAGCTTGTGCTGTTGGAT 1139
 DB AATTGTTTGAAGAAACAAACGATGGGACATTTGATCTTGTCTCTGCTGATGAT 1134
 QY TGGTTTCATGAGGCTGACCTTCAATTTGAGCATCTGTTTCCAGAGATGCTAAG 1199
 DB TGGTTTCATGAGGCTGATTTCAATTTGAGCATCTGTTTCCAGAGATGCTAAG 1194
 QY TGGCATTTCAGAAATCTCACCATTTGTAACAACTTTGCGCAGAGATATTGTCTC 1259
 DB TGCACCTTAAGAAATCTGCGCTACGTGATGATTTGCAAGAAATATTGTCCT 1254
 QY TATGAACTGCTACATGTTGGAGGCGCAATTAATGATTAATCTCAACCTGCTGTG 1319
 DB TACAAATTAATGATCTTCTTCCAGGCGCAATTAATGATTAATCTCAACCTGCTGTG 1314
 QY GCTATGAAGCTAAGATGTTTCCAGGCGCAATTTCCAGAAACATGCTGGGAGGAAT 1379
 DB GCAATTCAGGCTAAGGATTAATCAAGGCGCTCCAGAAATTTGATGGAGGCTCT 1374
 QY AACATTTGCGGGAAGCTTATTAATCAAGTGTGCTTCCGCTAAAGGCTTCAG 1439
 DB CACATCTAGGTTTAAATTAATCACTTATGATTAATTAATTAATGATTAATGATCTCCTA 1434
 QY TCCCAATGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1469
 DB TGTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTT 1464

RESULT 4
AAT30395
ID AAT30395 standard; DNA; 1685 BP.
XX
AC AAT30395;
XX
DT 15-SEP-1996 (first entry)
XX
DE Borage delta-6-desaturase gene.
XX
KM Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;
KM polyunsaturated fatty acid; octadecatetrenoic acid;
KM chilling resistance; oilseed; ss; ds.
XX
OS Borage officinalis.
XX
FH Key Location/Qualifiers
FT CDS 44..1390
FT /tag= a
XX
PN WO9621022-A2.
XX
PD 11-JUL-1996.
XX
PF 28-DEC-1995; 95WO-1B01167.
XX
PR 30-DEC-1994; 94US-0366779.
XX
PA (RHON) RHONE POULENC AGROCHIMIE.
XX
PI Freyssiuet GL, Nuccio M, Nunberg AN, Reddy AS, Thomas TL;
XX
DR WPI; 1996-33397/33.
XX
DR P-PSDB; AAR98455.
XX
PT Transgenic plants comprising the borage delta-6-desaturase gene
PT show increased production of gamma linolenic acid and having
PT increased resistance to chilling
XX
PS Claim 2; Page 51-52; 75pp; English.
XX
CC A DNA clone (AAT30395) codes for borage delta-6-desaturase (AAR98455),
CC which catalyses the conversion of linoleic acid to gamma-linolenic
CC acid (GLA). It was isolated from a borage membrane-bound polysomal
CC library using probes based on abundantly expressed seed storage
CC protein cDNAs and with an isolated partial cDNA clone. The gene
CC can be incorporated into a vector, pref. incorporating a
CC tissue-specific promoter, for the expression of delta-6-desaturase
CC in transgenic plants, esp. sunflower, soybean, maize, tobacco,
CC peanut, carrot or oilseed rape, resulting in increased GLA prodn.
CC Alteration of plant lipids may also lead to improved chilling
CC resistance.
XX
SQ Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 other;

Query Match 38.0%; Score 559.4; DB 17; Length 1685;
Best Local Similarity 62.8%; Pred. No. 3.2e-158;
Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;

QY 60 AAGAAGCAATTTGCGAAGCAGACCTTGCAGAGCAATGAACACCGAGATTTATGATC 119
DB 59 AAGAATATCATTTACTCATGATGAATCAAGAACCAAGATTAACCCGAAATCTATGATC 118
QY 120 TCTATCAAGGAAAGATTACGATATCTCAAGTGAGCTAAAGAGCATCCGGTGGTAG 179
DB 119 TCGATTCAAGGGAAGACCTATGATTTTGGATTGGGTGAAGACCATCAGGTGGCAGC 178
QY 180 CTCCTATTTAAAGTTTGGCCGCAAGATGTCATGATGCGTTCAATTCCTTACCTCT 239
DB 179 TTTCCCTGAAGAGCTTGCTGGTCAAGAGTAACTGATGCAATTTGTTGCAATTCATCT 238

QY 240 GGCACCTGTCGCAATACCTTGACAGGTTCTTTACTGGGTACTAGCTTCAAGATTACTCT 299
DB 239 GCTCTACATGGAAGAACTTGATAGTTTTCACCTGGGTATTAATCTTAAAGATTACTCT 298
QY 300 GTCTCTGATGTCACAGGACTACAGAAAGCTCGTCTGAGTTTCTTAAGTGGTTTG 359
DB 299 GTTCTGAGGTTTCTTAAGATTAATAGGAAGCTGTGTTGAGTTTCTTAAGTGGTTTG 358
QY 360 TTCAAGACACAGGAAAGGGGTCTACGTCACATCTTTTCGTCTGTGTGTTGCT 419
DB 359 TATGACAAAAGGTCATATTAATGTTTGCACATTTGCTTTATAGCAATGCTGTTGCT 418
QY 420 CTGAGTGTTAAGGTTCTCTACTGCAAGACACCTGGCTCATCTTGTCTGCTGTTG 479
DB 419 ATGAGTGTTAAGGTTTGTGTTGAGGGTGTGTTGTAACATTTGTTTCTGGGTCT 478
QY 480 CTAATGGGTATGCTATGCTCCAGAGTGGTGGGTCAGATGATCTTGTCTACTACCA 539
DB 479 TTGATGGGGTTTCTTTGATTCAGAGTGGTGGATTTGACATGATGCTGGCATTAATG 538
QY 540 GTTATGCTTAACCGTAACCTTAATGCTCTTTTCAATCATTCGAGAAATGATGCT 599
DB 539 GTAGTGTGATTCAGAGCTTAATTAAGTTTATGGGTATTTTGTGCAAAATGCTTCA 598
QY 600 GGTGTAGTGTGATGCTGAGGTTGGAAGTTGACCATTAACCCATCACTTGGCTTAATAGC 659
DB 599 GGAATTAAGTATTTGTTGGTGGAAATGGAACCATTAATGACATCATATGCTGTAATAGC 658
QY 660 GCCAATCTGATCTGATATTCAGACCTTCTTAATGTCANATCCCAAAATTTTTC 719
DB 659 CTGAAATATGACCTGATTTACAAATATATACCATCTTGTGTGCTTCCAAAGTTTTC 718
QY 720 AACTCCCTTACATCTACTATACACACTGCAAAATGACCTATGATGCGGCTGCCAGTT 779
DB 719 GGTTCACCTCCTTCATTTCTATGAGAAAGTTTGTGACTTTTGTATCAAGATTC 778
QY 780 TTTGTACCTTTCAGACCTGACATTTTATCTGTCATGTTTAAAGGCTTATGCTTACT 839
DB 779 TTTGTAAGTTATCAATTTGACATTTTATACCTTATATGTCGTGCTAGGCTCAATAG 838
QY 840 TTTATCTGCTTTTAAAGGTGTTTTCACACAAAGGATATACAGAAAGTCAAG 899
DB 839 TATGTAACATCTCTCATATATGTTTGAACCAAGAAAT--GTGTCATGACACTCAG 895
QY 900 GAAATTTAGGCTATGACGCTTCTTGACTGTGATTTCTTACTCTTCTGCTCAACC 959
DB 896 GAACTCTTGGGATGCTGATGTTCTGCAATTTGGTACCCGTTGTTCTTGTGTTGCT 955
QY 960 AATTGGCCGAAAGGATGATGATTTCAAGTCGTCGTTTGAAGTGGCGGGTTCCAACT 1019
DB 956 AATTGGGGTGAAGAAATTAATGTTTATTTGCAAGTTTATGATCTGGAATGCAACAA 1015
QY 1020 TGGCAGTTTCAAGCTTGAATCACTTGTCTTATGTTTACACTGTGTTGCTAGCCGTA 1079
DB 1016 GTTCAGTTCTCTTGAACCACTTCTTCAAGTGTATTTGTTGAAGGCTTAAGGAAT 1075
QY 1080 GATTGCTTACACAGACAAAGGCAAGCTCAACATPAACGCTTCTGTTGGGTAT 1139
DB 1076 AATTGGTTGAGAAACAAAGGATGGGACACTTGCAATTTCTTGTCTTCTGATGAT 1135
QY 1140 TGGTTTCAAGGCTGCTGACCTTCAAGTTGATGATCTGATCTTCAAGAGTGGCTAAG 1199
DB 1136 TGGTTTCAAGGCTGCTGATTTCAAAATTTGACATCTTGTCTTCCAAAGTGGCTAAG 1195
QY 1200 TGGCATTTCAGAAATCTCAACCATTTGTGAACAACTTTGCGAGAGCATTAATTTGTC 1259
DB 1196 TGCACCTTGAAGAAATCTCGCCCTAGCGATTCGATTAATGCAAGAAACATPAATTTGCT 1255
QY 1260 TATGAACTGCTACATGTTGGAGGCAATTAATATGTAATCTCAACCTGTGCTGTG 1319
DB 1256 TACAATTAATGATCTTTCTTCCAAAGGCCAATGAATGAACACTGAGAACTTGGAAACA 1315
QY 1320 GCTATGAGAGTAAAGATGTTTACCAAGCAAGTTCACAAAGAACATGCTGGAACAATG 1379

Db 1316 GCATTGAGGCTGAGGATATACCAAGCCCTCCGAAAGATTGTATGGGAAGCTCTT 1375
 QY 1380 AACACTTGGGGGGAACCTATNAACATGAGTGTCTTCCCTAAAGCTTCAG 1439
 Db 1376 CACACTCATGTATTAATTACCTTGTGATGATTAATTAATGATTAATCTCTTA 1435
 QY 1440 TCCCAATGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1469
 Db 1436 TGTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1465

RESULT 5
 ABK49502
 ID ABK49502 standard; DNA: 1685 BP.
 XX
 AC ABK49502;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE DNA encoding Borago officinalis delta6-desaturase.
 XX
 KM delta6-desaturase; sunflower; soybean; maize; tobacco;
 KM peanut; carrot; oil seed rape; gamma linolenic acid; GLA;
 KM chilling tolerance; gene; ds; borago.
 XX
 OS Borago officinalis.
 XX
 FH Key Location/Qualifiers
 FT CDS 44..1390
 FT /tag= a
 FT /product= "delta6-desaturase"
 FT /transl_except= (pos:1151..1153, aa:Ser)
 XX
 PN US635861-B1.
 XX
 PD 12-MAR-2002.
 XX
 PF 19-SEP-1997; 97US-0934254.
 XX
 PR 13-OCT-1992; 92US-0959952.
 PR 10-OCT-1991; 91US-0774475.
 PR 08-JAN-1992; 92US-0817919.
 PR 14-SEP-1994; 94US-0307382.
 PR 28-JAN-1997; 97US-0789936.
 XX
 PA (RHON) RHONE-POULENC AGROCHIMIE.
 XX
 PI Thomas TL;
 XX
 DR WPI: 2002-380944/41.
 DR P-PSDB; AAU9830.
 XX
 PT Novel nucleic acid encoding evening primrose delta6-desaturase which
 PT converts linolenic acid to gamma linolenic acid useful for producing
 PT gamma linolenic acid in transgenic plant or bacteria -
 XX
 PS Example 9; Column 29-32; 53bp; English.
 XX
 CC The invention describes an isolated nucleic acid encoding an evening
 CC primrose Delta6-desaturase. The nucleic acid and a vector expressing the
 CC nucleic acid are useful for producing a plant such as sunflower, soybean,
 CC maize, tobacco, peanut, carrot or oil seed rape plant, with increased
 CC gamma linolenic acid (GLA) content, and also for inducing or increasing
 CC production of GLA in a bacteria or plant deficient, lacking in or
 CC producing low levels of GLA. The nucleic acid is also useful for inducing
 CC chilling tolerance in plants. This sequence encodes the borago delta6
 CC desaturase involved in the production of gamma linolenic acid.
 CC
 XX Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 other;
 SO

Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;
 QY 60 AAGAGACATTTGGAGAGACCTTGAACATTAAGAACAGAGATTAATGATC 119
 Db 59 AAGAAATACATTAACCTCAAGTGAATCAAGAACAGATTAACCGAGATCTATGATC 118
 QY 120 TCTATCAAGGAAAGATTACATATCTCAAGTGAATCAAGAGATCCCGGTGTGAG 179
 Db 119 TCGATTCAAGGAAAGATATGATGTTGGATGGGTGAAGAACATCAGGTGGAGC 178
 QY 180 CTCCCATTTGTAATTTTGGCGGCAAGATGTCATGAGCTTCAATGCTTCAATCCT 229
 Db 179 TTTCCCTTGAAGAGTCTTGTGTCAAGAGTAACTGATGATTTGTGATTCATTCCT 238
 QY 240 GGCACGTCTGGCAATACCTTGACAGTCTTACTGGGACTAGCTTCAAGATTTCTCT 239
 Db 239 GCTTCAATGAGAAATCTTGATTAATTTTCTAGGAGTATTAATCTTAAGATTAATCT 238
 QY 300 GTCTGAGATGTCAGAGCTCAAGAGCTGCTGAGTCTTCTAAGATGGGTTTG 359
 Db 299 GTTCTGAGGTTCTAAGATTAATAGAGCTTGTGTGAGTTTCTAAGATGGGTTTG 358
 QY 360 TTCAAGACACAGGCAAGGGGCTACTGCTCAATCTTTTGTGTGTGTGTGCT 419
 Db 359 TATGACAAAAAAGGTATATATGTTGCAACTTGTGCTTATAGCAATGCTGTGCT 418
 QY 420 CTGAGTGTAGGAGTCTCTCACTGACAGAGCACTGGGCTCATCTTGTCTGTGTTG 479
 Db 419 ATGAGTGTATAGGGGTTTGTGTGTGAGGGTGTGTGTGTGTGTGTGTGTGTGTGT 478
 QY 480 CTATAGGATATGCTATAGCTCCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 539
 Db 479 TTGATGGGTTCTTGTGATTAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 538
 QY 540 GTTATGCTTACCGCTAAGCTTAATGCTTTTCAATCATGTCAGAAATGATGCT 559
 Db 539 GTAGTCTGATTCAGAGCTTAATTAATGAGTATTTGTGTGTGTGTGTGTGTGTGT 558
 QY 600 GGTGTAGTGTGCAAGTGTGAAGTGAACATTAACCATCACTTGTGTGTGTGTGTGTGT 659
 Db 599 GGAATAGATATGTTGTGTGAATGAATGAACATTAAGCAATGCTGTGTGTGTGTGTGT 658
 QY 660 GCCAATGTGATCTGATATTAAGCACTTCTATTAATGCAATATCCCAAAATTTTTC 719
 Db 659 CTGATATGATGACCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 718
 QY 720 AACTCCCTTAATCATATATCAAACTGCAAAATGACCTATGATGCGGTGACGTT 779
 Db 719 GGTTCACATCACTCTCATTTCTATGAGAAAGGTGACCTTTATCAAGATTC 778
 QY 780 TTTGTAGCTTTCAGACCTGACATTTTATCTGCAATGTAAGGTTAGGCTTATCTT 839
 Db 779 TTTGTAATTAATCAATGACATTTTACCTTATATGTGTGTGTGTGTGTGTGTGTGT 838
 QY 840 TTTATCTCTCTTTTAAAGT 899
 Db 839 TATGTATCATCTCTATATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 895
 QY 900 GAAATTTAAGGCTTACAGCTTCTTGAATTTCTATCTCTTCTTCTGCTTACC 959
 Db 896 GAACTCTTGGAGTGTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 955
 QY 960 AATGCGCTGAAAGGTCATGATTTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1019
 Db 956 AATGCGGGAAGAAATTAATGTTTGTATGCAAGTTTATCAAGTGTGTGTGTGTGTGT 1015
 QY 1020 TGGCAGTGTAGCTTGAATCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1079
 Db 1016 GTTCACTTCTCTTGAACACATTTCTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1075
 QY 1080 GATGTGTTTACACAGCAAAAGGACGCTCAACATTAACAGCTTGTGTGTGTGTGTGT 1139
 Db 1076 AATGTGTTGAAGAAACAAAGGATGGACATTTGATGATTTCTTGTGTGTGTGTGTGTGT 1135

Query Match 38.0%; Score 559.4; DB 24; Length 1685;
 Best Local Similarity 62.8%; Pred. No. 3..2e-158;

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OY 1140 TGGTTTCAGTGGCCCTGACATTTGAGTGCATCTGTTCAGAGATGCTTAG 1199
DB 1136 TGGTTTCAGTGGCCCTGACATTTGAGTGCATCTGTTCAGAGATGCTTAG 1195
OY 1200 TGGCATTTCAGGAAATCTCACCATTGTGAACAACTTGCAGAGATATTTGCTC 1259
DB 1196 TGCACCTTCAGGAAATCTCACCATTGTGAACAACTTGCAGAGATATTTGCTC 1255
OY 1260 TATGAACCTGCTACCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1319
DB 1256 TACCAATTATGACATCTTCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1315
OY 1320 GGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1379
DB 1316 GCAATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1375
OY 1380 AACACTTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1439
DB 1376 CACACTCAGTGTAAATTAACCTTATGATGATATTAATTAATTAATTAATTAAT 1435
OY 1440 TCCCAATGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 1469
DB 1436 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1465

RESULT 6
ABX15366
ID ABX15366 standard; cDNA; 1685 BP.
AC ABX15366;
XX
XX 17-APR-2003 (first entry)
DE Borage delta-6-desaturase #1 cDNA.
XX
XX Delta-6-desaturase; gene: ss: delta-12-desaturase; sunflower; soybean;
KW maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
KW octadecatretenoic acid; alpha-linolenic acid; delta-15-desaturase;
XX borage.
XX Borage officinale.
XX
XX Key Location/Qualifiers
FH CDS 44..1390
FT /tag= a
FT /product= "Borage delta-6-desaturase #1"
FT /transl_except= (pos:1151..1153, aa:Ser)
XX
XX US2002108147-A1.
XX
XX 08-AUG-2002.
XX
XX 21-DEC-2001; 2001US-0029756.
XX
XX 13-OCT-1992; 92US-0959952.
XX 19-SEP-1997; 97US-0934254.
XX 10-OCT-1991; 91US-0774475.
XX 08-JAN-1992; 92US-0817919.
XX 14-SEP-1994; 94US-0307382.
XX 28-JAN-1997; 97US-0789936.
XX
XX (THOM/) THOMAS T L.
XX
XX Thomas TL;
XX
XX MPI; 2003-066659/06.
XX P-PSDB; ABG73095.
XX
XX Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
XX for producing plant with increased gamma linolenic acid content, and
XX for inducing octadecatretenoic acid production in plant -
XX

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PS Example 9; Fig 5A; 55pp; English.
XX
XX The invention relates to a nucleic acid encoding an evening primrose
CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
CC for producing a plant (such as sunflower, soybean, maize, tobacco,
CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
CC acid (GLA) content by transforming a plant cell with the nucleic acid or
CC vector and regenerating a plant with increased GLA content from the plant
CC cell, for inducing or increasing production of GLA in an organism lacking
CC in or producing low levels of GLA and for inducing production of
CC octadecatretenoic acid in at least one of a plant deficient or lacking
CC in or producing low levels of octadecatretenoic acid, a bacterium which
CC produces alpha-linolenic acid or a bacterium which exhibits a
CC delta-15-desaturase activity on a GLA substrate. This sequence represents
CC cDNA encoding a borage delta-6-desaturase polypeptide.
XX
XX Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 other;
SQ
Query Match 38.0%; Score 559.4; DB 25; Length 1685;
Best Local Similarity 62.8%; Pred. No. 3.2e-158;
Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;
OY 60 AAGAAGCAGATTTCCGACAGACCTTGCAGATTAAGCAACAGAGATTTATGATC 119
DB 59 AAGAATATCTTACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 118
OY 120 TCTATCAAGGAAAGTTTACGATATCTCCAGTGAAGTAAAGAGATCCCGTGTAG 179
DB 119 TCGATTCAGGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 178
OY 180 CTCCTATGTTATGTTTCCCGGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 239
DB 179 TTTCCCTGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 238
OY 240 GGCATGCTTGGCAATPACCTTGACAGGTTCTTACTGAGTATACGTTCAAGTATCTCT 299
DB 239 GCTCTACATGGAAGAACTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 298
OY 300 GTCTCTGAGATGTCAGAGACTACAGAGGCTGCTCTGAGATTTCTTAAAGTGGTTTG 359
DB 299 GTTCTGAGGTTCTTAAAGATTAAGAGAGCTGTTGATGATGATGATGATGATGATGATGATGAT 358
OY 360 TTCAAGACACAGGAGGAGGCTACGCTCAATCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 419
DB 359 TATGACAAAAGGCTATATATATATATATATATATATATATATATATATATATATATATATAT 418
OY 420 CTGAGTGTTCAGGTTCTCTACTGCAAGACCTGGCTCATCTTGTCTGTGTTG 479
DB 419 ATGAGTGTTCAGGTTCTCTACTGCAAGACCTGGCTCATCTTGTCTGTGTTG 478
OY 480 CTATGAGTATGCTATGCTCCAGAGTGGTGGTGGGAGATGATTTCTGATCAACAA 539
DB 479 TTGATGGGGTTCTTTGATTCAGAGTGGTGGTGGGAGATGATTTCTGATCAACAA 538
OY 540 GTTATGCTTACCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 599
DB 539 GTTATGCTTACCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 598
OY 600 GGTGTTAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 659
DB 599 GGTGTTAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 658
OY 660 GCCAATCTGATCTGATATTCAGACCTTCTATATATGCAATATCCCAAAATTTTTC 719
DB 659 CTTGAAATATGACCTGATATTCAGACCTTCTATATATGCAATATCCCAAAATTTTTC 718
OY 720 AACTCCCTTACATATATATATATATATATATATATATATATATATATATATATATATATAT 779
DB 719 GGTGTTAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 778
OY 780 TTTGTTAGCTTACAGACCTGATTTATCTGATGATGATGATGATGATGATGATGATGATGAT 839

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Db	779	TTGTAAATGATCAACATTGGACATTTTACCCTATTATGTGTGCTGATGGCTCAATATG	838
Qy	840	TTTATTTCTGCTTTTAAAGTGCTGTGTTTCCAAACAACAAGGATTAACAAGAAAGTCAAG	899
Db	839	TATGTACATCTCTCATATATATGTGTGACCAAGAAAT---GTGTCTATGAGCTCAG	895
Qy	900	GAATTTTAGGCTATGACGCTTTCCTTGAAGTTATCTCTACTCTCTCGCTACCC	959
Db	896	GAACTCTTGGGATGCTAGTGTGTTCGATTTGGTACCGGTTGCTTTTGTGTTTGCT	955
Qy	960	AATTGGCTGAAGGATCATGTATTTCAACGTCCTGTTTGAAGTCGCCGAGTTCCACAT	1019
Db	956	AATTGGGATGAAGAAATATGTTTGTATTGCCAAGTTATCAGTACATCGAATGCAACAA	1015
Qy	1020	TGGCAGTTGACGTTGATCACTCTGCTCTATGTTTACAGTCGGTTGCTAGGCGTAT	1079
Db	1016	GTTCAAGTTCTCTTGAACCACTTCTCTTCAAGTGTATTATGTTGAAGCCTTAAGGAAAT	1075
Qy	1080	GATTGGTTTCAACAGCAGACAAAGGACGCTCAACATACAGCTTCGTGTGTGGAT	1139
Db	1076	AATTGGTTTGAAGAAACAACGAGATGGACACTTGACATTTCTGTCTCTGTGATGGAT	1135
Qy	1140	TGGTTTCAATGATGCGCTGACCTTTCAGATGAGCATCATCTGTTCCAAAGATGCTTAAG	1199
Db	1136	TGATTTCATGATGGATTTGCAATTCGAATGACATCATGTTTCCAAAGATGCTTAAGA	1195
Qy	1200	TGCCATTTCAAGAAATCTCAACCCATTTGTGAACAACCTTGGCCAGAAACATATTTGTCC	1259
Db	1196	TGCAACCTTAGAAGAAATCTCGCGCCATGATGATGATGATGATGATGATGATGATGATG	1255
Qy	1260	TATGAACTGCTACCATGTGGAGGCGCAATTAATGATATCTCAACCTCGCTGCTGTG	1319
Db	1256	TACAAATTAATGATCTTTCTCCAAAGCCAAATGAAGACATCAGAACTATGAGAACACA	1315
Qy	1320	GCTATGGAAGCTAAGATGATTAACCAAGCCAGTCCCAAGAACATGATGATGATGATGATG	1379
Db	1316	GCATTGCAAGCTAAGGATATATACCAAGCCGCTCCGAGAAATTTGATATGGAAGCTCTT	1375
Qy	1380	AACATTTGGGATGAACCTTATTTAAACATCAAGTGTCTCTTCCCGTAAAGCTTCCAG	1439
Db	1376	CACACTCATGTTTAAATTAATTAACCTTAGTCAATGATATTAATTTGAGATTAATGATCTCTA	1435
Qy	1440	TCCCAATGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	1469
Db	1436	TGTTTGTCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT	1465
RESULT 7			
AAD01352			
ID AAD01352 standard; cDNA: 1934 BP.			
XX AAD01352;			
AC AAD01352;			
XX 12-OCT-2000 (first entry)			
XX 12-OCT-2000 (first entry)			
DE Soybean sphingolipid desaturase cDNA #2.			
XX Soybean, sphingolipid desaturase; membrane-bound desaturase;			
KM transgenic plant; fatty acid; ss.			
XX Glycine max.			
XX Glycine max.			
FH Key			
FT CDS			
FT location/Qualifiers			
FT 305..1657			
FT /*tag= a			
FT /product= "Sphingolipid desaturase"			
XX WO200032790-A2.			
XX 08-JUN-2000.			
XX 02-DEC-1999; 99WO-US28589.			

PR	03-DEC-1998;	98US-0110784.
XX		
PA	(DUPO) DU PONT DE NEMOURS & CO E. I.	
XX		
PI	Cahoon EB, Cahoon RE, Hiltz WD, Kinney AD;	
XX		
DR	WPI; 2000-412336/35.	
XX		
DR	P-P5DB; AAV71554.	
XX		
PT	Polynucleotide encoding delta-6 desaturase enzyme useful for producing	
XX		
PT	transgenic plants and for producing antibodies specific to which is	
XX		
PT	useful for screening cDNA expression libraries	
XX		
PS	Claim 2; Page 46; 57pp; English.	
XX		
CC	The present sequence is a cDNA encoding sphingolipid desaturase	
XX		
CC	from clone 861.pB0017.b4:fls isolated from soybean seedling cDNA	
XX		
CC	library, ssl. The present sequence is useful for producing	
XX		
CC	transgenic plants having altered levels of sphingolipid desaturase which	
XX		
CC	in turn would alter the fatty acid composition. The enzyme is useful	
XX		
CC	for producing polyclonal or monoclonal antibodies. The polynucleotide	
XX		
CC	is also useful as primer or probe for screening cDNA libraries to	
XX		
CC	isolate desired full-length cDNA clones.	
XX		
SQL	Sequence 1934 BP; 505 A; 367 C; 448 G; 614 T; 0 other:	
Query Match	35.8%; Score 526.4; DB 21; Length 1934;	
Best Local Similarity	61.3%; Pred. No. 3.3e-148;	
Matches	864; Conservative 0; Mismatches 542; Indels 3; Gaps 1.	
49	TGGAAGAGCCAAAGAGACATTTTCGACAGACGCTTGCAAGCATAGACACCGAG	108
DB	315 TTGAGAGAGAGAGAGATGACATTAACCTCAGAGAGCTTAAGGTCACACAGAGGAG	374
QY	109 ATTTATGATCTCTATCAAGGAGAAAGTTTACGATATCTCCAGTGAAGTAAAGACATC	168
DB	375 ATTTATGATCTCAATTCAGTAAAGGTGATCAATATGTCAGATTGGTCAAGAGACAC	434
QY	169 CCGGTGTGAGCTCCCATTTGTAAGTTTGGCCGACCAAGATGTCATGATGCTTATTG	228
DB	435 CTGGTGTGATGTTTCAATCTCAACCTTGGCTGGCCAGAGATGATCATTCATTACATG	494
QY	229 CTTCACATCCCTGGAGCTGCTTGGGAATACCTTGACAGGTTCTTTATCTGGGTAACGTTT	288
DB	495 CATCCATCCCTGGAGCAGACAGATGTCACCTTGAAAAATTTCTACCTGGCTACACCTCA	554
QY	289 AAGATTACTCTGTCTGAGATGTCACAGAGCTACAGAAAGCTGCTCTGAGTTTCTA	348
DB	555 GTGACTTCAGAGTCTCTGAGGTGTCCAAAGACTACAGAAAGCTTGCATCTAGTTCTCA	614
QY	349 AGATGGGTTTGTCAAGACACACAGGCAAAAGGGGTCTACTGCTCAATCTTTTTCGTCTG	408
DB	615 AATTGGGCTTTTGTGACACCAAAAGGGGACATGTCATTCAATGACACCTTGTCATCTGTTGCTG	674
QY	409 TGTGTTCCTGCTGAGTGTTTAAGGTGTTCTCTACTGCAAGACACCTGGGCTCATCTTT	468
DB	675 TTATGTTCTCATTTGTACTTATGATGTTTCTGAGGTGACATGATGTGTGGCTCATTTGG	734
QY	469 GCTCTGTTTGTCTATGGGATATGCTATGAGCTCCACAGAGTGTGGGTGGGATGATTTCTT	528
DB	735 GTTACAGGATGCTCTTGAAGGTGTGCTTTTGAAGCAAGTCTTATGTGGGCATATTTCTG	794
QY	529 GTCACTACCAAGTTATGCTTAAACCGTAAATCGCTTTTTCAAATCATTTGACGAA	588
DB	795 GCCACTATATGTGTTATGACCAACCAATGGTTTCAACAAGTTTGACACAGATCTCTCTGGGA	854
QY	589 ATGTGATTTGCTGTGTATAGTGTTCATGATGTGAAAGTTGACCATTAACCCATCACTTTG	648
DB	855 ACTGCTTGACCGGATTAAGCAATTCCTGTGTGGAAGTGAATCAACATATGCTCACACATTTG	914
QY	649 CCTGTAAATAGCGCAATCTGGATCTGTATATTCAGACACCTTCCTATATTCGCAATATCC	708
DB	915 GTGTCAACAGCTTGACCATATACCTTGATCTTGACGACATATCCGGTCTTTTGAGTTTGT	974

QY	709	CAAATTTTTCACATCCCTTACATCATATCATACCAACTGGAAATATGACTATGATGCG	768
Db	975	CGCGGCTTTCATATTCATTAACCTCTCATTTCTATGGAGGAAGTGGAGTTTGATTTTCA	1034
QY	769	CTGCGAGGTTTTTGTATGTAGCTTTGACGACTGGACATTTTATCTGCAATGTGTTAAAGCTT	828
Db	1035	TYGCTAGGTTCTTGATCTGCTACGACGACTTTTACTTTTACCCTGTAATGTGTGGCA	1094
QY	829	GGCTCTATCTTTTATTTCTGTCTTTTAAAGTGGGTTTTTCCACACAAAAGGTTATCA	888
Db	1095	GGGTCAACTGTGATCTGCAACAATTCGTATTTGTTTTCAGAGCGGAAAA--GTGCGAG	1151
QY	889	AGAGAGTCAGAAATTTTAAAGTCTATGACAGCTTCTTGACTTGGTATTTCTACCTCTT	948
Db	1152	ATGAGCCTTGAAACATTAATGGGGAATCTTGTGTTTTTGAACTTGGTCCCTCTTTAGTGT	1211
QY	949	CTGCGCTAACCAATTTGGCTGTAAAAGGTCATGTATTTTACGTCCTGTTTAAAGTCGCG	1008
Db	1212	CTTCTCGTCCCAATTTGGCTGTAGAGGGTTATGTTTGTCTTGCTAGCTTTGTGTGTTGT	1271
QY	1009	GGTTCCAACTATTGGCAGTTCAAGCTTGAATCACTTTGCTCTTAATGTTTACACTGTTTGC	1068
Db	1272	CCATTCAGACAACTTCAAGTCTGTTTGAATCACTTTGTCGCAAAATGTAATGTGCGGCGAC	1331
QY	1069	CTAGCGGTAAATGATTTGTTTCAACGACGACAAAGGCGACGCTCAACATTAACAGCTTCTG	1128
Db	1332	CGAGTGGGAATGACTGTTTAAAGACGACAAAGGTATCAATGATATCTCTGTGCTT	1391
QY	1129	CTTGTGGGATTTGTTTCTATGTTGCGCTGCACTTTCAATTTAGCATCATCTGTTTCCA	1188
Db	1392	CTTGATGATGATTTGTTTTCGTGGCTTGACAGTTTCACTTGAGCATCATTTGTTTCCA	1451
QY	1189	GGATGCGCTAATGTCATTTACGAAAAATCTACCATTTGTGAACAATTTTGGCAGAAC	1248
Db	1452	GGCTACCTCGGTGCCAATTTGGAAGATTTGCTTGTGTTAGTACCTTTTGCAGAAAGC	1511
QY	1249	ATAATTTGTCTATGAATACTGCTACATGTGGGAGGCCAATTAATGTTATCTCCACC	1308
Db	1512	ATAATTTGCCTTATAGAGCTGTGTCTATTTTGGAGGCGCAATCAAGTGACATTTAGAACCC	1571
QY	1309	TGCGTGCTGTGGCTATGGAAGCTTAAGATGTTAACCAAGCCAGTTTCCAAGAAATGTC	1368
Db	1572	TCAGAGACTGTGCGCTTACAACTAGGGACTTAAACAACCTGCGCCCTTAAGAAATTTGTTGT	1631
QY	1369	GGGAAGCAATGAACAATTCGGGTGAACTTATTAATAATCAAGTGTCTTTCCCTTA	1428
Db	1632	GGGAAGCTGTTAATTAACCATGCTGAGGCAATTTGGAGTTTAAAGTTTAAAGATTTTGTCTC	1691
QY	1429	AAAGCTTCCAGTCCCAATGTTTCTTTT	1457
Db	1692	AAAGTCTTTTTTTTTTGTCTCTTT	1720
RESULT 8			
AAZ44851			
ID	AAZ44851 standard; DNA; 1606 BP.		
AC	AAZ44851;		
XX			
XX	27-APR-2000 (first entry)		
DE	Spingolipid desaturase DNA.		
XX			
KM	Spingolipid desaturase; aldi; spingobase; ceramide; capnoid;		
KM	transgenic plant; crop plant; delta-8-unsaturated long-chain base;		
KM	tolerance; resistance; soil salinity; ion stress; toxicity; drought;		
KM	cold; frost; phytopathogenic microorganism; flowering time; cosmetic;		
KM	pharmaceutical; food; chemical raw material; de.		
XX			
OS	unidentified.		
XX			
TH	Key	Location/Qualifiers	

FT	CDS	88..1464	/*tag= a
FT		/product= "Sphingolipid desaturase"	
XX	DE19828850-A1.		
XX	30-DEC-1999.		
XX	27-JUN-1998;	98DE-1028850.	
XX	27-JUN-1998;	98DE-1028850.	
XX	(GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.		
XX	Heinz E, Zaehring U, Schmidt H, Sperling P;		
XX	WPI; 2000-127549/12.		
XX	P-PSDB; AAY51348.		
XX	New sphingolipid desaturase that selectively introduces double bond		
XX	into sphingolipids and capnoids -		
XX	Disclosure; Fig 15; 62pp; German.		
XX	This invention describes a novel sphingolipid desaturase that selectively		
XX	introduces a double bond into the sphingobase of the ceramide residue of		
XX	sphingolipide and capnoids. A DNA sequence encoding the sphingolipid		
XX	desaturase, or a vector containing the DNA sequence, can be used to		
XX	produce transgenic plants, especially crop plants, with an increased or		
XX	decreased delta-8-unsaturated long-chain base content or an altered		
XX	delta-8-unsaturated long-chain base cis/trans ratio, especially to		
XX	compensate for a delta-8-unsaturated long-chain base deficiency, to		
XX	exclude production of delta-8-unsaturated bases, to increase tolerance		
XX	or resistance to soil salinity, ion stress or toxicity, drought, wet		
XX	conditions, cold or frost and/or phytopathogenic microorganisms, or to		
XX	alter size growth and flowering time. Cells, transgenic organisms or		
XX	plants containing the DNA sequence can be used to produce sphingolipids		
XX	and capnoids with unsaturated sphingobases. The sphingolipids or capnoids		
XX	can be used in cosmetics, pharmaceuticals and foods and as chemical raw		
XX	materials. This sequence encodes a sphingolipid desaturase protein		
XX	described in the method of the invention.		
XX	Sequence 1606 BP; 412 A; 338 C; 370 G; 486 T; 0 other;		
XX	Query Match 31.3%; Score 460.8; DB 21; Length 1606;		
XX	Best Local Similarity 59.2%; Pred. No. 2e-128;		
XX	Matches 805; Conservative 0; Mismatches 552; Indels 3; Gaps 1		
QY	42 ACTCTAATGAGAGCCAAAGACACATTTCCGACAGACCTTGCAGACATAGCAA	101	
DB	115 AATTCATTTGCTGATGGAATAAATATACATACATCAAAAGATTAAAGACATTAAC	174	
QY	102 CCAGGAAATTTATGATCTCTATCAAGGAAATTTATCGATCTCCAGTGGACTAA	161	
DB	175 CTTATATACCTTTGATCTCAATTTTGGGCAAGTTTACACGTTACGAATGGCTTAA	234	
QY	162 GAGCATCCGGTGTGAGCTCCCATTTGTAAGTTTGGCCGCAAGATGTCATGATCG	221	
DB	235 GAGATCCGGGTGGCGATGCCCCGTTGATTAATCTCGCGGCGCAAGATGTAACGACGA	294	
QY	222 TTCAATGCTTACCATCTCGCATCTGTCGCAATCTTGACAGGTTCTTTACTGGGATC	281	
DB	295 TTTATCCATTTTCACTCCCGGATCTGCGTGAAGCATCTAGCAAACTATTAACCGGGTAT	354	
QY	282 TAGCTTCAAGATTACTGTCCTCGATATGCCAAGACTACAAAGGCTGCTCTGAG	341	
DB	355 CACTTAAAGATTACAGGTTTCTGACATTTCTAGAGACTACCGGAACTGGCTTCAGAG	414	
QY	342 TTTTCTAAGATGGGTTTGTTCAGACACACAGGCAAGGGGCTCTACTGCTCAATCTTTTC	401	
DB	415 TTTTGCAAAAGCGGTAATGTTTGAGAAAGAAAGTCAAGGTGAATTAATTACTACTTTGTTTC	474	
QY	402 GTGTCTGTGTGTTGCTCTGATGTTTACCGGTTTCTTACTGCAAGACGACTGGGCT	461	

Db	475	GTGTGCTACTGCTTCCGCTTGTGTGTATGCGCGTTATATATCCGGAAGCTTTCGAT	534
Qy	462	CATCTTTCCTCGTTTGTCTTAATGGGTAATGCTATGGCTTCAGAGTGTGGTGGCGAT	521
Db	535	CATATGCTTTCGGGGCCATATTTGGGAATTAGCATGGAATGCAAAATGCTATTTGGGTCAT	594
Qy	522	GATCTTTCCTACCTACCAAGTTATGCGCTAACCGCTAAGCTTAAATGCTTTTCAATTCAT	581
Db	595	GACCGGGGTCAATTACCAATATATGGCCAGCCCGGGGTGGMAACAATTTCCGGAAATTTT	654
Qy	582	CGAAGAAATGTGATTCGTGTGTATGTTGATGATGCTGAGTGGAGTTGACCAATTAACCAT	641
Db	655	ATCGGGAATTTGATTAACCGGAATAAGCATCGGCTGTGGAAATGAGACCATTAACCCAT	714
Qy	642	CACTTTGCCTGTAAATAGGCCCAATGTGATCCTGATTCCTAGACCTTCCTAATATGCC	701
Db	715	CACATCGCTTGTAAACAGTCTGATTAATATCTGATCTTCAGCATTTAACCGATTTGTAGCC	774
Qy	702	ATATTCGCCAAATTTTTCACCTCCCTTATCATCATATCATATCAACATGCAAAATGACAT	761
Db	775	GTTTCTTTCAGACTTTTAACTCAATTAATCTGTCTTTCTAATGGAGACAGTGTACCTTT	834
Qy	762	GATGCGCTGCCAGGTTTTTTTGTATAGCTTTACAGACTGAGCAATTTATATCTGACTTTGA	821
Db	835	GACCCGTAGCCCGGCTTCTGTGTAGCTACAGCAATTCATTAATATCCGATCATGTGT	894
Qy	822	AGCGTTAGGCTCTATCTTTTATTTATGTCTTTTAAGTGTGTGTTTCCAAACAACAAAG	881
Db	895	GTGGCCGGGTCAACCTCTATTTACAAACATCTGTGTGTATTTCAAAACAGAAAG--	952
Qy	882	GTATTAACAAGAGTCAAGAAATTTTAGGCTATGCAAGCTTTCTTGACTTGTATTTCTTA	941
Db	953	-TTCCGACAGAGGTTTAAACATATCTCGAACCCTTAATCTCTGAGCGGTTCCTGTA	1011
Qy	942	CTCCTTTCGCGCTAACCAATTTGGCGCTGAAGGGCTAGTATTTCAACGCTCGTTTAGA	1004
Db	1012	CTTGTCTTCGCTTACCGAATCTGCGCCGAACCGCGGCTTTGTGTGTATGCTTCGT	1071
Qy	1002	GTGCGCGGGTTCCAACATTTGGCAGTTTCAGCTTGAATCACTTGTCTTAATGTTTAACT	1061
Db	1072	GTAAACGGGTATATAACAATATTACAGTTTACATGAAACATTTTTCGGGGATGTTAACGG	1133
Qy	1062	GCTTTCCTACCGGTAATGATTTGCTTTACACAGCAGACAAAGGCAACGCTCAACATTAAC	1122
Db	1132	GGCCCGCCAAAGAGACAAATTTGTTGAGAAACAAACGCGTGGACCAATGATATCGG	1191
Qy	1122	GCTTCGCTTGGTGATTTGTTTCATGAGTGCGCTGCACTTTCATTTAGCATATCTG	1181
Db	1192	TGTTCTTCTTGGATGGAATTTGTTTTTGGGAGGTTTACAGTTTCAACTTGAAGCACATTTG	1251
Qy	1182	TTTTCAGAGATGCTTAAGTGCATTTACAGAAATCTCAACCATTTGTGAACAACCTTTCG	1244
Db	1252	TTTCTTAGGTTCCACCGGTGTCACTGTAGTGATTTCTCTATATGTAGAAACCTTCG	1311
Qy	1242	CAGAAGCAATATTTGCTCATGAACCTGTACCATGTGGAGGCAATTAATGTTATAC	1304
Db	1312	AAGAAATATTAATTAATCTTAATGTAGTTTGTGTCTTTATGATGCAATGTAAACACTTG	1371
Qy	1302	TCCACCTGTGCTGTGGCTATGGAAGCTAAGATGTATTAACCAAGCAATTTCCAAAGAC	1361
Db	1372	AAGACGCTTAAGACAGCGGCTTCAAGGCAAGTACCTTAAGAACCCCGGCCACAGAAAT	1431
Qy	1362	ATGATCTGGGAAGCAATGAACATTTCCGGTGAACCTTAT	1401
Db	1432	TTAGCTTGGGAAGCTTTCAACCAACCATGATGTTGAACCTTCT	1471

[illegible]

QY 240 GGCACTGCTGGCAATACCTTGACAGGTTCTTACTGGGACTACGTTCAAGATTACTCT 299
DB 249 GGAACCGCATGSGCCCACTCGAAACCTTCAACAGGCTACACGTTGAAAGACCCAC 308
QY 300 GTCTCTGAGATGTCACAGACTACAGAAAGGCTGCTCTGAGTTTCTTAAAGATGGGTTTG 359
DB 309 GTGTCCGACGTGTGGGTGACTACCGTTCGTTAGCCGCGGAGTTTCCAAAGCGGACTC 368
QY 360 TTCAAGACACAGGCAAGGGGCTCTACTGCTCAATCTTTTGGTGTCTGTGTTGGCT 419
DB 369 TTGGAATAAAAGAGTCAAGTCTTTTACACCTCAACGCTCCCTGCAATGCTCGCG 428
QY 420 CTGAGTTTACAGGTTCTCTACTGCAAGACACCGGCTCATCTTTGCTGTGTTG 479
DB 429 GCGGTTGATACGGTGTGTTGATGACAGCAATAGGCGCACTTAATATCCCGCTC 488
QY 480 CTAAATGGATATGCTATGCTCCAGAGTGTGGGTGGGCGCATTTCTGTCACTACCA 539
DB 489 TTGCTGGGCTTCTCTGATACAGAGGCTTACGTGGACATAGACTGTGCTATTACAC 548
QY 540 GTTATGCTTACCGTAACTTAATCGTCTTTTCAATCATTCGAGAGAAATGATGCT 599
DB 549 GTGACGTCAACGAGCGGTGTAATACTGTCAGCTTCTGTGTGTAATCTCATACC 608
QY 600 GGTGTAGATGTCATGCTGAGTGGAGTGGACATTAACCCATCTTGTCTGTAATAGC 659
DB 609 GGGATATCGATCGGTGTGGAAATGAGCGCATTAACGCTACCATATCTTGTTAATAGT 668
QY 660 GCCAATCTGATCTGATATATTCAGCACTTCTATATATGCAATCCCAAAATTTTC 719
DB 669 CTGACACAGATCTCTATCTCCAGCAATCCCTGTCTAGCGGCTTCCAAAGTTCTTT 728
QY 720 AACTCCCTTACATCACTACTACCAACTGCAAAATGACTATGATGCGCTGCCAGTTT 779
DB 729 AAGTCATGACGTCTCAGCTTCTATGAGGAGAAAGTTGACGTTCACTCACTGATTC 788
QY 780 TTGTGATGCTTACAGCTGAGATTTATCCGCAATGTTAGCCGTAGGCTCTATCTT 839
DB 789 TTGATGAGCTACCAACACTGTGTGTTTATCCATCATGTGTGGGAAATCAATCTC 848
QY 840 TTATATCTGCTTTTAAAGTGTGTTTCCAAACAAAGGATATCAAGAGAGTCAAG 899
DB 849 TTATATCCAAAGCTTACTTTTGTATTTCTGAGACGTTAC---GTTCTGATCGAGCTTG 905
QY 900 GAAATTTAGGCTATGCACTTTCTGACTTGTGATTTCTTACTCTTTCTGCTTACC 959
DB 906 AACATAGCTGGGATTTCTGTTTCTGGAAGTGTGTTCTCTTTAGATCTCTTACCA 965
QY 960 AATTGGCCGAAAGGCTATGATTTTCACTCTGTTTACAGTCCGCGGTTCCAACT 1019
DB 966 AACTGGCAAGAGGATCATCTTGTCTTTTAAAGCATGGCCGTCAACGGGATTCAGCA 1025
QY 1020 TGCACTTACGTTGATCACTTGTCTTAAATGTTTAACTGCTTACGCGGTAAAT 1079
DB 1026 GTTCAAGTTCTGTTTAAACATTTTGGCGGAGATGTTTACCGGCTTAATGGGAC 1085
QY 1086 GATTGGTTTACAGCAAGAAACAGCTGGTAGCTGATATCGTGTAGGTGTATATGAT 1145
DB 1140 TGCTTTCATGCTGCTGCTGCTGCTTTCAGATTTGATGATATCTGTTTCCAGAGAT 1199
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QY 1206 TGCACTTACGAGGAGTGTGCTGCTGCTGCTTTCAGAGATTTGTAAGAGCATTAATCT 1265
QY 1260 TATGAACTGCTTACATGCTGAGAGGCAATAAATGATATCTTCAACCTGCTGCTGTG 1319
DB 1266 TATAGAGTCTTTCGTGTGTGGAGGCTAATGTGTGAGCGCTCAGAGACTTGAAGAAAGCG 1325

QY 1320 GCTATGAGACTAAGATGTTTACCAAGCCAGTTCCCAAGACATGCTTGGAGCAATG 1379
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AC AAC42244;
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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 34823.
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KW Hybridization assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
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PF 25-FEB-2000; 2000EP-0301439.
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Query Match

Best Local Similarity 30.5%; Score 448.6; DB 21; Length 1465;
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DB 134 AAGAGATACCTTACAGCAGCAGATTGAAAAAACACACAAACCTCGAGATTATGATC 193

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 DB 254 GCAGCATCTCAATCTCGCGGCGCAAGATGTCACGACGCGCTTCAATCTCCATCC 313
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 QY 300 GTCTCTGAGATGTCAGAGACTACAGAAAGCTGCTCTGAGTTTCTAAGATGAGTTG 359
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 DT 17-OCT-2000 (first entry)
 XX
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 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.
 OS Arabidopsis thaliana.
 XX
 EN EP1033405-A2.
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 PF 25-FEB-2000; 2000BP-0301439.
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DB 283 GCGATTCAAGGCAAGGCTTACAAAGCTCCGATTGATTAATACTATCCGAGCGAG 342
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DB 343 ACGGTATCTCAATCTCGTGGTCAAGAGCTCAAGATGCTTCAATGCTTCAATCTCC 402
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DB 403 GGAACCGTTGGCACCATCTCGACCATCTTTCACCGGTTACCATCAAGATTTCCAA 462
QY 300 GTCTCTGAGATGTCAGAGACTTCAGAGGCTGCTCTGAGTTTCTTAAGATGGGTTG 359
DB 463 GTCTCGAAGCTCAAGCATTAACGCTGATGCTGCGAGTTTGTAAATCGGCTTC 522
QY 360 TTCAAGACACAGGCAAGGGGCTCTAGTCAATCTTTTGGTGTGTTGGCT 419
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QY 540 GTTATGCTTACCGTAAAGCTTATGCTTTTCAATATGACAGAAATGATGCT 599
DB 703 ATCATCTCAACAAATCTTATTAACAATTCGCTACCTTCTCTCGGTAATCTCTCAC 762
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DB 1003 TTCAATCAACAGTTTCTTGTCTTCTCCAAACGTGA---GTACCAATGCTGCTTA 1059
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DB 1060 AACTTTCGCGGAATCTTATGCTTCTGAGCTTCCACTCTTATCTCATGCTTACCA 1119
QY 960 AATTGCTGAAAGGCTCATGTTTCAAGTCTGTTTGAAGTCCGCGGTTCAACAT 1019
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RESULT 12
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DT 18-OCT-2000 (first entry)
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KM Hybridization assay; genetic mapping; gene expression control;
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KW metabolic pathway; promoter; termination sequence; ss.
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OS Arabidopsis thaliana.
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PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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XX Claim 11, Fig 3; 62p; German.

CC This invention describes a novel sphingolipid desaturase that selectively
 CC introduces a double bond into the sphingosine of the ceramide residue of
 CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to
 CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered
 CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
 CC compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingosines. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 CC materials. This sequence encodes the Arabidopsis thaliana sphingolipid
 CC desaturase sldi protein described in the method of the invention.

CC Sequence 1678 BP; 416 A; 408 C; 339 G; 515 T; 0 other;

Query Match 29.5%; Score 433.4; DB 21; Length 1678;
 Best Local Similarity 58.1%; Pred. No. 4e-120;
 Matches 783; Conservative 0; Mismatches 562; Indels 3; Gaps 1;

QY 60 AAGAGACATTTGCGAAGAGAGCTTGAAGATGAGACAGGAGATTATGATC 119
 DB 190 AAAAGATCTTTCGAGAGAGATCTTAAAGACAGAGATCTATGATC 249
 QY 120 TCTATCAGGAGAAAGTTTACATCTCCAGTGAAGAGATCCCGTGTGAG 179
 DB 250 GCGATTCAGGAGAGGCTTCAAGCTCCGATTTGATTAATCTCCGAGGAGAC 309
 QY 180 CTCCTATGTTAGTTTGGCGGCAAGATGCTGATGCTTATGCTTACCTCT 239
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 QY 240 GGCATGCTTGGCAATCTTGAAGGCTTCTTACTGAGTCAAGTCAAGTCTCT 299
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 DB 490 TTGAGAAACAGAGATGCTTCTGCTCAATCTTCTGCTGCTGCTGCTGCT 549
 QY 420 CTGAGGTTTGAAGGCTTCTGCTCAATCTTCTGCTGCTGCTGCTGCTGCT 479
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 QY 480 CTGATGAGTATGCTGCTGCTCAAGATGCTGCTGCTGCTGCTGCTGCTGCT 539
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 DB 730 GGAATCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 709
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RESULT 14
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 DT 21-JAN-2003 (first entry)
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 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 558.
 XX
 KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 PN W020021655-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 24-AUG-2001; 2001WO-US26685.
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 PR 24-AUG-2000; 2000US-227866P.
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 PR 26-JAN-2001; 2001US-264647P.
 XX
 PR 22-JUN-2001; 2001US-300111P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Harper JF, Kreps J, Wang X, Zhu T;
PI
XX WPI, 2002-304127/34.

XX Identifying a stress condition to which a plant cell has been exposed
XX and producing plants with increased tolerance to these abiotic stresses
PT
XX

PS Claim 6; SEQ ID NO 558; 577bp + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant
XX cell has been exposed, comprising:
CC (a) contacting nucleic acid representative of expressed polynucleotides
CC in the plant cell with an array or probes representative of the plant
CC cell genome; and
CC (b) detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stresses. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
CC in methods of the invention.
CC Note: The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied to Derwent by
CC the European Patent Office.

XX Sequence 1350 BP; 325 A; 359 C; 274 G; 392 T; 0 other;

Query Match 29.2%; Score 429.4; DB 24; Length 1350;
Best Local Similarity 58.1%; Pred. No. 5.8e-119;
Matches 776; Conservative 0; Mismatches 556; Indels 3; Gaps 1;

QY 60 AAGAACCAATTTCCGACAGACCTTGCAAAAGCATACCAACAGAGATTTATGATC 119
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DB 79 GGGATTCAAGGAGGATCTACACGCTCGATGATTAATACTATCCGAGGCGAC 138
QY 180 CTCACATGTTAAGTTTCCGCGCAAGATGTCATGATGCGTTCAATTCATACCT 239
DB 139 ACGGATATCTCAATCTCGTTGGTCAAGAGTCACGATGCTTTATGCAATTTATCC 198
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DB 259 GTCTCGAAGTCTACAGCGATTAACGTCGATGCGCGAGTTGTAACCTCGGCTC 318
QY 360 TTCAAGACACAGGCAAGGAGGCTACTGCTCAATCTTTTGGTGTGTTGCT 419
DB 319 TTGCAAAACAAAGATGACGTTACTCTTACATCTGACCTTGCTGCGCCATGTTCTC 378
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XX Wheat; sphingolipid desaturase; membrane-bound desaturase;
KW transgenic plant; fatty acid; ss.
XX
XX Triticum aestivum.
OS
XX
XX
FH Key Location/Qualifiers
FT CDS 124..153
FT /tag= a
FT /product= "sphingolipid desaturase"
XX
XX PN MO20032790-A2.

XX 08-JUN-2000.
 PD 02-DEC-1999; 99MO-US28589.
 XX 03-DEC-1998; 98US-0110784.
 XX (DUPO) DU PONT DE NEMOURS & CO E.I.
 PI Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;
 DR WPI, 2000-412336/35.
 XX P-PSDB; AAY71555.
 PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries.
 PS Disclosure; Page 48-49; 57pp; English.
 XX The present sequence is a cDNA encoding sphingolipid desaturase
 CC from clone wrel.ph0004.c7.f15 isolated from wheat etiolated
 CC seedling root cDNA library, wrel.
 CC The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is also useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
 XX
 SQ Sequence 1972 BP; 382 A; 616 C; 490 G; 484 T; 0 other;
 Query Match 27.2%; Score 399.4; DB 21; Length 1972;
 Best Local Similarity 58.1%; Pred. No. 8.4e-110;
 Matches 763; Conservative 0; Mismatches 542; Indels 9; Gaps 3;

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 DB 245 CGAGCGACCTCTGATCTCATCTCGGGGACGTCTAGAGTACGACGCGTGGCC 304
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 DB 305 ACCACCGGCGGAGAGTCCCGCTCATCACCCCTGCGCGGACGAGACGACGACCCCT 364
 QY 223 TCATTGCTTACATCTCCGAGCTGTTGGAATCACTTGAAGGTTCTTAACTGGTACT 282
 DB 365 TCATTGCTTACATCTCCGAGCTGTTGGAATCACTTGAAGGTTCTTAACTGGTACT 282
 QY 283 AGCTTCAAGATTAATCTCTGAGTGTCAAGAGTCAAGAGGCTGCTGAGT 342
 DB 422 GCCTCTCGAATACAGCTCCCGCCGCTCCGCGCATTCGCGCGCTCTCGCGGAGC 481
 QY 343 TTTCTAAGATGGTTTGTAAAGACACGACGCAAGGAGGCTTACTGCTCAATCTTTTTCG 402
 DB 482 TCTCTCCGCGGCTCTTGAAGCGCTCGGACACACCCCAAGTTCTCTGCTGCAAA 541
 QY 403 TGTCTGCTGCTGCTCTGAGTGTAAAGTGTCTTCTTCTTCAAGAGACCTGGGCTC 462
 DB 542 TGTCTGCTGCTGCTCTGAGTGTAAAGTGTCTTCTTCTTCAAGAGACCTGGGCTC 462
 QY 463 ATCTTGTCTGCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 522
 DB 602 ACATGTTCTGCGGGGCTCATTTGCTTCACTGATGATGATGATGATGATGATGATGATG 661
 QY 523 ATTCTTGTCTGCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 582
 DB 662 ACTCCGCGCACCAATATCAACGAGACCCCGGCTCAACCGGCTCTGCAAGTGTCT 721
 QY 583 CAGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 642
 DB 722 CCGGAACTGCTCAACGCGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 781
 QY 643 ACTTTCCTGTAATAGCGCAATCTGATCTGATATTCAGACCTTCTATATTCGA 702

DB 782 ACATCTCTGCAACAGCTCTGACATGATGACCGGACCTCCAGCACTTGCGCTTGGCGG 841
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 QY 823 GCGTTAGGCTTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 882
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 QY 1003 TCGCCGGGTTCCAACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1062
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Search completed: December 31, 2003, 16:16:32
 Job time: 284.13 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:48:07 ; Search time 2241.82 Seconds
(without alignments)
15947.709 Million cell updates/sec

Title: US-09-857-524B-1
Perfect score: 1471
Sequence: 1 cttccctgtctctggaattt.....ttttttttttttttttttttt 1471

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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2: em_esthum:*
3: em_estin:*
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27: em_gse_vrl:*
28: gb_gse1:*
29: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	352	23.9	1764	11	AY103762 Zea mays
2	326.4	22.2	721	11	CB972537 CAB30001
3	299.8	20.4	651	13	BQ409001 GA_Ed001
4	295.6	20.1	721	13	BQ64828 BQ64828 QGC27M12.

RESULT 1	LOCUS	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	
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2	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
3	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
4	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
5	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
6	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
7	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
8	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
9	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
10	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
11	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
12	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
13	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
14	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
15	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
16	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
17	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
18	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
19	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
20	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
21	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
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23	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
24	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
25	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
26	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
27	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
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29	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
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33	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
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37	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
38	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
39	AY103762	AY103762	AY103762.1	GI:21206840	HTC.	Zea mays	1764 bp	mRNA	linear	HTC 16-OCT-2002	BO861565	QGC18P18.	BO861565	QGC18P18.	BO861565	QGC18P18.
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ALIGNMENTS

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ACCESSION AY103762
VERSION AY103762.1 GI:21206840
KEYWORDS
SOURCE HTC.
ORGANISM Zea mays
REFERENCE
AUTHORS Hayney, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
1 (bases 1 to 1764)
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of
JOURNAL Overgo Probes
REFERENCE Unpublished (2002)
AUTHORS Coe, E.H.
TITLE Direct Substitution
JOURNAL Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the

maize cDNA sequences is either Virginia Malbot, Stanford or Pat Schabale, Iowa State, then clones may be requested from ZMBB: www.zmbb.iastate.edu.

FEATURES

Source

Location/Qualifiers

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/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

BASE COUNT 310 a 602 c 456 g 396 t

ORIGIN

Query Match 23.9%; Score 352; DB 11; Length 1764;

Best Local Similarity 55.9%; Pred. No. 6.8e-52; Matches 730; Conservative 0; Mismatches 566; Indels 9; Gaps 3;

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189 CCGACGACCTCTGGATCTCATCTCGGCGACGTAAGATGACGCCCTGCCCC 248
163 AGCATCCGGTGTAGCTCCCATTTTAAAGTTTGCAGGCAAGATGATGATCGT 222
249 ACCACCCGGGCGGACCTCCGCTTCTACCCCTGCGGGGAGAGCGCACGACCT 308
223 TCAATGCTTACCATCTCGGACCTTGGCAATACCTGACGTTCTTACTGGGACT 282
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1203 GCTCTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1262
1183 TTTCAAGATGCTTAAAGTGCATTTGAGAAATCTCACCATTGTGAACAACTTTGCC 1242
1263 TTTCCCGCTTACTCGCTGCTGACCTTGCACAGGTTGACACGCGCGCTCCGACCTTTGCA 1322
1243 AGAAGATATTTTGTCTTATGAAATGCTTACCAATGTTGGAAGGCAATTAATGATTAAT 1302
1323 AGAAGATAGGCTTCACTTATTTCTGACGACCAATTTCTGGGATGCAAAATGTCTTACATGA 1382
1303 CCACCTGCGGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1359
1383 AGACACTCAGGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1442
1360 ACATGCTTGTGGAAGCAATGAACACTTTCGGGTGAACCTTATTA 1404
1443 ATTGTATGAGGAGGCTGTGAACACCATGATTAATGATGATGA 1487

RESULT 2

CB972537

LOCUS

CB972537 721 bp mRNA linear EST 01-MAY-2003
CAB30001.1a Pa_D04 Cabernet Sauvignon Berry Stage I - CAB3 Vitis

winifera_cDNA clone CAB30001.1a_Pa_D04 5', mRNA sequence.

CB972537 GI:30295743

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Expressed sequence tags from Vitis vinifera 'Cabernet Sauvignon' berries at various developmental stages
Unpublished
Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
Seq primer: ACGTACCGACATATAGCC.
Location/Qualifiers
1. 721
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"

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/cxone="CAB30001.1Ita_Fa_D04"
/sex="Hermaphrodite"
/dev_stage="Berry stage 1"
/lab_host="DH5alpha"
/clone_1ib="Cabernet Sauvignon Berry Stage 1 - CAB3"
/ncote="Organs: Berry; Vector: pDNR; Site 1: Sfil; Site 2:
Sfil; CAB3 is a cDNA library of Vitis vinifera 'Cabernet
Sauvignon' Clone 8 berries. Samples were collected after
berry set from field-grown vines during stage 1 of berry
growth, 17 days after full bloom. The average berry size
was 6 millimeters. Sampled vines were located at the
University of California, Davis, Experimental Vineyard.
cDNAs were made by oligo-dT priming and directionally
cloned. 5' and 3' adaptors were used in cloning as follows
5'-AAGCAGGTGTATCAACGACGAGGTGGCATTTACGGCGGG-3' and
5'-ATTCTAGAGCGCCGAGCGCGGCGCATGTG-dT(30)NN-3'. Library was
constructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."

```

	Query Match	22.2%	Score 326.4	DB 14	Length 721	
	Best Local Similarity	65.8%	Pred. No. 2.8e-47			
	Matches	474	Conservative	0	Mismatches	246
					Indels	0
					Gaps	0
QY	91	AGCATTAAGCAAC	CAGAGATTATATGATCTCTATCAAGGAAAGATTACGATATCTCCA	150		
DB	2	AGCATTAAGCAAC	CCAGGGGATCTGTGATATCTCTATCAAGGTAAGGTTTACATGTCACGG	61		
QY	151	AGTGGACTTAAGAG	AGATCTCCGGTGTGAGCTCCCATTTGTAAAGTTTTCGCGCCAAAGT	210		
DB	62	ATTGGTCTAAGAG	TTTCATCCGGGTGGGACATCCCTCTCTGAATTTGGCTGGCCAAAGT	121		
QY	211	TCACGTAGCGCTTCA	TGCTTACCATCTCGGACATGCTTGGCAATACCTTGACAGGTTCT	270		
DB	122	TTACAGACGCTTCA	TGCTTACCATCTCGGACATGCTTGGCAATACCTTGACAGGTTCT	181		
QY	271	TTACTGGGTACTAG	CGTTCAAGATTACTGTCTCTGAGATGTCCAAGACTACAGAAAGC	330		
DB	182	TTACTGGGTATTA	TCTCAAGACCTTCAAAAGTCTGGAGGTGTCCAAAGACTTCAGAAAC	241		
QY	331	TCGTCTCGAAGTTT	CTAAGATGGGTTTGTTCAGACACAGGCAAGGGGCTTACTGCT	390		
DB	242	TCGCTAATGAATTT	CAAAACCTTGGGTTGTGTAACAAAGGCCATGAAATCTGTACA	301		
QY	391	CAATCTTTTGGTGT	CTGTGGTCTCGAGAGTTTGAAGGATGTCATCTACTGCAAGA	450		
DB	302	CTGTGTCATATGA	ATTCCTTTGTCATGAGTGTGATTAAGGATTTTGTGTGTGATA	361		
QY	451	GCACCTGGGCTCAT	CTTGTGCTCTGGTTGTCTAATGGGATGCTAATGAGCTCAGAGTGGT	510		
DB	362	GTTTCTGGGTTCA	TCTGGGTGTGTGTCATTACTGGGGTTTCTAAGATTCAAGATCTT	421		
QY	511	GGGTGGGCGATGA	TTCTTGTCTACCAAGATTATGCTTAACCGTAAGCTTAATGCTTTT	570		
DB	422	ATCTGGGTCATGA	ATCTGGGATTAATCAATATGTCAGATCTGGGTTTAATAAGCTTG	481		
QY	571	TTCAATATATGCA	AGGAATGATGTTGGTGTGATTAAGTGTGCAAGTGGGAAGTTGAC	630		
DB	482	CTCAAAATGCTTA	TTAAGGAATGCAATACCGGGATTAAGATTTGGTGGGAAGTGGACT	541		
QY	631	ATAACACCCATCAT	CTTGTGCTGTGTAATACGCCAATCTGGAATCTGATTAATACGACCTTC	690		
DB	542	ATAATGCCCATCA	TATAGCTGTGTAATAGCTTTGATTAATGATTCCTTACGCAATATTC	601		
QY	691	CTATTAATGCAAT	ATCCCAAAATTTTCAACTCCCTTAACATCATATCAACAATGCA	750		
DB	602	CAGTGTGTGCAAG	TTCTTCAGACTGTTCGATTCATATACTGTCTTTAATGGAGAA	661		
QY	751	AAATGACCTAATGA	TGCGCTGCCAGGTTTTTTGTATAGCTTTCAGACATCGACATTTTATC	810		
DB	662	TATTAAGAAATTA	GTATCTGTGTGATAGTTTTTTGTATAGTTTACAGACATCGACATTAATTC	721		

FEATURES	REFERENCE	ORGANISM	KEYWORDS	VERSION	ACCESSION	LOCUS	RESULT 3
<p>Source</p> <p>1. 651</p>	<p>Wing, R.A., Friesch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A. An integrated analysis of the genetics, development, and evolution of the cotton fiber</p> <p>Unpublished</p> <p>Contact: Wing RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Total High Quality bases = 563 Seq primer: TAATACGACTCACTATGCG High quality sequence stop: 628. Location/Qualifiers</p>	<p><i>Gossypium arboreum</i></p>	<p>GI:21096688</p>	<p>BQ409001.1</p>	<p>GA_EB0014D02r <i>Gossypium arboreum</i> T-10 dpa fiber library <i>Gossypium arboreum</i> cDNA clone Ga_EB0014D02r, mRNA sequence.</p>	<p>BQ409001</p>	<p>EST 22-MAY-2002</p>

[illegible]

	QY	403	TGTCGTGGTGTTCGCCTCAGTGTTAA CGSGTGTTCCTACTCGCAAGACACCTGGGCTC	462
	Dd	405	TAGATATTCGTCTTTCTATCATCGTGTTTA ACGSTGTTTTATGCTCTTAACAGCCCTTTGGTGC	464
	QY	463	ATCTTTCCTCTGTTTGCTAA TGGGTA TGCTATAGGCTCCAGAGTGTTGGTGGGCGATG	522
	Dd	465	ATTCTCTTTCCGGGTGCTTTACTCGGAATTC TCATGGATTCAGA GATGGGGATTTGGAACATG	524
	QY	523	ATTCTTGTGCTACCAGCTTATG CCTAACCGCTAAGCTTAATCGTCTTTTCGAATCATG	582
	Dd	525	ATTCCGGGCATATCACAGTTA ATGTCAGCAAAAATTC AAAGGGTGTCTAGATCTTTA	584
	QY	583	CAGAAATATGATGATTCGTG GTTTAGTGTGATGATGGTAGAATGTGGAACCATTAACCCATC	642
	Dd	585	CTGGGAATGCTCTTGCA GCGATCATGATATGTTGTGTGGAATGGAACCAACAATGCTCAAC	644
	QY	643	ACTTTGCC 649 	
	Dd	645	ACATTTGC 651 	
RESULT_4				
B0864828				
LOCUS				
DEFINITION			721 bp mRNA linear EST 14-AUG-2002	
ACCESSION			OGC27M12.YG.ab1 QG_ABCDI lettuce salinas Lactuca sativa CDNA clone	
VERSION			BOB64828	
KEYWORDS			BOB64828.1 GI:22250293	
SOURCE			EST.	
ORGANISM			Lactuca sativa	
REFERENCE			Lactuca sativa	
AUTHORS			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Lactuca. 1 (bases 1 to 721)	
JOURNAL			Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Liu,H., Van Damme,M., Lavelle,D., Chevalier,P., Ziegler,D., Ellison, P., Kolman,J.J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.	
COMMENT			Lettuce and Sunflower ESTs from the Compositae Genome Project http://composetome.ucdavis.edu/ Unpublished Contact: Alexander Kozik (R.W.Michelmore) Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Asmndson Hall, UCD, Davis, CA 95616, USA Tel.: 1-(530)-742-1742 Fax: 1-(530)-752-9659 Email: akozik@atgc.org [michelmore@vegmil.ucdavis.edu] belongs to contig OG_Ca_Config2376, see http://cgdb.ucdavis.edu/ for details. Plate: QGC27 row: M column: 12.	
FEATURES			Location/Qualifiers	
Source			1..721	
			/organism="Lactuca sativa"	
			/mol_type="mRNA"	
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			/db_xref="taxon:4236"	
			/clone="QGC27M12"	
			/lab_host="E.coli"	
			/clone_lib="QG ABCDI lettuce salinas"	
			/note=Vector: pBRCDNASfiAB. The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgdb.ucdavis.edu/ TAG_Lib-QG_ABCDI lettuce salinas	

BASE COUNT	194 a	153 c	163 g	211 t	ORIGIN
Query Match	20.1%;	Score 295.6;	DB 13;	Length 721;	TAG TISSUE=flowers pre-fertilized
Best Local Similarity	65.7%;	Pred. No. 6.6e-42;			TAG_SEQ=GCCTGACGGG"
Matches 430;	Conservative 0;	Mismatches 224;	Indels 0;	Gaps 0;	
QY	29	CTTCCTCTGTTGCACCTTCATATGAGAGCCCAAGACACATTTGGCAGACACCTTCC	88		
DB	51	CTTTCGCTTACAGCTTTTTCATATGAGAGAGCCCAAGAGGTATGTCACTAGTAAAGGCTCAA	110		
QY	89	AAACGATTAGCAACCAAGAGATTATATGATCTCATGAAGSAAAGTTTATACGATATCTC	148		
DB	111	AACGACAAACCAACCAAGAGATTATATGATCTCATGAAGSAAAGTTTATACGATATCTC	170		
QY	149	CAAGTGGACTAAAGAGATCCCGGTGGTGAAGCTCCATTTGTAAGTTTTCGCGCCCAAGA	208		
DB	171	AGAGTGGATGAAGAAACCAACCTGGTGGTGAAGCTCCATTTGTAAGTTTTCGCGCCCAAGA	230		
QY	209	TGTCACTGATGCGTTCAATTTGTTACCATCTGAGCACTGCTTGGCATATCTTGAACAGTT	268		
DB	231	CGTCAACGATGCTTACCGCTCGCTTTCACTCATCATCATCTGCTGGCAATATCTCGCAAGTT	290		
QY	269	CTTACACGGGATCAAGCTTAAGATTTACTGCTGCTGATGATGTCGAAGATCAAGATCAAG	328		
DB	291	CTTCAATGGGATTAATCTCAAGATCAAGCCGTTTCCGAGATCTCCAAAGATTACAGAA	350		
QY	329	GCTCGCTCTGAGTTTCTTAAGATGGGTTTGTTCGAAGACACAGGCAAGGGGCTTACTG	388		
DB	351	GCTTACTCTGCAATTCACAAAATGGGTTTGTTCGAAGAAAGGATGAGATTTGAT	410		
QY	389	CTCAATCTTTTGTGCTGTGTGTGTTGCTCTGAGTGTTCACGGTCTTCTTCACTGCAA	448		
DB	411	ATTCATGGTGTCTACCAATGATGTTCTCCGATGTGTATATGATTTTATTCACCCA	470		
QY	449	GAGCACTGGGCTATCTTGTCTGTGTGTTGCTTAATGGATATGTAAGGCTCCAGATGG	508		
DB	471	GAGGCTTTTGTATTTGATTTGGCGATGATTAATGGGTTTCTTTGAAATCCAAATGG	530		
QY	509	TTGGGTGGGATGATTTCTGTCTACCTACCAAGTATGCTTAAAGCTTAACTGCT	568		
DB	531	GTGGCTAGGCTATATTCGGGCACTATCAGATATATATGATGCGAAATTCATATCTTT	590		
QY	569	TTTTCAATCATTTGACAGAAATGTATGTCTGTATGATGTTGATGATGAGAAATTGA	628		
DB	591	TGCTCAGATCTTGAACCGAAATTTGTCTCGCGGAATCAGATTTGCGTGGAGAAAGAA	650		
QY	629	CCATTAACACCATCATTTGCTGTATATAGCGCAATCTGATCTCATATTTCA	662		
DB	651	CCACACTGCACATCATATCGCTGTATTAACAGCTTGAATATGATCTTCACTTCA	704		
RESULT 5					
CEB02504/c					
LOCUS	CEB02504	674 bp	mRNA	linear	EST 10-JAN-2003
DEFINITION	VWB017E10.131866	An expressed sequence tag database for abiotic stressed leaves of <i>Vitis vinifera</i> var. Chardonnay	<i>Vitis vinifera</i>		
ACCESSION	CEB02504				
VERSION	CEB02504.1	GI:27579809			
KEYWORDS	EST.				
SOURCE	<i>Vitis vinifera</i>				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.				
REFERENCE	1 (bases 1 to 674)				
AUTHORS	Cramer,G.R. and Cushman,J.C.				
TITLE	An expressed sequence tag database for abiotic stressed leaves of <i>Vitis vinifera</i> var. Chardonnay				
JOURNAL	Unpublished				

COMMENT

Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

FEATURES

source

BACKWARD: T3 20mer
Plate: 0 row: E column: 10
Seq primer: T3 20mer
High quality sequence stop: 674.
Location/Qualifiers

BASE COUNT

236 a 183 c 125 g 130 t

ORIGIN

Query Match 19.7%; Score 289.8; DB 14; Length 674;
Best Local Similarity 65.3%; Pred. No. 6,9e-41;

Matches 442; Conservative 0; Mismatches 232; Indels 3; Gaps 1;

497 GCTCCAGAGTGGTGGGGGATGATTTCTCACTACCAAGTATGCTTAACCGTAA 556
674 GATTCAGAGTGGGATGGGACATTCCTGGGACATACAGGATGATGAAACGCG 615
557 GCTTATCGCTTTTCAATCATTCAGAGAAATGATGCTGCGTGTAGTTCGACG 616
614 TTGAAACCGCTTGTGTCAGGTGCTGAGTGGAAATGCTTGGGGGATCGATTCG 555
617 GTGGAAGTGGACCATTAACACCATCACTTGGCTGTAAATAGGCGCAATCTGAT 676
554 GTGGAAGTGGAAATCAACAGCTCATCACTGCTGCAACGCTGATTCGATCGGA 495
677 TATTCAGACCTTCTAATAATGTCATATCCCAAAATTTTCACTCCCTTACAT 736
494 TCTTCAGCATATGCTGATTCGCGATTCCTCAAGCTTTCACTCCCTTACAT 435
737 CTATCACTGAAATGACCTATGATGCGCTGCCAGGTTTTTTGTTAGCTTGA 796
434 TTTCATGGAAGAAATGATGATTTGATGCTGAGTTTCTAGTGATGATCAGCA 375
797 CTGACATTTTATCTGCAATGTTTAAGCGTTAGGCTCTAATCTTATCTGCTTT 856
374 CTGGAATTTTATCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 315
857 GGTGATGTTTCCAAACAAAGGATATCAAGAGAGTCAAGAAATTTTAAAGCT 916
314 TTGTTGTTGTC---CAAGAGAGGGGTGCTACAGGCGCTCAAGAGATTTTGG 258
917 AGCTTTCTGACTTGTGATTTCTACTCCCTTTCTCGCTACCAATTTGGCGTGA 976
257 TGTGTTTGGATTTGTAACCTTTACTGTTTCTATCTGCTGCTGCTGCTGCTG 198
977 CATGATTTCAAGCTGCTGTTTACAGTGGCGGGGTTCCAAATTTGAGTGA 1036
197 GATGTTTGTGTTCTGAGTTTCTCTTACTGGAATTCACAGATGCTCAATTC 138
1037 TCACATTGCTTCAATGTTTACACTGTTTGCCTAGCGGTAATGTTGTTTCA 1096
137 TCATTTCTCATTCAGTGTGTTATGTTGGTCTCTCAAGTGGGAATGTTGTTGA 78

QY 1097 GACAAAGGCGACGCTCAACATACAGCTTCTGTTGGTGGATTGGTTTCAGTGG 1156

DB 77 GACTCATGGGCTCTTCGATTAATTTCCGCTCTTGGATGAGCTGTTTCATGG 18

QY 1157 GCACCTTCAGATTGAGC 1173

DB 17 GCAGTTTCAGATTGAGC 1

RESULT 6

CB002410/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

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Fax: 775-784-1650

Email: jcushman@unr.edu

PCR Primers

FORWARD: T3 20mer

BACKWARD: T7 20mer

Plate: 0 row: E column: 06

Seq primer: T3 20mer

High quality sequence stop: 673.

Location/Qualifiers

1. 673

source

499 TCCAGAGTGGTGGTGGGATGATTTCTGCTACTACCAATTAATGCTTAACCGT 558
672 TTCAGAGTGGTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 613
559 TTAATGCTTTTTCAAATCATTCAGAGAAATGATGATGATGATGATGATGATG 618
612 TGAACCGCTTTTGAAGGATGATGATGATGATGATGATGATGATGATGATGAT 553
619 GGAAGTGGACCATTAACACCATCACTTGTGCTGATGATGATGATGATGATGAT 678

Db	Accession	Source	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Db	552	GGAATGGAAATCAACAAGCCTCATATGCTGCTGCAACAGCCTGATTTTCATCCGACCT											
Qy	679	TTGACGACCTTCCTATTAATTTGGCATTATCCCAAAATTTTTCACCTCCTTACATCATCT											
Db	492	TTGACGAAATATGCTGTATATTCGGGATATCTTCACAGCTTTTCAGTTCCCTTACATCTTAT											
Qy	739	ATTCACATGTGCAAAATGACATATGATTCGGGCTGCACAGGTTTTTGTATGCTTTACGACT											
Db	432	TCTATGAAAGAGATGAAATTTTATATGTGTGGCTAAGGTTTCTTACTGATGATTAACGACACT											
Qy	799	GGACATTTTATCTCGCATTTGTTTAAAGCTTAAGCTCTATCTTTTATCTGTCTTTTAAAG											
Db	372	GGACCTTTTATCTCGTGTATGTGTGTGTGCTAATTAATCTATTTTCTCAGTCTGTGCTT											
Qy	859	TGTGTCTTTCCAAACAACAAAGGATATCAAGAGAGATGACGAAATTTTAGGCTATGACG											
Db	312	TGTTGTGTC---CAAGAGAGAGGGTTCCTACAGGAGCTCAGAGATTTTGGGGCTGTGG											
Qy	919	CTTCTCTACCTTGGATATCTCTACTCCTTCTCGCTTACCCATTTGGCGCTTAAAGGCTCA											
Db	255	TGTTTGGATTTGGATCCCTTACTTGTTCATGTCTGCCCAATTTGGGAAAGATGA											
Qy	979	TGTAATTTGACGCTCCTGTTTACGATCGCGGGTTTCCACATTTGGCAGTTGACCTTAATC											
Db	195	TGTTTGTGTTCTGATGTTCTTCCTTACTGGAATCAGACATGTTCAATTCCTGTTGAATC											
Qy	1039	ACTTGTCTTCTPAATGTTTACACTGGTTTGCCTAAGCGGTAATGTTGTTTACACAGCAGA											
Db	135	ATTTCTCATTCACAGTGTATATGTGGGTCTCCCAAGTGGGAATGATGTGTGAGAAGCAGA											
Qy	1099	CAAGGGCAGCCTCAACATTAACAGTTCTGCTGTGTGGATTTGTTTATATGTGTGCTTCG											
Db	75	CTCATGGGTCTCTCGAATATTCCTGCTCCTCTTGATGATGACTGTTTCATGATGGGCTGC											
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Db	15	AGTTTCAGATTGAGC 1											
RESULT 7													
BO861565													
LOCUS	BO861565												
DEFINITION	OGC18P18.yg.ab1 OG.ABCD1 lettuce satinas Lactuca sativa cDNA clone												
ACCESSION	OGC18P18												
VERSION	BO861565												
KEYWORDS	BO861565.1 GI:22247030												
SOURCE	EST.												
ORGANISM	Lactuca sativa												
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	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;												
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;												
	asterids; campanulids; Asterales; Asteraceae; Cichorioideae;												
	Cichorioideae; Lactuca.												
	1 (bases 1 to 696)												
	Kozik,K., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,												
	Liu,H., van Damme,W., Lavelle,D., Chevalier,P., Ziegler,U., Ellisson												
	,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,												
	Church,S., Jackson,L. and Bradford,K.												
	Lettuce and Sunflower ESTs from the Compositae Genome Project	</											

Query Match	Best Local Similarity	19.1%	Score 280.8	DB 13	Length 696	
Matches	435	Conservative	0	Mismatches 237	Indels 2	Gaps 1
Db	78	GCAGACCTTGCAAAAGCATTAAGCAACAGAGATTTATGATCTATCAAGGAAAGTT	137			
Qy	8	GAAAGAGCTCAAAAGCTCAACAAACCAAGGGGATCTGTGATCTATACAGGAAAGTT	67			
Db	138	TACGATATCTCCAAAGTGAATTAAGAGATCCCGGTGTGAGCTCCCATTTGATGTT	197			
Qy	68	TATGACGCTCAGAGTGAATGAAGAAACCAACCTGTGTGAGACTTCCATTTGATCTT	127			
Db	198	GCCGGCCAAAGATGCTAGTATGCGTTCAATGCTTACATCCCTGGCACTGCTGGCAATAC	257			
Qy	128	GCTGTCAAGAGCTACCGATGCTTACGTGCTTTCATCATCATCATGCTTGGCAATAT	187			
Db	258	CTTGAACAGTTCTTACTGTGGTACTACAGTTCAAGATTAATCTGTCTGTGAGATGTCAG	317			
Qy	188	CTCGACAGTTCTTCAATGGGATATATCTCAAAAGACTAGCGCGTTCCGAGGCTTCGAA	247			
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Qy	308	GGAAGTTTGAATCATGATGCTCATACAGATGATGTTCTCCGTGTGTATATGATGTT	367			
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Qy	368	TTATTTACCCAGAGTGCTTTTGTTCATTTGAATTCGGGATGATATATGGGTTTCTTGG	427			
Db	498	CTCCAGATGTTGGGTGGGCGATATTTCTTGTCTACTACCAAGTATGCTTAACGTAAG	557			
Qy	428	ATTCAAGATGGGTGCTGAGCCATATTCGGGCACTATCAGATATATGATGTCGAAA	487			
Db	558	CTTATAGCTCTTTTCAATCATTCAGAGAAATGATGCTGAGTGTGATGTTGATGATG	617			
Qy	488	TTCAATGCTTTTGTCTCAATCTTTCACGGAAATTTGTCTGCCGGAATCAGCATTTGCGTGG	547			
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Qy	608	CTTCA--CACATACAGATGTGCGGTTTCTTCAAAATCTTGACATCTCTTATATCAAT	665			
Db	738	TATCAACACTGCA 751				
Qy	666	ACTACGAAAGAAA 679				

RESULT 8
 LOCUS BG647198
 DEFINITION BG647198 783 bp mRNA linear EST 24-APR-2001
 EST508817 HOGA Medicago truncatula cDNA clone pHOA-15P24 5' end,
 mRNA sequence.
 ACCESSION BG647198
 VERSION BG647198.1 GI:13782310
 KEYWORDS EST
 SOURCE Medicago truncatula (barrel medic)
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 REFERENCE 1 (bases 1 to 783)
 Hahn,M.G., Ojane-Reuhs,T., Samac,D., Town,C.D., Van Aken,S.,
 Uterback,T., Cho,J. and Fraser,C.M.
 ESTs from roots of Medicago truncatula treated with
 oligogalacturonides of DP 6-20
 JOURNAL Unpublished
 COMMENT Contact: Michael G. Hahn
 Complex Carbohydrate Research Center
 University of Georgia
 220 Riverbend Road, Athens, GA 30602-4712, USA
 Tel: 706-542-4457
 Fax: 706-542-4412
 Email: hahn@ccrc.uga.edu
 G390804e TIGR sequence name: MTMBV96TK More information is
 available at: www.medicago.org
 Seg primer: Skmod (CTA gaa cta gtc gat cc).
 Location/Qualifiers
 FEATURES
 source
 1..783
 /organism="Medicago truncatula"
 /mol_type="mRNA"
 /cultivar="A17"
 /db_xref="taxon:3880"
 /clone="pHOA-15P24"
 /tissue_type="3 day old seedling roots"
 /dev_stage="24 hours after treatment in the dark at 26 C
 with 0.5 mg/ml oligogalacturonides (DP 6-20) in the
 presence of 100 ug/ml Gentamicin"
 /lab_host="XLOLR"
 /clone_1lb="HOGA"
 /note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2:
 XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
 was directionally ligated into the Unizap XR vector from
 Stratagene and packaged using Gigapack III Gold packaging
 extracts. Plasmids containing cDNA inserts were excised
 from the recombinant lambda-Zap phage using Ex-aseIst
 helper phage and propagated in SOLR cells."

Db 181 TTGCTTGGAAGAAATGACTCATATATGCTCATATATGCTTGCAATAGTCTTGATTANG 240
 Qy 670 ATCTGATATATGAGCACTTCCATATATGGCAATATCCCAAAATTTTCAATCCCTTA 729
 Db 241 ATCTGATATGAGCAATATCCCTTGTTGCTGCTCTCATATCCGATTCCTTTGATTA 300
 Qy 730 CATCATATCATCAACAATGCAAAATGACCTATGATGCGGTGCGAGTTTGTAGCT 789
 Db 301 ATCTGATATGATATGATATGAGCAATTAAGTTGATGCTTTGATGAGTTTCTATAGTT 360
 Qy 790 TTGACATGAGCAATTTATCTGCAATGTTAAGCTTAAGCTTAATCTTTATCTGT 849
 Db 361 ACCAGCATATCACTTTTACCTGCTGTTGTTTCCAAAGGCTTAACCTGTACCTTCAA 420
 Qy 850 CTTTAAAGTGGTCTTTCACCAACAAGGATATACAAGAAATGAGAAATTTAG 909
 Db 421 CATTTTGGCTTGTGTTTCCATCAAGAAATGCTTGAATGAGCTTTACAAATCATGG 480
 Qy 910 GCTATGCACTTCTTCTGATGTTGATTCCTTCTCTGCTTCTGCTTACCAATTTGCGCTG 969
 Db 481 GATCGGTGTTCTGCTGATGTTGCTTCCCTGCTGATGTTGAGCTTCCCAAGTTGGCAG 540
 Qy 970 AAAGGTCATATATTTACAGTCTCTTTAGCAAGTCCGGGTTCCAAATTTGCAAGTTCA 1029
 Db 541 AAAGGTCATATGTTGTTGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 600
 Qy 1030 GCTTGAATCACTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1089
 Db 601 GTTGAACATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 660
 Qy 1090 ACCAGAGCAAAAGGCAAGCTCAATCAATCAAGCTTCTGTTGGTGGATTTGTTGATG 1149
 Db 661 AGAAACAAACAGCTGAAACATTTGATATCACTTTGTTCAACATGATGATGTTGTTG 720
 Qy 1150 GTGGCTGCACTTTCAGATTGAGCATATCTGTTTCCAAAGATGCTTAAGTGCATT 1206
 Db 721 GTGGTTGCAATTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTT 777

RESULT 9
 LOCUS CB893839
 DEFINITION EST646631 HOGA Medicago truncatula cDNA clone HOGA-29M7, mRNA
 sequence.
 ACCESSION CB893839
 VERSION CB893839.1 GI:30101008
 KEYWORDS EST
 SOURCE Medicago truncatula (barrel medic)
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 REFERENCE 1 (bases 1 to 817)
 Hahn,M.G., Ojane-Reuhs,T., Samac,D., Town,C.D., Van Aken,S.,
 Uterback,T., Cho,J. and Fraser,C.M.
 ESTs from roots of Medicago truncatula treated with
 oligogalacturonides of DP 6-20
 JOURNAL Unpublished
 COMMENT Contact: Michael G. Hahn
 Complex Carbohydrate Research Center
 University of Georgia
 220 Riverbend Road, Athens, GA 30602-4712, USA
 Tel: 706-542-4457
 Fax: 706-542-4412
 Email: hahn@ccrc.uga.edu
 TIGR sequence name: MTMDK76TK
 More information is available at: www.medicago.org
 Seg primer: Skmod (CTA gaa cta gtc gat cc).
 Location/Qualifiers
 FEATURES
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 1..817
 /organism="Medicago truncatula"
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/cultivar="A17"
 /db_xref="taxon:3880"
 /clone="HOGA-29M7"
 /tissue_type="3 day old seedling roots"
 /dev_stage="24 hours after treatment in the dark at 26 C
 with 0.5 mg/ml oligogalacturonides (OP 6-20) in the
 presence of 100 ug/ml Gentamicin"
 /lab_host="XLOLR"
 /clone_1lb="HOGA"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
 was directionally ligated into the Unizap XR vector from
 Stratagene and packaged using GigaPack III Gold packaging
 extracts. Plasmids containing cDNA inserts were excised
 from the recombinant lambda-Zap phage using Ex-assist
 helper phage and propagated in SOLR cells."

BASE COUNT 217 a 110 c 183 g 307 t
 ORIGIN

Query Match 19.0%; Score 279.4; DB 14; Length 817;
 Best Local Similarity 64.7%; Pred. No. 4,2e-39;
 Matches 415; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

QY 50 GGAAGAGCCAAAGACATTTGCAAGACCTTGCAAGCATTAAGCAACGAGAGA 109
 DB 177 GGTGAGAGAAAGAGATACATCTGAGAACTGAAAGCATGACAAAGAGGGA 236
 QY 110 TTATGATGTCATCAAGGAAAGTTACATCTCCAGTGGACTAAAGCATCC 169
 DB 237 TCTATGATCTCAATTCAGGTAAGGTTTCAATGTTTCAAGTTGAGGCTTAAACATCC 296
 QY 170 CGGTGGTGAAGCTCCCATTTGTAAGTTTGGCGGCAAGATGTCATGATCGTTTCATTCG 229
 DB 297 TGGTGGAGAGGTTTGTGTAATCTTGTGTCAGAGATGTAATCATTCATTCATAGC 356
 QY 230 TTACCATCTGSCACTGCTTGGCAATACCTTGAACAGTTCTTTTACGGTACTACCTTCA 289
 DB 357 ATATCATCTCGTTGACATGAAACATCTTGACACAGTTTTCACCTGCTATTACCTTGA 416
 QY 290 AGATTACTGCTGTCGAGATGTCGCAAGCTACAGAGAGCTACAGAGAGCTGCTCTAGATTCTTA 349
 DB 417 GGAATTTAAGATCTGAAGTTTCTAAAGATTAAGAGACTGTTCTGAGTTTGTCAA 476
 QY 350 GATGGTTTGTCAAGACACAGCAAGGAGTCTACTGCTCAATCTTTTGTGCTGT 409
 DB 477 AATGGTTTGTGAAAGAAAGAAACATGTTCTTATTACATTAACATCTGTTCTAT 536
 QY 410 GTTGTTCCTGAGTGTTCAGGTGTTCTTCACTGCAAGAGACCTGGGCTCATCTTTG 469
 DB 537 TAGCTTGTCTATGTTGTTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTAGG 596
 QY 470 CTCTGGTTTGTCAATGGGTAATGCTATGCTCCAGAGTGGTGGGGGATGATTTCTTG 529
 DB 597 TCTGTATGATGTTGGGTTTGTATGATGAGCAAGACTATATATGTTGATATTTCTGG 656
 QY 530 TCACCTCAAGATGATGCTTACCGTAAGCTTAATGCTTTTCAATCATTCAGAGAA 589
 DB 657 TCAATTGAGGTTATGTCAGAGTGAAGTTATTAACAATTAAGCAAAATTTTGTGTTAA 716
 QY 590 TGTGATGCTGTTGTTAGTGTTCATGTTGAAAGTTGAGACATTAACACCATTCATTCG 649
 DB 717 TGTATGACGTGATTAAGATGCTTGTGTTGAAATGAGACATTAATGCTCATATTTGC 776
 QY 650 CTGTATAGGCAATCTGATCTGATATTCAGCATTC 690
 DB 777 TTGCAATAGCTTGAATTAATGATCTGATTTGACAGATATCC 817

RESULT 10
 CD005403/c 652 bp mRNA linear EST 02-MAY-2003
 LOCUS VVB047G10.325360 An expressed sequence tag database for abiotic
 DEFINITION stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera

ACCESSION CD005403
 VERSION CD005403.1 GI:30322141
 KEYWORDS EST.
 SOURCE Vitis vinifera
 ORGANISM Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 Vitaceae; Vitis
 1 (bases 1 to 652)

REFERENCE Cramer, G.R. and Cushman, J.C.
 AUTHORS An expressed sequence tag database for abiotic stressed leaves of
 TITLE Vitis vinifera var. Chardonnay
 JOURNAL Unpublished
 COMMENT Contact: Cushman JC
 Department of Biochemistry
 University of Nevada
 MS200, Reno, NV 89557-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu
 PCR Primers
 FORWARD: T3 20mer
 BACKWARD: T7 21mer (backward)
 Plate: 0 row: G column: 10
 Seq primer: T3 20mer
 High quality sequence stop: 652.

FEATURES
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 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /db_xref="taxon:29760"
 /clone="VVB047G10"
 /tissue_type="leaf"
 /dev_stage="juvenile and adult"
 /clone_1lb="An expressed sequence tag database for abiotic
 stressed leaves of Vitis vinifera var. Chardonnay"
 /note="Vector: lambda Uni-Zap XR, Bluescript SK-; Site 1:
 EcoRI; Site 2: XhoI; library construction was performed
 according to Stratagene's recommended protocol for the
 Lambda UnizapXR vector and cDNA synthesis kit."

BASE COUNT 230 a 172 c 124 g 126 t
 ORIGIN
 Query Match 18.7%; Score 275.8; DB 14; Length 652;
 Best Local Similarity 64.9%; Pred. No. 2e-38;
 Matches 425; Conservative 0; Mismatches 227; Indels 3; Gaps 1;
 QY 519 CATGATTTGTCACACCAAGTTATGCTTAACCGTAAGCTTATGCTTTTCAATC 578
 DB 652 CAGATTTCTGGGACATCAAGAGTATGATGAAACAGCGTTTGAACGCTTTGTGCAAGTC 593
 QY 579 ATTGAGGAATGTGATGCTGTTGTTAGTGTTCAGTGTGAGAGTTGAGACATAACACC 638
 DB 592 CTGAGTGGGAATGCTTCCGGGGATCAGTATGTCGTGTGGAAGGAAATCAACAGCT 533
 QY 639 CATCACTTTGCTGTATTAAGCCCAATCTGATCTGATATTCAGACACCTCTCTTAAT 658
 DB 532 CATCACTTTGCTGTATTAAGCCCAATCTGATCTGATATTCAGACACCTCTCTTAAT 658
 QY 699 GCCATATCCCAAAATTTTCAACTCCCTTACATCACTATCAACAACGAAATGACC 758
 DB 472 GCGGTATCTTCCAGGTTTTCAGTTCCCTTACATCTTATTCTATGAAGAAAGATGAAT 413
 QY 759 TATGATGCGCTGCCAGGTTTGTGTTAGCTTACAGACATGACATTTATCTGATTC 818
 DB 412 TTGATGTTGTGCTAGGTTTCTAGAGATTAACAGACATGACATTTATCTGTGANG 353
 QY 819 TTAAGCTTAAGCTCTATCTTTTATTTCTGCTTTTAAAGTGTGTTTCAACAACAA 878
 DB 352 TGTGTTGCTAAGATTAATCTATTTGCTCAAGTCTGCTCTTGTGTTGTC---CAAGAG 296
 QY 879 AGGATTAACAAGAGAGTCAAGAAATTTTAAGCTATGACGCTTTCTTGAAGTGTATCT 938

Db 295 AGGGTTCGCTACAGGGCTCAGAGATTTTGGGGCTGCTTGTGTTTGGATTGGATCCCT 236
 Qy 939 CTAATCCTTTCTTCGCTACCAATTTGGCTGAAGGTCATGTATTTCAGCTCTTTA 998
 Db 235 TTACTGTTTCATGTCTGCCAATTTGGGAAAGATGATGTTGTTCTTGATTTTC 176
 Qy 999 GCAATGCCGGGTTCCAACTTTGGCAGTTTCAGCTTAATCATCTTCTTAATGTTAC 1058
 Db 175 TCTTTACTGGAATCCAGCATGTTCAATTTCTTTTAATCATCTTCAATCCAGTTTAT 116
 Qy 1059 ACTGTTTCCCTAGCCGTAATGATTGTTTCACACAGACAAAGGCAAGCTCAACATA 1118
 Db 115 GTGGGCTCTCAAGTGGAGATGATTGTTGAGAACAGACTGAGGCTCTGCATATT 56
 Qy 1119 AAGCTTCTGCTTGGTGGGATTTGTTCAATGTTGCGCTGACCTTTAGATTGAC 1173
 Db 55 TCCTGCTCTCTTGTGATGACTGTTTCATGTGGGCTCAGATTTCAGATTGAC 1
 RESULT 11
 Bf268631 957 bp mRNA linear EST 07-MAR-2001
 LOCUS Bf268631
 DEFINITION GA_Eb0002G08f Gossypium arboreum 7-10 dpa fiber library Gossypium
 arboreum cDNA clone GA_Eb0002G08f, mRNA sequence.
 ACCESSION Bf268631
 VERSION Bf268631.1 GI:11199626
 KEYWORDS EST.
 SOURCE Gossypium arboreum
 ORGANISM Gossypium arboreum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosid II; Malvales; Malvaceae; Malvoideae; Gossypium.
 1 (bases 1 to 957)
 REFERENCE Wing,R.A., Fritsch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
 D., Wood,T.C., Leslie,A. and Wilkins,T.A.
 An integrated analysis of the genetics, development, and evolution
 of the cotton fiber
 TITLE Unpublished
 JOURNAL Contact: Wing RA
 COMMENT Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: twing@clemson.edu
 Seq primer: TAATACGACTCACTATAGG
 High quality sequence stop: 714.
 FEATURES
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 /organism="Gossypium arboreum"
 /mol_type="mRNA"
 /strain="AKA"
 /cultivar="8400"
 /db_xref="taxon:29729"
 /clone="GA_Eb0002G08f"
 /issue_type="Fibers isolated from bolls harvested 7-10
 dpa"
 /lab_host="E. coli"
 /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
 /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
 BASE COUNT 258 a 179 c 233 g 287 t
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 Query Match 18.3%; Score 268.8; DB 10; Length 957;
 Best Local Similarity 61.9%; Pred. No. 2,8e-37;
 Matches 426; Conservative 0; Mismatches 262; Indels 0; Gaps 0;
 Qy 37 GTTGCACTTCATGAGAGCCAAAGACACATTTGGCAAGCACTTTCAGAACATA 96
 Db 165 GTTGAGGTTCAATGAGGAGGAGAAAAAGATACATTAGTGGCAAGAGCTGAAGACATA 224
 Qy 97 AGCAACGAGAGATTATGATCTATATCAAGGAAAGTTTACGATATCTCCAACTGA 156

Db 225 ACAAATCGGGATTTTGTGATCTCAATCCAGGCAAGTTTACAGATGTTTCAGAGTGG 284
 Qy 157 CTAAGAGATATCCGGGTGTGAGCTCCCATTTTAAAGTTTTCGGGCAAGATGTACTG 216
 Db 285 CAAAGAGATATCCGGGTGTGAGCTCCCATTTTAAAGTTTTCGGGCAAGATGTACTG 344
 Qy 217 ATGCGTTCAATGCTTACCATCTGGGCACTGTTGGCAATACCTTGAACAGTTCTTACTG 276
 Db 345 ATGCGTTCTGCGATATCACTTGAACCGCTTGGCAGATTTTGAACAGTTCTTACTG 404
 Qy 277 GGTACTAGTTTCAGATTAATCTGTTCTGAGATGTCAGAGACTACAGAGGCTGTCT 336
 Db 405 GTTATCATCTCAAAAGATTTTCAGAGTGTGAGATATCCAAAGATTAATAGAGGCTGTCT 464
 Qy 337 CTGAGTTTCTTAAGATGGGTTTTCAGACACAGGCAAGAGGCTTACTGCTAATCT 396
 Db 465 CGAGATTGCGCAAGCCGGTATGTAAGAAAGAAAGACATGTAGCCCTTTTTCATTGA 524
 Qy 397 TTTTGCTGTGTTGTTGCTGAGTGTTAAGGTTTCTTACTGCAAGACACCT 456
 Db 525 CAGCTGTAGCTTATTTATCTTATGCTCTTTATGTTTATAGATGTGATAGCTGT 584
 Qy 457 GGGCTCATCTTGTCTGTGTTGCTAATGGTATGCTCCAGAGTGTGGTGG 516
 Db 585 GGGCAATCTTGGGTGGGCACTTGTGGGCTTGTGGATGAGAAAGGCAATACATTG 644
 Qy 517 GGCATGATCTTGTACTACCAAGTTATGCTTAACCTTAAGTCTTTTCAAA 576
 Db 645 GTACAGATTAAGTATTAACAGTAAATGATGATGCTGCTTACCAAGCTTCGCTCAGA 704
 Qy 577 TCATTGCAAGAAATGATGATGCTGTGTTAGTTCAGATGTAAGTTGACCAATAACA 636
 Db 705 TTTTATCTGGGATTTTAAACCGGATCAGCATTTGCTGGGAAATGACTCAAAAG 764
 Qy 637 CCATCATCTTGTCTGTATAGCGCAATCTGATCTGATTTTACGACCTTCTATTA 696
 Db 765 CTCACCAATTTGGCTGCAACAGCTGACACAGATACCAATCCAGACATATCTGTT 824
 Qy 697 TTGCATATCCCAAAATTTTCAATCTC 724
 Db 825 TTGCCGTCTTTTACCACTTTTAATTTCC 852
 RESULT 12
 Bf111411 772 bp mRNA linear EST 20-JUL-2001
 LOCUS Bf111411
 DEFINITION EST5313161 GESD Medicago truncatula cDNA clone pGESD10F10 5' end,
 mRNA sequence.
 ACCESSION Bf111411
 VERSION Bf111411.1 GI:14985738
 KEYWORDS EST.
 SOURCE Medicago truncatula
 ORGANISM Medicago truncatula (barrel medic)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosid I; Fabales; Fabaceae; Papilionoideae; Trifoliales;
 Medicago.
 1 (bases 1 to 772)
 REFERENCE Grusak,M.A., Samac,D.A., Town,C.D., Van Aken,S., Uterback,T., Cho
 J. and Fraser,C.M.
 ESTs from developing reproductive tissues of Medicago truncatula
 Unpublished
 JOURNAL Contact: Michael A. Grusak
 USDA/ARS Children's Nutrition Research Center
 Baylor College of Medicine
 1100 Bates Street, Houston, TX 77030-2600, USA
 Tel: 713-798-7044
 Fax: 713-798-7078
 Email: mgrusak@bcm.tmc.edu
 B398266e
 TIGR sequence name: MTPAT29TK
 More information is available at: www.medicago.org

Db 240 TATCAACATGTTCACTTGTGTTGAACCATTTCTCGTAGGTTTACGTCGCCGCC 299
 QY 1070 TGGCGTATGATGTTTTCACAGACAGCAAGGCGACCTCAATACAGCTTCTGC 1129
 Db 300 GAACGGGAATGATGTTTTCAGAAACAAACCGAGGACGCTTAATATGTTGTCGTC 359
 QY 1130 TTGTTGGATGTTGTTTCATGTTGGGCTGCACCTTTCAGATTGAGCATCATCTGTTCCAG 1189
 Db 360 TTGGATGATGTTGTTTCTATGTTGGGTTTGCATTTCCAGTTTGAGCATCATTTGTTCCGAG 419
 QY 1190 GATGCTTAAGTGCATTTGAGAAATCTCCACATTTGTAACAACTTTGCCAAGA 1249
 Db 420 GTTGCTAGTGCATTTAGGACAAATTCACCATTTGTTAAGAGTTGTAAGAAACA 479
 QY 1250 TAATTGTCTTGAAGTCTCAATGTTGGAGGCGCATTAATGATATCTCCACCT 1309
 Db 480 CAATTTGGCTTAAATGTTGCTTCTTTTGGAAAGCTAATGACATGAGACACT 539
 QY 1310 GCGTGTGCTATGAGGCTAAGAGTGTACCAAGCCAGTTCCAGAACTGCTG 1369
 Db 540 TAAATAGCTGCTTCAAGCTTACGCTTTACCAATGCTGTTCCAAAACCTTGCTG 599
 QY 1370 GGAAGCAATGAACACTTGGGT 1392
 Db 600 GGAAGCTGTCACACACATGGGT 622

RESULT 14
 A1729306 668 bp mRNA linear EST 11-JUN-1999
 LOCUS BNLGH11080 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar
 DEFINITION to (AF007561) delta 6-desaturase [Borago officinalis], mRNA
 sequence.

ACCESSION A1729306 GI:5048158
 VERSION A1729306
 KEYWORDS EST.
 SOURCE Gossypium hirsutum (upland cotton)
 ORGANISM Gossypium hirsutum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 1 (bases 1 to 668)
 AUTHORS Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.
 TITLE ESTs from developing cotton fiber
 JOURNAL Unpublished

COMMENT Contact: Ben Burr
 Biology Department
 Brookhaven National Laboratory
 Upton, NY 11973, USA
 Tel: 516-344-3396
 Fax: 516-344-3407
 Email: burr@bnl.bnl.gov
 Seq primer: T3 Primer.

FEATURES
 source Location/Qualifiers
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 /organism="Gossypium hirsutum"
 /mol_type="mRNA"
 /cultivar="Acala Maxxa"
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 /cvsue_type="immature fiber"
 /dev_stage="Six days post anthesis"
 /lab_host="XLI-Blue"
 /clone_lib="Six-day Cotton fiber"
 /note="Vector: pBluescript II KS+."

BASE COUNT 184 a 134 c 131 g 219 t
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Query Match 17.6%; Score 259.4; DB 9; Length 668;
 Best Local Similarity 65.8%; Pired. No. 1,4e-35;
 Matches 377; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

QY 34 TCTGTGCACTTCAATGAAGCAAGCAAGCAATTCGCAAGACGACTTGCAGAAC 93

Db 89 TATTGAGACATCAATGGCGGATTCAGAGGGGTACATTTCCAAAACAGAGCTGAACCC 148
 QY 94 ATTAGCAACAGAGATTTATGATCTCTATCAAGGAAAGATTATCATCTCCAACT 153
 Db 149 ACAAACAAACATGATCTTGTGATCTCAATCCAGGCAAGATCTATGATGTAATCTCAAT 208
 QY 154 GGAATAAAGAGATCCCGGTGGTGAAGCTCCCATTTGTAATTTTGGCGGCAAGATGTA 213
 Db 209 GGAATCCACACACCTGTGTGGCCACTTCCATTTACTGAACCTCGCGGTCAAGACCCA 268
 QY 214 CTGATGCGTTCAATGTTGTTACATCTGAGCACTGCTGGCAATACCTTGAACAGTTCTTA 273
 Db 269 CCGATGCTTTCAATGATTTATCATCCCGGATAGCTTGCATATATCTCGAAGTTCTTCA 328
 QY 274 CTGGGATCAAGTTCAAGATTACTCTGTTCTGAGATGTCAGAGACTACAGAGCTG 333
 Db 329 CTGGTATTAACCTTGAAGGTACTTACTCTGATATATCCAAAGATTTATGAAAGCTAG 388
 QY 334 TCTGTAGTTTCTAAGATGGGTTTGTTCAGACACACAGGCAAGGGGCTACTGCTCA 393
 Db 389 CTGTGAGTTCTCAAGATGGGCTTTTGAACAAGAAAGACATGGACATGATTATAC 448
 QY 394 TCTTTTCGTGCTGTGTTGCTGCTGAGTGTTCACGTTCTCTACTGCAAGACA 453
 Db 449 TTACATCATACATGATGCTGTTTTCATCTGTTATGTTATGTTATGTTGACAAA 508
 QY 454 CCGGGCTCATCTTGTCTGCTGTTGCTAATGGATGCTATGCTCCAGAGTGTGGG 513
 Db 509 CTGGGTTTCATCTGTTGTTGCTGTTGATGGGTTTATGATGATCAAGGTTGGA 568
 QY 514 TGGGGATGATCTTGTGCTACCAAGTATGCTTAACGCTAAGCTATATGCTTTTC 573
 Db 569 TAGACATATTCAGACATTAACCTGATCTTATATAAAACCTCAACAGTTGCTC 628
 QY 574 AATCATTCAGAAATGATGATGCTGTTA 606
 Db 629 AACTTCTTACAGGAATGTCTTGTGGGATCA 661

RESULT 15
 BQ281359 744 bp mRNA linear EST 13-MAY-2002
 LOCUS WHE3020_D06_H12ZS Wheat unexpressed seedling shoot normalized cDNA
 DEFINITION library Triticum aestivum cDNA clone WHE3020_D06_H12, mRNA
 sequence.

ACCESSION BQ281359 GI:20548798
 VERSION BQ281359
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 1 (bases 1 to 744)
 AUTHORS Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
 P.S., Hsieh, C.C., Kang, Y., Lazo, G.R., Miller, R., Nguyen, H.T.,
 Rauech, C.J., Seaton, C.L., Tong, J.C. and Zhang, D.

TITLE The structure and function of the expressed portion of the wheat
 JOURNAL genomes - Normalized shoot cDNA library
 COMMENT Unpublished
 CONTACT: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818

FEATURES
 source Location/Qualifiers
 1..744
 Email: oanderson@w.usda.gov
 Sequences have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: SK primer.

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/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WH53020_D06_H12"
/tissue_type="Etiolated shoot"
/dev_stage="Five day old seedling"
/lab_host="E. coli DH10B"
/clone_lib="wheat unstressed seedling shoot normalized
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/notes="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK, Site_1: EcoRI, Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
pClose lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pBluescript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares'. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

```

BASE COUNT 144 a 219 c 197 g 184 t

Query Match 17.5%; Score 257.4; DB 13; Length 744;
 Best Local Similarity 60.2%; Pred. No. 3e-35;
 Matches 445; Conservative 0; Mismatches 291; Indels 3; Gaps 1;

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QY 512 GGTGGGCGCATGATTTCTGTCTACTACCAAGTTAGCCTTAACGCTTAATGCTTTT 571
DB 9 GATTGGCCATGACTCCCGCCACCAATACACGAGCACC CGCCTCAACGCTCTCT 68
QY 572 TCAATCATGCGAGAAATGATGCTGATGTTAGTGCATGCGGAAAGTTGACCA 631
DB 69 GCGAGTGGTCTCCGGAACTGCTCATCGGCTGGCATGCGCTGGGGAAGTTCAACCA 128
QY 632 TAACACCCATCATTTGCTGTATATAGCGCAATCTGATCTGATATTCAGCAGCTTCC 691
DB 129 CAACACACACCATCTCTGCAACAGCTGACATGACCCGAGCTCCAGAGCTTGCC 188
QY 692 TATAATTGCCATATCCCAAAATTTTCAACTCCCTTACATCATACTATACAACTGCA 751
DB 189 GCTCTTCGCGTTTCCAAAGCTCTTCAACACCTTGGTGGTCTGCTACGAGCGCAC 248
QY 752 AATGACCTATGATGCGGCTGCGAGGTTTTTTGTAGCTTTCAGCATGAGCAATTTATCC 811
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	559.4	38.0	1684	2	US-08-831-570-1 Sequence 1, Appl
2	559.4	38.0	1684	2	US-08-831-575-1 Sequence 1, Appl
3	559.4	38.0	1685	1	US-08-366-779-4 Sequence 4, Appl
4	559.4	38.0	1685	1	US-08-789-936-4 Sequence 4, Appl
5	559.4	38.0	1685	4	US-08-934-254-4 Sequence 4, Appl
6	377.8	25.7	1702	4	US-08-934-254-26 Sequence 26, Appl
7	122.6	8.3	291	4	US-09-313-294A-1966 Sequence 3256, Ap
8	93.4	6.3	266	4	US-09-313-294A-3256 Sequence 1, Appl
9	58.6	4.0	1617	2	US-08-834-655-1 Sequence 1, Appl
10	58.6	4.0	1617	3	US-08-834-655-1 Sequence 1, Appl
11	58.6	4.0	1617	3	US-09-363-574-1 Sequence 1, Appl
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13	58.6	4.0	1617	4	US-09-330-235-17 Sequence 17, Appl
14	57.4	3.9	449	4	US-09-439-261-38 Sequence 38, Appl
15	57.4	3.9	449	4	US-09-439-261-37 Sequence 37, Appl
16	57.4	3.9	655	4	US-09-439-261-3 Sequence 3, Appl
17	57.4	3.9	655	4	US-09-439-261-3 Sequence 3, Appl
18	57.4	3.9	864	4	US-09-439-261-12 Sequence 12, Appl
19	57.4	3.9	864	4	US-09-439-261-13 Sequence 13, Appl
20	57.4	3.9	1928	4	US-09-048-888-4 Sequence 4, Appl
21	55	3.7	2710	4	US-09-912-161-1 Sequence 1, Appl
22	54.2	3.7	473	4	US-09-439-261-37 Sequence 37, Appl
23	54.2	3.7	473	4	US-09-227-613-36 Sequence 36, Appl
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25	54.2	3.7	1335	4	US-09-227-613-1 Sequence 1, Appl
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28	48.8	3.3	1686	4	US-09-227-613-6	Sequence 6, Appl
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44	34.2	2.3	1884	1	US-08-789-936-3	Sequence 3, Appl
45	34.2	2.3	1884	4	US-08-934-254-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-831-570-1
Sequence 1, Application US/08831570
Patent No. 5959175
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Nunberg, Andrew N.
TITLE OR INVENTION: A SUNFLOWER ALBUMIN 5' REGULATORY REGION
TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,570
FILING DATE: 09-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10545
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 743-4366
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1684 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 43..1387
US-08-831-570-1
Query Match 38.0%; Score 559.4; DB 2; Length 1684;
Best local Similarity 62.8%; Pred. No. 1.6e-164;
Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;

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Oy	120	TCATCA	AGGAAA	AGTTTA	CGATAT	CTCC	AAAGTG	CACTAA	AGACAT	CCCGTG	TGAG	179		
Db	118	TCGAT	TCAAGG	AAAGCC	TATGAT	GTATT	CGGAT	TGGG	TGAAGA	CCATCT	CAAGTGG	CAGC	177	
Oy	180	CTCCAT	TGTTA	AGTTTG	CCGGCC	AAATG	CACTG	ATGCG	GTCA	TGTG	CTTAC	TCACT	239	
Db	178	TTTCC	CTTGA	AGAGCT	TGCTG	GTCA	AGAGGT	TA	CTGAT	GA	CTTGTG	CATTCAT	237	
Oy	240	GGCA	CTGCTTG	GCATAT	CTTGAC	AGCTT	CTTTAC	TGCGTA	CTAC	GGTCA	AGATTA	CTCT	299	
Db	238	GCCT	CTACAT	GGAA	GAATCT	GTAT	AAAGTTT	TTTCA	CTGGG	ATAT	CTTTAA	AGATTA	297	
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Db	298	GTTC	CTGAG	GTTC	CTAA	GAATTA	TATG	GAAGCT	TGTG	TTG	AGATTTT	CTTA	AAATGGG	357
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Db	358	TATG	CAAAAA	AGTCAT	TATAT	GTTTG	CAACTT	TGTCT	TAT	AGCA	ATGCTG	TTT	417	
Oy	420	CTG	AGTTT	TA	CGGTCT	CTACT	GTCA	AGAGAC	CACTG	GGCT	CAATCT	TGTCT	479	
Db	418	ATG	AGTGT	TAT	TAGGG	TTTGT	TGTG	TAGGG	GTGTTT	TGTG	ATCA	TTTGT	CTGG	477
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Db	778	TTTG	AATAT	ATCA	CAAT	TGAC	ATTTA	CC	TAT	TAT	TGTGTG	CTG	CTA	837
Oy	840	TTTA	TCTG	CTTTA	TAG	TGTGT	TTTTT	CCAA	CAAA	AGG	GTAT	TACA	AGAG	899
Db	838	TATG	A	CAATCT	CTCAT	TAT	GTGTTG	TGAC	CAAG	A	AAAT--	GTGT	CCAT	894
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Db	895	GAA	CTT	GGATG	GTCTG	ATGT	CTTC	GAAT	TGG	TA	CCG	TGT	CTT	954
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Db	955	AAT	TGG	GTGA	AA	GAAT	TAT	GTGTTT	ATG	CA	AGTT	TAT	CA	1014
Oy	1020	TGG	AGTT	CA	GTG	GAAT	CACTT	GTCTT	CTA	TGTTT	CA	CTG	TTTG	1079
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Oy	1080	GAT	TGG	TTTCA	CC	AGAC	CAAA	AGG	GC	CTCA	AT	TA	AG	1133
Db	1075	AAT	TGG	TTTGA	AA	CAAA	CGAT	TGG	CA	CTT	GA	CA	CTT	1134

Qy	1140	TGGTTTCATGGTGGCCGCGACCTTTCACATGAGCATCATCTGTTCCAGATGCTAAG	1139
Db	1135	TGGTTTCATGGTGGATTTGCAATTCGAAATGAGCATCATTTGTTTCCAGATGCTAAG	1194
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Db	1315	GCATTTGACGGGTAGGGAATATPACCAACCCGCTCCCGAAGAAATTTGGTATGGGAAGCTCTT	1374
Qy	1380	AACACTTTGGGGTACACCTTATNNAAATCAAGTCTGTTTCCGTAAGAACCTTCCAG	1439
Db	1375	CACACTCATGGTTAAATTAATCCCTTAGTCAATGTAATTAATTTAGATTATGATATCTCCTA	1434
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RESULT 2
US-08-831-575-1
; Sequence 1, Application US/08831575
; Patent No. 5977436
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Li, Zhongsen
; TITLE OF INVENTION: AN OLEOSIN 5'REGULATORY REGION FOR THE
; TITLE OF INVENTION: MODIFICATION OF PLANT SEED LIPID COMPOSITION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831.575
; FILING DATE: 09-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: DIGILLO, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1387
;
Query Match 38.0%; Score 559.4; DB 2; Length 1684;
Best Local Similarity 62.8%; Pred. No. 1.6e-164;
Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;

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QY 60 AAGACACATTTGCGAAGCAGACTTGAAGCATTAAGCAACGAGATTTATGATC 119
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 QY 1080 GATTGTTTACAGACAGACAAAGGCAAGCTCAACATTAACAGCTTCTGTTGTTGAT 1139
 DB 1075 AATTGTTTGAAGAAACAAAGGATGGGACACTTGACATTTCTTGTCTCTTGGATGAT 1134

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 QY 1440 TCCCAATGTTCTTTTCTTTTCTTTTCTTTT 1469
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RESULT 3 US-08-366-779-4 : Sequence 4, Application US/08366779

: Patent No. 5614393
 : GENERAL INFORMATION:
 : APPLICANT: Thomas, Terry L.
 : APPLICANT: Reddy, Avutu S.
 : APPLICANT: Nuccio, Michael
 : APPLICANT: Freysinet, Georges L.
 : APPLICANT: Nunberg, Andrew N.
 : TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 : TITLE OF INVENTION: DELTA 6-DESATURASE
 : NUMBER OF SEQUENCES: 25
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Scully, Scott, Murphy & Presser
 : STREET: 400 Garden City Plaza
 : CITY: Garden City
 : STATE: New York
 : COUNTRY: United States
 : ZIP: 11530
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/366,779
 : FILING DATE: 30-DEC-1994
 : CLASSIFICATION: 800
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Presser, Leopold
 : REGISTRATION NUMBER: 19,827
 : REFERENCE/DOCKET NUMBER: 8383ZYXW
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (516) 742-4343
 : TELEFAX: (516) 742-4366
 : TELEX: 230 901 SANS UR
 : INFORMATION FOR SEQ ID NO: 4:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1685 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: both
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA (genomic)
 : US-08-366-779-4
 : Query Match 38.0%; Score 559.4; DB 1; Length 1685;
 : Best Local Similarity 62.8%; Pred. No. 1,66-164;

Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;

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QY 60 AAGAGACATTTGCGAAGACGACCTTGCAGAGATAGACACGAGAGATTTATGATC 119
DB 59 AAGAAATACATTTACTCAGATGAACTCAAGAACACAGATAAACCGAGATCTATGATC 118
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QY 360 TTCAAGACACGAGCAAAAGGGCTCTACTGCTCAATCTTTTCTGCTGTGCTGCT 419
DB 359 TATGACAAAAGGTCATATATATGTTGCAACTTGTGCTTATAGCAATGCTGCT 418
QY 420 CTGAGTGTTAAGGTTCTCTACTGCAAGACCTGGGCTACTTGTCTGGTTG 479
DB 419 ATGAGTGTTAAGGTTGTTGTTGAGGGGTGTTTGGACATTTGTTCTGGGTGT 478
QY 480 CTATGAGTATGATGCTCTCAGAGTGTGAGTGGGAGATGATCTTGTCTACTACAA 539
DB 479 TTGATGGGTTTCTTGTGATTCAGAGTGTGATGAGATGATGCTGGCATTAATAG 538
QY 540 GTTATGCTTAACGTAAGCTTATGCTTTTCAATTCATGAGAGAAATGATGCT 599
DB 539 GTAGTGTCTATTCAGAGCTTAAATGATTAAGGATTTTGTGCAAAATGCTTCA 598
QY 600 GGTTGATGTTGATGAGTGAAGTGAACATTAACCATCACTTGTCTGTATAGC 659
DB 599 GGAATAGATGTTGTTGAGAAATGAAACATATACATCAATGCTGTAAATAGC 658
QY 660 GCCATCTGATCTGATATTCAGACCTTCTATATTTGCCATATCCCAAAATTTTC 719
DB 659 CTGGAATATGACCTGATTTACATATATATACATCTCTGTGTGCTTCCAAATTTT 718
QY 720 AACTCCCTTAATCAATATCACTACACTGCAAAATGACTATGATGCGCTGCAAGTT 779
DB 719 GGTTCACCTACCTCTCATTTCTATGAGAAAGGTTGACTTTGACTTTATCAAGATTC 778
QY 780 TTTGTTAGCTTTCAGCACTGACATTTTATCCCTGATTTGAACCTTAGGCTTATCT 839
DB 779 TTTGTAAGTATCAACATGAGCAATTTTACCTATATATGCTGTGCTAGGCTCAATAG 838
QY 840 TTTATCTGCTTTTAAAGTGTGTTTTCACAACAAGGATATCAAGAGATGAG 899
DB 839 TATGTAACAATCTCTCAATATGTTTGTGACCAAGAAAT---GTGCTTATCAGCTCAG 895
QY 900 GAAATTTTAAAGCTATGAGCTTTCTGATGTTGATTTCTACTCTCTTCTGCTTACC 959
DB 896 GAACTTTGGGATGCTAGTGTCTCGATTTGGTATCCGTTGCTGTTTCTGTTTCTCT 955
QY 960 AATTGGCTTAAAGGCTATGATTTTACGCTGTTTACAGTCCGGGTTTCCACAT 1019
DB 956 AATTGGGTTAAAGAAATATGTTTGTATATGCAAGTTATCAGATGGAATGCAACAA 1015
QY 1020 TGGCAGTTTCAAGTATGATTTGCTTATATTTTAACTAGGTTTCCAGGATTAAT 1079
DB 1016 GTTCAAGTTTCTTGAACCACTTCTCTTCAAGTGTATATGTTGAAGGCTTAAAGGAAT 1075
QY 1080 GATTGTTTCAACGAGACAAAGGAGCGCTCAACATTAACAGTTTCTGCTGTGGAT 1139
DB 1076 AATTGTTTAAAGAAACAAAGGATGGACATTTCTTGTCTCTGCTGTGATGAT 1135

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QY 1140 TGGTTTCATGTTGCGCTGACCTTTCAGATTCATCTGTTTCCAGAGATGCCTAAG 1199
DB 1136 TGGTTTCATGTTGCGCTGACCTTTCAGATTCATCTGTTTCCAGAGATGCCTAAG 1195
QY 1200 TGGCATTTCAGAAAATCTGACCATTTGTGAAACAACTTTGCGAAGATTAATTTGTC 1259
DB 1196 TGCACCTTAGGAAAATCTGCGCTTACGTGATGATGATGCAAGAAACATTAATTTGCT 1255
QY 1260 TATGAACTGCTACATGTGGAGGCCATTAATATGATATCTCCACCTGCGCTGTG 1319
DB 1256 TACAAATTCATCTTCTTCCAGGCGCAATGAATGACCTGCAACATTTAGAGAACACA 1315
QY 1320 GCTATGAGCTTAAGATGTTTACCAAGCCAGTTCACCAAGAACTGCTGGAAGCAATG 1379
DB 1316 GCAATGCAAGCTTAGGATATTAACCAAGCCGCTCCGAAAGATTTGATGGAAGCTTT 1375
QY 1380 AACACTTTCGGGTGAACCTTATTAACATGCAAGTGTCTTTCCGTAAGACCTTCCAG 1439
DB 1376 CACACTCATGTTAAATTAATTCCTTAGTTCATGTAATTAATTTGAGATTAATCTCTTA 1435
QY 1440 TCCCAATGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1469
DB 1436 TGTGTGTCTTGTCTTGTGTTCTACTGTT 1465

```

RESULT 4
US-08-789-936-4
Sequence 4, Application US/08789936
Patent No. 5789220
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Reddy, Annu S.
APPLICANT: Nuccio, Michael
APPLICANT: Freysaine, Georges L.
APPLICANT: Numbert, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789, 936
CLASSIFICATION: 435
FILING DATE: 28-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/366, 779
FILING DATE: 30-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83832YXX
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1685 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-789-936-4

Query Match 38.0%; Score 559.4; DB 1; Length 1685;
 Best Local Similarity 62.8%; Pred. No. 1.6e-164;
 Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;

QY 60 AAGAACACATTTCCGACAGACCTTGCACATTAAGCAACCAAGATTTATGATC 119
 DB 59 AAGAAATACATTACCTCAGATGAATCAAGAACCAAGATTAACCGAGATCTATGATC 118
 QY 120 TCTATCAGGAAAAGTTTACATCTCCAGATGCACTAAGAGATCCCGGTGTAG 179
 DB 119 TCCATTCAGGAAAAGCTATGATGTTTCCGATTTGGATGAAGACCATCCAGGTGGCAG 178
 QY 180 CTCCTCATTTGATTTTGGCCGCAAGATGTCATGATGCTTCAATGCTTACATCT 239
 DB 179 TTTCCCTTGAAGAGCTTGTGCTCAAGAGTAACTGATGCTTGTGATTCACATCT 238
 QY 240 GGCACCTGTGCAATACCTTGAACAGTCTTACTGGTACTAGCTTCAAGATTAATCT 299
 DB 239 GCCTCTACATGAGAAATCTTGAATTAAGTTTTCACCTGGGATTAATCTTAAAGATTA 298
 QY 300 GTCTCTGAGATGTCAGAGATCAAGAGGCTGCTCTGAGTTTCTAAGATGGGTTTG 359
 DB 299 GTTCTGAGGTTTCTAAGATTAAGAGAGCTTGTGATGATTTCTAAGATGGGTTTG 358
 QY 360 TTCAACACACAGGCAAGGGGCTACTGCTCAATCTTTTGTGTGTGTGTGTGTGT 419
 DB 359 TATGACAAAAGAGTCATTAATTAATTTGCAACTTTGTGCTTAAACAAATGCTGTGTGT 418
 QY 420 CTGAGTGTTAAGGTTTCTCTACTGCAAGAGACCTGGGCTCATCTTGTGCTGTGT 479
 DB 419 ATGAGTGTTAATGAGGTTTGTGTTGTGAGGGTGTGTTGTGATCAATTTGTTTGTGGGT 478
 QY 480 CTAAATGGATATGCTATGCTCCAGAGTGTGTGGGTGGGATGATCTTGTCTACTCA 539
 DB 479 TTGATGAGGTTTCTTGTGATTCAGAGTGTGTGATTTGACATGATGCTGGGATTAATG 538
 QY 540 GTTATGCTTAACCGTAACTTAATGCTTTTTCAAATCATTCGAGAAATGATGATGCT 599
 DB 539 GTAGTCTGATTCAGAGGCTTAATTAATGATGATTTTGTCTCAAAATGCTCTTGA 598
 QY 600 GGATGATGTTGTCATGTCAGAGTGTGACATTAACCATCACTTGTGCTGATTAATG 659
 DB 599 GGAATTAAGATTTGTTGTGAGAAATGAAACATTAATGACATATGCTGTTAATGAG 658
 QY 660 GCCAATCTGATCTGATATTCAGACCTTCTAATATGTCATATGCCCAAAATTTTTC 719
 DB 659 CTGAAATATGACCTGATTTTACAATATATATACATCTGTTGTGTCTTCAAGTTTTC 718
 QY 720 AACTCCCTTAATCATATCACTCAACTGCAAAATGACTATGATGCGCTGCAAGTTT 779
 DB 719 GGTTCACACCTCTCATTTCTATGAGAAAAGTTGACCTTTTACCTTATCAAGATTC 778
 QY 780 TTTGATGCTTGAAGAGTGAATTTTATCCGATGTTAGCGTTAGGCTTATCTT 839
 DB 779 TTTGATGATTAACATTTGAGATTTTACCTAATATGTTGCTCTGAGCTCAATATG 838
 QY 840 TTTATCTGCTTTTAAAGTGTGTTTCCAAACAAGGATATATCAAGAGATGAG 899
 DB 839 TATGTCATCTCTCATTAATGTTTGTGACCAAGAAAT---CTGTCTATGAGCTCAG 895
 QY 900 GAAATTTTAAAGCTTATGAGCTTGTGATGTTTCTACTCTCTTGTGCTACCC 959
 DB 896 GAACTCTGAGAGCTAGTGTCTGATTTGTGATCCCGTGTCTTGTGTTGCT 955
 QY 960 AATTGCGTGAAGGATGATTTTCAAGCTGTTAGCACTCCCGGCTTCAACAT 1019
 DB 956 AATTGGGGTGAAGAAATATGTTTGTATGCAAGTTTATCACTGATGCAAGATGCAACA 1015
 QY 1020 TGGCAGTTCAAGCTTGAATCACTTGTCTAATGTTTAACTGTTGCTAGCGGTAAT 1079
 DB 1016 GTTCAAGTTCTCTTGAACCACTTCTCTCAAGTGTATGTTGAGAAAGCTTAAGGAAT 1075

QY 1080 GATGTTTACACAGACAGAAAGGCAAGCTTCAATACAGCTTGTGTTGGGAT 1139
 DB 1076 AATTGTTTGAAGAAACAAAGGATGAGACATTTGTTGCTCTTGTGATGAT 1135
 QY 1140 TGGTTTCAAGTGTGCTGCTGACCTTTCAGATTTGAGCATCTGTTTCAAGATGCTTAAG 1199
 DB 1136 TGGTTTCAAGTGTGATTTGCAATTTGAGCATCTGTTTTCAGAAATGCTTA 1195
 QY 1200 TCCATTTCAAGAAATCTCAACCATTTGTAACAACTTTGCCAAGATTAATTTGTC 1259
 DB 1196 TCCAACTTGAAGAAATCTGCTTACGATGATGATGCAAGAAATTAATTTGCT 1255
 QY 1260 TATGAACGTACACATGAGGAGGCAATTAATGATTAATCAACCTGTGCTGTG 1319
 DB 1256 TACAAATTAATGATCTTCTTCCAGGCAATGAATGACCTAGAACTTGAAGAACACA 1315
 QY 1320 GCTATGSAAGCTAAGATTTTACCAAGCCAGTTCCCAAGACATGCTGGAGCAATG 1379
 DB 1316 GCATTTGCAAGCTAAGGATTAACCAAGCCGCTCCGAAAGATTTGTTATGGAGCTTT 1375
 QY 1380 AACACTTGGGTGAACCTTAATMAACATCAAGTGTCTTCCGTAAAGCTTCCAG 1439
 DB 1376 CACACTCATGTTAAATTAACCTTAGTTCATGATTAATTTGAGATTAATGATCTCTTA 1435
 QY 1440 TCCCAATGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1469
 DB 1436 TGTGTGTCTTGTCTGTTGTTCTACTTGT 1465

RESULT 5
 US-08-934-254-4
 ; Sequence 4, Application US/08934254
 ; Patent No. 6355861

GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.
 TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A

TITLE OF INVENTION: DELTA 6-DESATURASE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

CITY: Garden City

STATE: New York

COUNTRY: United States

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,254

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Presser, Leopold

REGISTRATION NUMBER: 19,827

REFERENCE/DOCKET NUMBER: 8383ZYXWVU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1685 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-934-254-4

Query Match 38.0%; Score 559.4; DB 4; Length 1685;

Best Local Similarity 62.8%; Pred. No. 1,6e-164;
Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;

QY 60 AAGAGACATTTTCGCAAGACGACCTTGCAGAAAGATAGACACAGAGATTTATGATC 119
DB 59 AAGAAATACATTTACTCAGATGAACTCAAGAACACAGATTAACCCGAGATCTATGATC 118
QY 120 TCTATCAAGGGAAGATTTACGATATCTCCAGTGAATGAAGAGATCCCGGTGTGAG 179
DB 119 TCGATTCAGGGAAGGCTATGATGATTTGGATTTGGGTGAAGACATCCAGGTGGAGC 178
QY 180 CTCCATTTGTTAAGTTTTCGCGCAAGATGCTAGATGCTTATGCTTACATCT 239
DB 179 TTTCCTTGAAGAGCTTGTGCTGCAAGAGGATCATGATGATTTGTTGATTCATCT 238
QY 240 GGCACTGCTTGGCAATCTTGAAGGCTCTTATCTGGTATCTACGTTCAAGATTTCT 299
DB 239 GCTCTACATGGAAGATCTTGAATGATTTTCACTGGATATATCTTAAAGATTTACT 298
QY 300 GCTCTGAGATGCTCAAGACATACAGAAAGCTGCTCTGAGTTTCTAAGATGGTTTG 359
DB 299 GTTCTGAGTTTCTAAGATTAAGAGAGCTTGTGATGATTTCTAAGATGGTTTG 358
QY 360 TTCAAGACACGAGCAAGGGGCTACTGCTCAATCTTTTCTGCTGTGTGTTGCT 419
DB 359 TATGACAAAAAGGCTCATATATGTTGCAACTTTGCTTATAGCAATGCTGTGCT 418
QY 420 CTGAGTGTATACGGTGTCTCTACTGCAAGACACCTGGGCTACTTGTCTGTGTTG 479
DB 419 ATGAGTGTATAGGGGTTTGTGTTGAGGGGTTTGTGACATTTGTTTCTGGGTGT 478
QY 480 CTATAGGATATGCTATGCTCTCAAGTGTGTGGTGGGAGATGTTCTGTCTACTACAA 539
DB 479 TTGATGGGTTTCTTGTGATTCAGAGTGTGTGATGACATGATGCTGGGATTAATG 538
QY 540 GTTATGCCCTAACGCTAAGCTTAATGCTTTTCAATTCATGAGAGAAATGATGCT 599
DB 539 GTAGTGTGATGATCAAGGCTTAATGATGATGATGATTTTGTGCAAAATGCTTTCA 598
QY 600 GGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 659
DB 599 GGAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 658
QY 660 GCAATCTGATCTGATATCTACAGACCTTCTAATGATGATGATGATGATGATGATG 719
DB 659 CTGATATATGACCTGATATCTACATATATGATGATGATGATGATGATGATGATG 718
QY 720 AACTCCCTTACATATCTATCACTGCAAAATGATGATGATGATGATGATGATGATG 779
DB 719 GGTTCACCTACCTCTCATTTCTATGAGAAAGGTTGACTTTTGACTTTATCAAGATTC 778
QY 780 TTGTGATGCTTGGACCTGACATTTTATCCCTGATGATGATGATGATGATGATGATG 839
DB 779 TTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 838
QY 840 TTATCTGCTTTTAAAGTGTGTGTTTCCAAACAAAGGATATCAAGAGATGATGATG 899
DB 839 TATGTACATCTCTCATATGATGATGATGATGATGATGATGATGATGATGATGATG 895
QY 900 GAAATTTAAGCTATGAGCTTTTGAATGATGATGATGATGATGATGATGATGATGATG 959
DB 896 GAACTCTTGGATGCTAGTGTCTCATTTGATGATGATGATGATGATGATGATGATGATG 955
QY 960 AATGGGCTGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1019
DB 956 AATGGGCTGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1015
QY 1020 TGGAGTTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1079
DB 1016 GTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1075
QY 1080 GATTTGTTTACCAAGACAAAGGAGCGCTCAACATTAACAGCTTGTGTTGGTGGAT 1139

DB 1076 AATTTGTTGAGAAACAAACGATGAGACATTTGATTTCTGCTCTTGATGAT 1135
QY 1140 TGGTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1199
DB 1136 TGGTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1195
QY 1200 TGGCATTTGAGGAAATCTCAACCATTTGATGATGATGATGATGATGATGATGATGATG 1259
DB 1196 TGCACCTTGAAGAAATCTGCGCTGATGATGATGATGATGATGATGATGATGATGATG 1255
QY 1260 TATGAATGCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1319
DB 1256 TACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1315
QY 1320 GCTATGAGCTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1379
DB 1316 GCACTTCAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1375
QY 1380 AACACTTTCGGTGAACCTTATTAACATCAAGTGTGCTTCCGTAAGATTTCCAG 1439
DB 1376 CACACTCAAGCTTAAATTAACCTTATGATGATGATGATGATGATGATGATGATGATG 1435
QY 1440 TCCCAATGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1469
DB 1436 TGTGTTGCTTGTCTGTTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTT 1465

RESULT 6
US-08-934-254-26
Sequence 26, Application US/08934254
Patent No. 6355861
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
NUMBER OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
City: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1702 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1406
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1406

US-08-934-254-26

Query Match 25.7%; Score 377.8; DB 4; Length 1702;
 Best Local Similarity 57.6%; Pred. No. 8.9e-108;
 Matches 717; Conservative 0; Mismatches 522; Indels 6; Gaps 2;

50 GGAGAGCCAAAGACACATTTGCGAAGCAGACTTGCAGAAAGCATAGCAACAGAGAG 109
 53 GGGCGAAGGTAGAGATATATCAAGGGAGAGACTCCGGCCACAGCAAGTCCGGCA 112
 110 TTTATGATCTCTATCAAGGAAAAGTTAGATATCTCAAGTGAAGTAAAGACATCC 169
 113 TCTCTGATCTCATCAAGGGCAAGGTCTACGACTCTCTCGGTGGGGCGGAGAGACC 172
 170 CGGTGAGAGCTCCCATTTGTTAGTTTTCGGGGCAAGATGATCACTGATCCGTTTCG 229
 173 CGGGGAGAGTCCCTCTCTCAGTCTGGGGCCAGAGATCAAGACGCTTCATTCG 232
 230 TTACATCTGAGCAGTGTGGCAATACCTTGACAGGTTCTTACTG---GTAACAT 286
 233 GTACCAACCGGGGACGCGGCGGCGCATCTGATCCGCTCTTACCGGCTACTACTACT 292
 287 TCAAGATTAATCTGTCTCTGAGATGTCAGAGACTACAGAGGCTGCTCTGAGTTTC 346
 293 CAAGGACTTCAGAGTCTGAGAGATCTCAAGGACTACCGAGGCTTTGAACGAGATGC 352
 347 TAGATGGGTTGTGAAGCACAGGCAAGGGGTCTACTGCTCATCTTTTTCGTC 406
 353 GCGGTCGGGATTTGAGAGAGAGGCGCCACATCATGTGAGCGTTCTCGGCGTTCG 412
 407 TGTGTTGCTGCTGATAGTTTACGTTGTTCTCTACTGCAAGAGACCTGGGCTCATCT 466
 413 GGTCAATGATGCGGCAATCTCTACGCGGCTGCGGTGGAGTCCGTCGAGATTACAT 472
 467 TGTCTGTGTTGCTATAGGATAGCTATGCTCCAGAGTGTGGGTGGGCGATATTC 526
 473 GCTCTCGGGGCACTGCTGGCTTGTGATGATCAAGCGGCTATGTGGGCGATGATC 532
 527 TTGTCTACTACAGATTATGCTTAACGTAAGCTTAATCGCTTTTCAATCATTTGAG 586
 533 CGGCGATTACAGAGTATGCAACCGGTGATCAACAGATACCGCACTCATACAGG 592
 587 AATGATGTTGCTGTTAGTGTGATGATGAGAGTGAAGTTGACATTAACCCATCACT 646
 593 CAACATCTTAACCGGATACGATCGGCTGTGAGAGTGAAGCCACACACCACT 652
 647 TGCCTTAATAGCGCAATCTGATCTGATATTCAGCACTTCTTAATATTCATATC 706
 653 CGCTCAACAGCTCGACTAGAACCCGACCTCCAGCAATCCCGTATGTGCGCTTC 712
 707 CCCAAAATTTTAACTCCCTTACATCATATCAACACTGCAGAAATGACTATGATCG 766
 713 CACCCGACTTCACTCACTCACTCGCTCTTCTATGCGCGAGTCCGTAATTCAGCA 772
 767 CGCTGCAAGTTTGTGTTAGCTTTCAGACTGGAATTTATCTGCATGTGTAAGCG 826
 773 AGTGGACGCTTCTATGATCACTACAGCACTGACCTACTACCGGTATGATCTTCG 832
 827 TAGCTCTATCTTTTATCTGCTTTTAAAGTGTGTTTCCAGAAACAAAGGATATA 886
 833 CGAGTCAACCTTCTATCAAGACCTTTTATGTCTCTACAGAGGCGA---CGTCC 889
 887 CAAGAGAGTCAAGAAATTTTAGGCTATGAGCTTTCTGACTTGTATTTCTACTCT 946
 890 TGACCCGCTCTAACTATAGGTATCGCGTTTCTGAGACGTGATCCCGCTTCCTG 949
 947 TTCTGCTTACCAATTTGCTGAGAGGCTCATGTAATTTACGCTCTGTTTACAGTCG 1006
 950 ATCTTGTCTCCAACTGCGCTTAAGCTTTGCGGTCTGCTCTATCAAGCTTTGCGG 1009
 1007 CGGATTCACATTTGAGAGTGTGATGATCACTTGTCTTATGTTTACACTGCTTT 1066
 1010 GCGGATTCAGCACTGCACTTCAAGCTTCAGCACTTCTCGGGGAGCAATAGCTGGGCC 1069

1067 GCTAGCGGTAAATGATGTTGTTTACACAGAGACAAAGGCGACGCTCAACATACACTTC 1126
 1070 CCCAAGGCGCACTAGTGTGAGAGAGACAGAAAGGACATGATATCACTGCGCC 1129
 1127 TCGTGTGGGATTTGTTTATGTTGCTGCTGCACTTTCAGATTGACATCATCTGTTTC 1186
 1130 ACCGTGATGATGATGTTGTTGTTGCTGCTGCACTTTCAGATTGACATCATCTGTTTC 1189
 1187 AAGATGCTTAAGTGCATTTTACAGAAATCTACCCATTTGTAACAACTTTGCCAGAA 1246
 1190 TAGGCTCCGCGTGTGACCTTACAGAGATGATGCGCTTGTGCTCGGACTTGTGAAGA 1249
 1247 GCATATATTTGCTCTATGAAGTGTACATGATGAGAGGCGCAATTA 1291
 1250 GACGGGATCCGTATAGAGCTTCGGGTTTGGAGCGACGCTTA 1294

RESULT 7
 US-09-313-294A-1966
 ; Sequence 1966; Application US/09313294A
 ; Patent No. 6476212
 ; GENERAL INFORMATION:
 ; APPLICANT: Lalquid, Raghunath V.
 ; APPLICANT: Ito, Laura Y.
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OR INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 ; FILE REFERENCE: PL-0017 US
 ; CURRENT APPLICATION NUMBER: US/09/313,294A
 ; NUMBER OF SEQ ID NOS: 7600
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1966
 ; LENGTH: 291
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 6476212 700551823H1
 ; LOCATION: 256
 ; OTHER INFORMATION: a, t, c, g, or other

US-09-313-294A-1966

Query Match 8.3%; Score 122.6; DB 4; Length 291;
 Best Local Similarity 65.3%; Pred. No. 1.8e-28;
 Matches 179; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

940 TACTCTTCTGCGCTACCAATGCGCTGAGAAAGGCTCATGATTTACAGTCTGTTAG 999
 7 TGTGTGCTTCTGCGCTGCGCAATGCTGGAAGAGGCTCGGTTGTCTTTACGCTCA 66
 1000 CAGTCCGCGGTTTCCAACTTGGCAGTTGATGATCACTTGTCTTAAATGTTTACA 1059
 67 CCATGCGGGGATTAAGACAGTCAATTTGCTGTAACACTTCTGTCGAGAGTATG 126
 1060 CTGTTGCTTACCGGTAATGATGTTTCCACAGCAGCAAAAGGCGACGCTCAACATA 1119
 127 TCGGGGCAACCAAGGCAATGACTGTTTGAAGAGCAGCGCAGGCAAGCTTCGATCC 186
 1120 CAGCTTCTGCTGTGAGGATGTTTCAATGATGAGGCTGACCTTTCGATTGAGCATATC 1179
 187 TGTGCTCTCTTGAATGATGATGTTTCAAGGCTGAGGCTTTCGATTGAGACCATATC 246
 1180 TGTTCACAGATGCTTAAGTCCATTTTCAGGA 1213
 247 TGTTCCTCCNCTACTAGTGCACCTCCGTA 280

RESULT 8
 US-09-313-294A-3256
 ; Sequence 3256; Application US/09313294A
 ; Patent No. 6476212

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300.USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-834-033A-1

Query Match 4.0%; Score 58.6; DB 3; Length 1617;
Best Local Similarity 52.2%; Pred. No. 4.8e-08;
Matches 130; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 453 ACCTGGGCTCATCTTGTCTGCTGTTGCTTAATGGGTATGCTTCCAGAGTGTGG 512
DB 518 ACCCTGCCAAGTGTCTGCTGCTGCTGCTTGGGTCTGTCTGGCAGAGTGGATGG 577
QY 513 GTGGGGCATGATTTCTGTCACTACCAAGTTATGCCCTAACCCTAAGCTTATCGTCTTTT 572
DB 578 TTGGCTCAGACTTTTGTGATCACCAGTCTTCCAGACCGTTTGGGGTATCTTTTC 637
QY 573 CAATCATTCAGAGAAATGTGATGCTGTGTTAGTTGATGTCAGTAAGTTGACCAT 632
DB 638 GGGCGCTTTCTGGAGAGTGTCTGCCAGGGCTTCTGCTCGTGGTGAAGACAGAC 697
QY 633 AACACCCATCACTTTCCTGTATATAGCGCCCAATCTGATCTGATATTCAGCACCTTCT 692
DB 698 AACACTCAGCAGCGCCGCCCAACGTCACAGCGGAGATCCGACATTCACACCCCT 757
QY 693 ATAATTGCC 701
DB 758 CTGTTGACC 766

RESULT 11
US-09-363-574-1
Sequence 1, Application US/09363574
Patent No. 6136574
GENERAL INFORMATION:
APPLICANT: KNUZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YONG-SHENG
APPLICANT: THURMOND, JENNIFER
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-09-363-574-1

Query Match 4.0%; Score 58.6; DB 3; Length 1617;
Best Local Similarity 52.2%; Pred. No. 4.8e-08;
Matches 130; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 453 ACCTGGGCTCATCTTGTCTGCTGTTGCTTAATGGGTATGCTTCCAGAGTGTGG 512
DB 518 ACCCTGCCAAGTGTCTGCTGCTGCTGCTTGGGTCTGTCTGGCAGAGTGGATGG 577
QY 513 GTGGGGCATGATTTCTGTCACTACCAAGTTATGCCCTAACCCTAAGCTTATCGTCTTTT 572
DB 578 TTGGCTCAGACTTTTGTGATCACCAGTCTTCCAGACCGTTTGGGGTATCTTTTC 637
QY 573 CAATCATTCAGAGAAATGTGATGCTGTGTTAGTTGATGTCAGTAAGTTGACCAT 632
DB 638 GGGCGCTTTCTGGAGAGTGTCTGCCAGGGCTTCTGCTCGTGGTGAAGACAGAC 697
QY 633 AACACCCATCACTTTCCTGTATATAGCGCCCAATCTGATCTGATATTCAGCACCTTCT 692
DB 698 AACACTCAGCAGCGCCGCCCAACGTCACAGCGGAGATCCGACATTCACACCCCT 757
QY 693 ATAATTGCC 701
DB 758 CTGTTGACC 766

RESULT 12
US-09-363-526-1
Sequence 1, Application US/09363526
Patent No. 6410288
GENERAL INFORMATION:
APPLICANT: KNUZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YONG-SHENG
APPLICANT: THURMOND, JENNIFER
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,526
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651

REFERENCE/DOCKET NUMBER: CGAB-201 USA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 433-4150
 TELEFAX: (415) 433-8716
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1617 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 US-09-363-526-1

Query Match 4.0%; Score 58.6; DB 4; Length 1617;
 Best Local Similarity 52.2%; Pred. No. 4.8e-08;
 Matches 130; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 453 ACCTGGGCTCATTTGCTGCTGTTGCTTAATGGGTAATGCTATGCTCAGAGTGTGG 512
 DB 518 ACCCTGCCAAGCTGCTCGGCTTGGGCTGTTGCGCAGCAGTGGGATGG 577
 QY 513 GTGGGGCATGATCTTGTCTACTACCAAGTTATGCTTAACCTTAATCGCTTTT 572
 DB 578 TTGGCTCAGACCTTTTGCATCACAGCTCTCCAGACCGTTTCTGGGCTGATCTTTTC 637
 QY 573 CAATATTCAGCAAAATGATGCTGCTGTTAGTGTTCAGTGGTGAAGTTGACCAT 632
 DB 638 GGGGCTTCTTGGGAGGTGTCTGCGAGGGCTTCTCGCTCTGTTGGTGAAGCAAGCAC 637
 QY 633 AACACCATCATCTTGTGCTGTAATAGGCGCAATCTGATCTGTAATTCAGACCTTCT 692
 DB 698 AACACTCAGCAGCCGCCGCCAAGTCCAGCGGAGATCCGCAATGACACCCACCT 757
 QY 693 ATATATGCC 701
 DB 758 CTGTTGACC 766

RESULT 13

US-09-330-235-17
 ; Sequence 17, Application US/09330235
 ; Patent No. 6459018
 ; GENERAL INFORMATION:
 ; APPLICANT: Knutson, Debbie
 ; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS
 ; FILE REFERENCE: MOCO.156.00US
 ; CURRENT APPLICATION NUMBER: US/09/330,235
 ; PRIOR FILING DATE: 1999-06-10
 ; PRIOR FILING DATE: 1998-06-12
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 17
 ; LENGTH: 1617
 ; TYPE: DNA
 ; ORGANISM: Mortierella alpina
 US-09-330-235-17

Query Match 4.0%; Score 58.6; DB 4; Length 1617;
 Best Local Similarity 52.2%; Pred. No. 4.8e-08;
 Matches 130; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 453 ACCTGGGCTCATTTGCTGCTGTTGCTTAATGGGTAATGCTATGCTCAGAGTGTGG 512
 DB 518 ACCCTGCCAAGCTGCTCGGCTTGGGCTGTTGCGCAGCAGTGGGATGG 577
 QY 513 GTGGGGCATGATCTTGTCTACTACCAAGTTATGCTTAACCTTAATCGCTTTT 572
 DB 578 TTGGCTCAGACCTTTTGCATCACAGCTCTCCAGACCGTTTCTGGGCTGATCTTTTC 637
 QY 573 CAATATTCAGCAAAATGATGCTGCTGTTAGTGTTCAGTGGTGAAGTTGACCAT 632

DB 638 GGGGCTTCTTGGGAGGTGTCTGCGAGGGCTTCTGCTGCTGTTGGAAGCAAGCAC 697
 QY 633 AACACCATCATCTTGTGCTGTAATAGGCGCAATCTGATCTGTAATTCAGACCTTCT 692
 DB 698 AACACTCAGCAGCCGCCGCCAAGTCCAGCGGAGATCCGCAATGACACCCACCT 757
 QY 693 ATATATGCC 701
 DB 758 CTGTTGACC 766

RESULT 14

US-09-439-261-38
 ; Sequence 38, Application US/09439261
 ; Patent No. 6428990
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pradip
 ; APPLICANT: Leonard, Amanda E.
 ; APPLICANT: Huang, Yung-Sheng
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
 ; FILE REFERENCE: 6295 US.P2
 ; CURRENT APPLICATION NUMBER: US/09/439,261
 ; CURRENT FILING DATE: 1999-11-12
 ; PRIOR APPLICATION NUMBER: US 08/833,610
 ; PRIOR FILING DATE: 1997-04-11
 ; PRIOR APPLICATION NUMBER: PCT/US98/07422
 ; PRIOR FILING DATE: 1998-04-10
 ; PRIOR APPLICATION NUMBER: US 09/227,613
 ; PRIOR FILING DATE: 1999-01-08
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 38
 ; LENGTH: 449
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (5)..(5)
 ; OTHER INFORMATION: k = g or t/u at position 5
 ; NAME/KEY: misc feature
 ; LOCATION: (6)..(6)
 ; OTHER INFORMATION: m = a or c at position 6
 US-09-439-261-38

Query Match 3.9%; Score 57.4; DB 4; Length 449;
 Best Local Similarity 58.5%; Pred. No. 5.4e-08;
 Matches 100; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 1080 GATTGTTTACGAGCAGCAAAAGGCGCATCAATACATACAGCTTCTGCTGGTGGAT 1139
 DB 167 GACTGGTTTCCACCCAGCTCCAGGCCACATGCAATGTCACAAAGTCTGCTCAATGAC 226
 QY 1140 TGGTTTCATGTTGGCTGCTGCACTTTCAGATTAGCATCATCTGTTCCAGAGTCTTAAG 1199
 DB 227 TGGTTTCATGTTGGCTGCTGCACTTTCAGATTAGCATCATCTGTTCCAGAGTCTTGA 286
 QY 1200 TGGCATTTGAGGAAATCTCACCATTGTTGACAACTTTGCCAGAGCAT 1250
 DB 287 CAAATATTCACAAAGTGGCTCCCTGCTGTCAGTCTTGTGTCAGAGCAT 337

RESULT 15

US-09-227-613-37
 ; Sequence 37, Application US/09227613A
 ; Patent No. 6432684
 ; GENERAL INFORMATION:
 ; APPLICANT: Mukerji, Pradip
 ; APPLICANT: Leonard, Amanda E.
 ; APPLICANT: Huang, Yung-Sheng
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
 ; FILE REFERENCE: 6295 US.P1
 ; CURRENT APPLICATION NUMBER: US/09/227,613A

LENGTH: 1685 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-10-029-756-4

Query Match 38.0%; Score 559.4; DB 14; Length 1685;
 Best Local Similarity 62.8%; Pred. No. 5,5e-164;
 Matches 885; Conservative 0; Mismatches 522; Indels 3; Gaps 1;

```

QY 60 AAGAGACATTTGCGAAGAGACCTTGAAGAGATAGACACGAGAGATTATGATC 119
DB 59 AAGAAATACATTACCTGAGATGAGACTCAAGAACAGATTAACCCGAGATCTATGATC 118
QY 120 TCTATCAGGGAAGATTACGATATCTCAAGTGAATAAGAGATCCCGGTGTGAG 179
DB 119 TCGATTCAGGGAAGGCTATGATGTTCCGATTTGGGTGAAGACATCCAGGTGGCAGC 178
QY 180 CTCGCAATGTTAAGTTTGCAGGCAAGATGTCATGATGCTTCAATGCTTACCATCT 239
DB 179 TTTCCTTGAAGAGCTTCTGCTGCAAGAGTAATGATGATGTTGCAATTCATCT 238
QY 240 GGCATGCTTGGCAATPACTTGAAGGTTCTTACTGGTACTACGTTCAAGATTAATCT 239
DB 239 GCGCTACATGGAAGATCTTGAATGTTTCACTGGATTTATCTTAAGATTAATCT 238
QY 300 GTCTCTGAGATGTCAGAGACTACAGAGGCTGCTCTGATGTTTCTAAGATGGGTTG 359
DB 299 GTTCTGAGGTTTCTAAGATTAAGAGACCTGTTGATGTTTCTAAGATGGGTTG 358
QY 360 TTCAAGACACGAGCAAGAGGCTACTGCTCAATCTTTTCGCTGCTGCTGCT 419
DB 359 TATGACAAAAGGCTATATTATGTTGCAACTTTGCTTATAGAAATGCTGTTGCT 418
QY 420 CTGAGTGTTCAGGCTGCTCTCTACTGCAAGAGACCTGGGCTCATCTTCTGCTGTTG 479
DB 419 ATGAGTGTATATGGGTTTGTGTTGAGAGGTTTGTGATCACTTTTCTGCGGTGT 478
QY 480 CTATGGGATGCTATGCTCTCCAGAGTGTGGTGGGAGATGTTCTTCTACTACAA 539
DB 479 TTGATGGGTTTCTTGGATTCAGAGTGTGGATGATGATGCTGGGCAATTAATG 538
QY 540 GTATGCTTACGAGTATGCTTATGCTTTTCAATCAATGAGAAATGATGCT 559
DB 539 GTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 558
QY 600 GGTGTTAGTGTGATGAGAGGTTGAGACCATTAACACCATCATCTTGGCTGTATAGC 659
DB 599 GGAATAGATGTTGGTGGTGAATGGAACCATTAATGACATGCTGCTGTATAGC 658
QY 660 GCCAATCTGATCTGATTAATGACACCTTCTATTAATGCTATGCTTATGCTTATGCT 719
DB 659 CTGGAATATACCTGATTAATGACATTAATGCTTCTTGTGCTTCAAGTTTGT 718
QY 720 AACTCCCTTACATCATCTATCAACTGCAAAATGACATATGCGGCTCAGGTT 779
DB 719 GGTTCATCTCTCTCTCTATGAGAAAGTTGCTTATGCTTATGAGAAATGCT 778
QY 780 TTGTGATGCTTACGAGTGAATTTATCTGATGCTTATGAGGTTAGGCTTATCTT 839
DB 779 TTGTGATGCTTACGAGTGAATTTATCTGATGCTTATGAGGTTAGGCTTATCTT 838
QY 840 TTATTTCTGCTTTTAAAGGTGTTTTCACAAACAAAGGTTATCAAGAGAGTCAAG 899
DB 839 TATGTAATCTCTCTATTAATGTTGTTGACCAAGAGAAAT---GTGCTTATGAGGCTCAG 895
QY 900 GAAATTTTAGGATGAGGCTTCTTCACTTGTGATTTCTACTCTTCTTCTGCGCTACCC 959
DB 896 GAACCTTTGGAGAGCTTGAAGTCTCGATTTGGAACCGTGTGCTTGTGTTTGTGCGCT 955
QY 960 AATTGGCTGAAAGGCTCATGTAATTTCAAGTCTGTTAGACAGTCCGCGGTTCCAACT 1019

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DB 956 AATTGGGGAAGAAATATGTTTGTATGCAAGTTATCAAGTCAAGTGAATGCAACAA 1015
QY 1020 TGGCACTTACGCTTGAATCACTTGTCTTAATGTTTACAGCTGTTTGGCTACGGTAAT 1079
DB 1016 GTTCAGTCTTCTTGAACCACTTCTCTTAAGGTTTATGTTGAAGAGCTTAAGGAAAT 1075
QY 1080 GATTGGTTTCAACAGAGACAAAGGAGGCTCAACATTAACAGCTTCTGCTTGGTGGAT 1139
DB 1076 AATTGGTTTGAAGAAACAAACGATGAGACATTTGATTTCTGCTTCTGATGAT 1135
QY 1140 TGGTTTCAATGTTGCTTGAACCTTTCAGATTGACATCATCTGTTTCCAAAGATGCTTAAG 1199
DB 1136 TGGTTTCAATGTTGATGCAATTCCAATTTGAGCATCATTTGTTTCCAAAGATGCTTGA 1195
QY 1200 TGGCATTTGAGAAATATTCACCATTTGTAACAACTTTGCAAGAGATTAATTTGTCTC 1259
DB 1196 TGCACCTTAAGAAATTCGCGCTTACGATGATGATGATGCAAGAAACATTAATTTGCT 1255
QY 1260 TATGAATGCTTACATGTTGGAGGCAATTAATGATTAATCTCAACCTGCTGCTGTG 1319
DB 1256 TACAAATTAATGATCTTCTTCCAAAGGCAATGAAATACACTGAAACATTTGAGAAACAA 1315
QY 1320 GCTATGAAGCTTAAGAGTGTATCAAGAGGCTTCCCAAGAAATGCTTGGGAAGCAATG 1379
DB 1316 GCATTCAGGCTTGGATTAATCAAGAGGCTCCGAAAGATTTGATGAGGAGCTCTT 1375
QY 1380 AACATTTGGGGAACCTTATTAACATCAAGTGTCTTCCGCTAAAGCTTCCAG 1439
DB 1376 CACACTCATGTTAAATTAACCTTATGATTAATTAATGAGATTAATGATCTCTTA 1435
QY 1440 TCCCAATGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1469
DB 1436 TGTGTTGCTTGTCTTGTGTTCTTACTTGT 1465

```

RESULT 2

US-09-938-842A-558
 ; Sequence 558, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938, 842A
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227, 866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264, 647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300, 111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 558
 ; LENGTH: 1350
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-938-842A-558

Query Match 29.2%; Score 429.4; DB 10; Length 1350;
 Best Local Similarity 58.1%; Pred. No. 2.7e-123;
 Matches 776; Conservative 0; Mismatches 556; Indels 3; Gaps 1;

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QY 60 AAGAGACATTTGCGAAGAGACCTTGAAGAGATAGACACGAGAGATTATGATC 119
DB 19 AAAAAATCATTTAGCAAGAGATCTTAATAAACAACAATCTGAGATCTATGATC 78
QY 120 TCTATCAGGGAAGATTATGATATCTCAAGTGAATAAGAGATCCGCGTGTGAG 179

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Db      79 GCGATTCAAGGCGAGCTACACGCTCCGATTGGATTAAATCATCCCGAGGCGAC 138
Qy      180 CTCCTCATTTAGTTTGGCGGCAAGATGCTAGATGCGTTTCTTACCTTCTTCT 239
Db      139 ACCGATATCTCATCTCGTTGTCAGAGCATGATGCTTCAATCGATTCTATCCC 198
Qy      240 GGCAGCTGTTGGCAATACCTTGAACAGTTCCTTACTGAGTACTAGCTTCAAGATTA 299
Db      199 GGAACGGCTTGGACACATCTCGACATCTTCAACCGGTTACACATCAGAGATTTCCA 258
Qy      300 GTCTCTGAGATGTCAGAGATCAAGAGGCTCTCTCTGAGTTTCTAAGATGGGTTTG 359
Db      259 GTCTCCGAGATCTCAGCGGATTTACCGTGTATGGCTGCGAGTTTGTAACTCGGCTTC 318
Qy      360 TTCAAGACACAGGCGCAAGGGGCTCTACTGCTAAATCTTTTCTGCTGTGTTGCT 419
Db      319 TTGCAAAACAAAGGTCAGCTTACTCTCTACCTCTGACCTTCTGCGCGCAAGTTCTC 378
Qy      420 CTGAGTGTATAGGCTTCTCTCTCTCAAGAGCAGCTGGGCTCATCTTGTCTGTTTG 479
Db      379 GGAATCTCTACGCTGTTTGGCTTGTACCTCGCTTCTGCTTACCAATCGCGCGG 438
Qy      480 CTAAATGGTATGCTATGCTCCAGAGTGTGGTGGGCGATGTTCTTGTCTACTACCA 539
Db      439 CTCTCGGCTCTCTCTGATCCAGAGCGCTTACATAGTCAAGATTCTGGTATTAAGT 498
Qy      540 GTTATGCCCTAACCGTAAGCTTAATGCTCTTTTCAATCATTTGACAGAAATGATGCT 599
Db      499 ATCATGTGCAAAATCTTATTAACAATTCGCTACACTTCTCCGCTAACTGTCTCAC 558
Qy      600 GGTGTAGTATGCTAGTGTGAAGTGGACATTAACCATCATCTTGCCTGTATATAG 659
Db      559 GGAATCTCATGCGCTGCTGAGAAATGACATCAACATGCTCATATCTAGCTTTGAAC 618
Qy      660 GCCAATCTGATCTGTATATGACACCTTCTATATATGCAATATCCCAAAATTTTTC 719
Db      619 CTCGATTACGATCCAGATCTACAAACATCCCTGTCTGCGCGCTCCACCAATCTTC 678
Qy      720 AACTCCCTTACATCATCTATCACTCACTGCAAAATGACCTATATGCGCTGCAAGT 779
Db      679 TCCCTATTAACCTCGAGATTTCTACATCGAAATCAAGTTGATCAAGTGGGAATTC 738
Qy      780 TTGTAGAGCTTTCAGAGCTGACATTTTATCTGCATGTTTAAAGCTTAAAGCTTAT 839
Db      739 TTAGTACGCTATCAACATTTACTTATATCAAGTTATGCTTGAAGATCAATCTTC 798
Qy      840 TTATATCTGTCTTTTAAAGTGTGTTTTCACACAAAGGATATATACAGAACTCAG 899
Db      799 TTCATTCAAAAGTTTCTCTTGTCTCTTCCAAAGTGA--GTACCAATGTGCTTAA 855
Qy      900 GAAATTTTAAAGCTATGACGCTTCTGACTGTGATTTCTTACTCTTCTGCGCTAAC 959
Db      856 AACTTGCAGGATCTTAACTCTCTGACTGTGCTTCCCACTTACTCTCATGTCTAAC 915
Qy      960 AATGAGCTGAAGAGGTCATGTTTTCAGTCTGTTTAAAGCTGCGCGGGTTCACAAAT 1019
Db      916 AACTGAGCTGAGAGATTTCTTCTGCTTTCACAGCTTCAACGCGGCTTCAACAC 975
Qy      1020 TGGCAGTTCAGCTTGAATCACTTGTCTTATATGTTTAACTGGTTCAGCGGTAAT 1079
Db      976 ATTCAATTAACGCTTAACATTTTCTGCTGATGTCTAAGTTGTCCACCCAGCTTAC 1035
Qy      1080 GATGTGTTTCAACAGACAGACAAAGGCGAGCTCAACATTAACAGCTTCTGCTGGT 1139
Db      1036 GACTGTGTGAGAGAGAGGCGGAGAACATGATATCTTGTATCATATCATGAT 1095
Qy      1140 TGGTTCATGATGCGCTGACCTTTCAGATTGAGCATCATCTGTTTCAAGAGATTAAG 1199
Db      1096 TGGTTCATGATGCGCTGACCTTTCAGATTGAGCATCATCTGTTTCAAGAGATTAAG 1155
Qy      1200 TGGCATTTCAGAGAAATCTCAACCATTTGTGAACAAATTTGCCAGAGATTAATTTG 1259
Db      1156 TGGCATCTCCGAGAAATTTCTCCGTTGTTCAAGAGCTTTGCAAGAGATTAATTTCCG 1215

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Qy      1260 TATGAACGTCTAACCATGAGGAGCAATAATGATATCTTCAACCTGCGTGTG 1319
Db      1216 TATGAGATATGTCGTGGTTTGAAGCAATGCTTGAACATTAACTTTGAAGACAGA 1275
Qy      1320 GCTATGAGAGCTAAGAGATTTACCAAGCCAGTTCCCAAGACATGCTTGGAGAGCAT 1379
Db      1276 GCTTATCAAGCTAAGAGAGCTGCTAATCCGTTGTTAAGAACTTGTGGAGAGCTT 1335
Qy      1380 AACACTTTCGGGTGA 1394
Db      1336 AATACTCATGCTTAA 1350

RESULT 3
US-10-029-756-26
; Sequence 26, Application US/10029756
; Publication No. US20020108147A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/029,756
; FILING DATE: 21-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/934,254
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 48..1406
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 48..1406
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-029-756-26

Query Match      25.7% Score 377.8; DB 14; Length 1702;
Best Local Similarity 57.6%; Pred. No. 4.8e-107;
Matches 717; Conservative 0; Mismatches 522; Indels 6; Gaps 2;

Qy      50 GGAAGAGCCAAAGAGACATTTTCCAGACAGACCTTGCACAAAGATTAAGCAACAGAGAGA 109
Db      53 GGGCGAAGCTAAGAGATATATACGCGGAGAGACCTCCGCGCACAAAGATCCGGCGA 112

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QY 110 TTATGATCTATCAAGGAAAAAGTTAAGATATCTCAAGTGAAGACTAAAGCATCC 169
 DB 113 TCTGTGATCTTCATCCAGGGAAGAGTCTACAGTGTCTTCGGGGGGGAGGAGCACC 172
 QY 170 CGGTGTGAGCTCCCATTTGTTAAAGTTTGGCCGCAAGATGTCACTGATGCTTATGTC 229
 DB 173 CGCGGGGAGAGTCCCGCTCTCTCAGTCTGGCCGCAAGAGTGTCAAGCAGCCCTTATGTC 232
 QY 230 TTACCATCTGGGAGCTGGGCAATACCTGACAGTTCTTTATCTG---GATCTAGT 286
 DB 233 GTACACCCGGGAGCGGGTGGCGGCAATGTGATCCCTCTTCAACCGGCTACTATCACT 292
 QY 287 TCAAGATTACTCTGTCTGAGATGTCCAGAGTCAAGAGAGGCTCGTCTGAGTTTC 346
 DB 293 CAGGACTTGAAGTGTGAGATCTCCAGAGTACCGAGAGCTTTGAAACGATGTC 352
 QY 347 TAAGATGGTTTGTTCAGACACCGGCAAGGGGTACTGCTCAATCTTTTTCGTGTC 406
 DB 353 GCGGTCCGGGATCTTCAGAAAGAGGCGCACACATCATGTGAGCGTTCGGCGGTTC 412
 QY 407 TGTGTTTGTGCTGTGATGTCTTACGTTTCTCTACTGCAAGAGCACCTGGCTCATCT 466
 DB 413 GGTATGATGGCGCAATCGTCTACCGCGTGGCGTGGAGTCCGTCCGAGTTCACT 472
 QY 467 TTGCTCTGTTGCTTAATGGGTATGCTATGAGCTCAGAGTGTGGTGGGCGCATGTC 526
 DB 473 GCTCTGGGGGCACTGCTGGGCTTGTGTGATCTCAAGCCGCGATGTGGCCATGATC 532
 QY 527 TTGTCACTACCAAGTATGCTTAAACGTTAATGCTTTTTCATTCATTTGAGG 586
 DB 533 CGGCAATACCAAGTATGCTTAAACGTTAATGCTTTTTCATTCATTTGAGG 592
 QY 587 AATGTGATGT 646
 DB 593 CAACATCTTAACCGGAATGAGCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 652
 QY 647 TGCCTGATATAGGCGCAATCTGATCTGATATTCAGACACCTTCTTAAATTTGCAATC 706
 DB 653 CGCTGCAAGAGCTGTGACACTGACACCCGCACTCCAGACATCCCGTATATCCGCTTC 712
 QY 707 CCAAAATTTTCACTCCCTTACATCATATCATCACTGCAAAATGACTATGATG 766
 DB 713 CACCCGACTCTTCACTCCATCACTCGTCTTCTATGCGGAGTCTGAAATTCAGCA 772
 QY 767 CGCTGCAGTCTTTTGTAGCTTTCAGCACTGACATTTTATCTCTATTTTAAAGCT 826
 DB 773 AGTGGACCGGTCTTACGTACGCTACAGCACTGACCTACTACCCGCTCATGATCTTCG 832
 QY 827 TAGGCTTATCTTTTATCTGCTTTTAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 886
 DB 833 CCGAGTCACTCTTCACTCAAGACCTTTTATGTCTCTCAACGAGGCGCA---CGTCC 889
 QY 887 CAGAGAGTCAAGAAATTTAGGCTATGAGCTTTTCTTGAATTTCTTACTCT 946
 DB 890 TGACCGGCTCTTAACTTATGAGTATCGGGTTTCTGAGCGTGTTCGCGCTTCGT 949
 QY 947 TTCTGCTTACCAATTTGCTGAGGATGATTTTCAAGTCTCTTTTGAAGTTCG 1006
 DB 950 ATCTTGTCTCCCAACGAGCTGAAAGCTGTGCGGTCTGCTCATCACTTTTGGGCTAC 1009
 QY 1007 CGGATTCACATTTGAGCTTGAATCACTTTGCTTAAATTTTAACTGTTT 1066
 DB 1010 GGGGATTCAGACGTCCAGTTTCAAGCTTCAACCTTTCCGGGCAACATATCGGGCC 1069
 QY 1067 GCCTAGCGTATGATTTGTTTCAACGAGCAAGAGGCGCTCAACATTAAGCTTC 1126
 DB 1070 CCCCAGGGGCAACAGTGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1129
 QY 1127 TGTGTGTGAGATTTGTTTATGTTGCTGCACTTTCAATTTGAGATCATCTGTTTC 1186
 DB 1130 ACCGTGATGAGTGTGTTCTTTTGTGGGTGAGTTCCAGTGTGAGACACCATTTGTTCC 1189

QY 1187 MAGATGCTTAAAGTCCATTTAGAAATATCTCAAGTGAAGACTAAAGCATCC 1246
 DB 1190 TAGGTCGGCGGAGAGTGAAGATGAGTGGCCCTTGTGGGACTTGTGTAGAA 1249
 QY 1247 GCATTAATTTGTCTTATGAATCTCTACATGTGGAGGCCAATAA 1291
 DB 1250 GCAAGGAGTCCGATATGAGTCTTGGGTTTGGAGAGAGCTTA 1294
 RESULT 4
 US-09-770-149-494/C
 ; Sequence 494, Application US/09770149
 ; Patent No. US2002005963A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goriach, Jörn
 ; APPLICANT: An, Yong-Qiang
 ; APPLICANT: Hamilton, Carol M.
 ; APPLICANT: Price, Jennifer L.
 ; APPLICANT: Raines, Tracy M.
 ; APPLICANT: Yu, Yang
 ; APPLICANT: Rameaka, Joshua G.
 ; APPLICANT: Page, Amy
 ; APPLICANT: Mathew, Abraham V.
 ; APPLICANT: Ledford, Brooke L.
 ; APPLICANT: Moesner, Jeffrey P.
 ; APPLICANT: Haas, William David
 ; APPLICANT: Garcia, Carlos A.
 ; APPLICANT: Krickler, Maja
 ; APPLICANT: Slader, Ted
 ; APPLICANT: Davis, Keith R.
 ; APPLICANT: Allen, Keith
 ; APPLICANT: Hoffman, Neil
 ; APPLICANT: Hurlan, Patrick
 ; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 ; FILE REFERENCE: 2024 (PARA-013PRV)
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 60/178,506
 ; PRIOR FILING DATE: 2000-01-27
 ; NUMBER OF SEQ ID NOS: 99
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 494
 ; LENGTH: 657
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-770-149-494
 Query Match 12.0%; Score 176.4; DB 9; Length 657;
 Best Local Similarity 59.9%; Pred. No. 3,7e-44;
 Matches 294; Conservative 0; Mismatches 197; Indels 0; Gaps 0;
 QY 917 AGCTTCTTGAAGTGTGATTTCTTACTCTTCTGCTTACCAATTTGCTTAAAGGCT 976
 DB 629 AGCTTCTGAGTGTGATTTCTTACTTGTATGCTATGCTTCAACAGTGGCTGAGATT 570
 QY 977 CATGATTTCAAGTCTCTGTTTACAGTCCGCGGTTCAACATTTGCAAGTTCAGCTTGA 1036
 DB 569 CTCTTCTGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 510
 QY 1037 TCATTTGCTTCAAGTGTGATTTCAAGTGTGATTTCTTACTTGTGCTTCAAGTGTGATTT 1096
 DB 509 CCAATTCGCTGCTGATGTCTACGTTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGT 450
 QY 1097 GACAAAGGCGAGCTCAACATTAACAGCTTGTGCTGTGAGTGTGATTTGATGAGTGT 1156
 DB 449 AGCGGGGGAACATGATATCTTGTAGATCATATGATGATTTGATTTGATTTGATTT 390
 QY 1157 GCATTTGATGATGATGATGATTTTCAAGAGTGTGATTTGATTTGATTTGATTTGATTT 1216
 DB 389 ACAGTTTCAAGTGTGATGATGATTTTCTTCTTCAAGTGTGATTTGATTTGATTTGATTT 330
 QY 1217 CTCACCATTTGATGATGATTTTCTTCAAGAGTATTTGCTTATGAACTGCTACAT 1276

Db 329 TTCTCCGCGTTCAGAGCTTTGCAAGACGATTAATCTCCGTATAGAGATGTCG 270
 QY 1277 GTGGGAGGCGCAATAAATGTATATCCACCCGCGTGTGTGGCTATGGAAGCTAAGA 1336
 Db 269 GTTTGAGCAAAATGTTGACCATTAACCTTTGAAGACGAGCTTATCAAGCTGAAGA 210
 QY 1337 TGTTCACCAAGCCAGTTCACCAAGACATGCTGTGGGAAGCAATGACACTTTCGGTGAAC 1396
 Db 209 CGTGGCTAATCCGCTGTATGAACCTTGTGGGAAGCTTTGAATATCATGCTTAAT 150
 QY 1397 CTTATNAACA 1407
 Db 149 GATTTATATCA 139

RESULT 5
 US-09-770-444-39
 ; Sequence 39, Application US/09770444
 ; Patent No. US2002023280A1
 ; GENERAL INFORMATION:

APPLICANT: Gorlach, Jorn
 APPLICANT: An, Yong-Qiang
 APPLICANT: Hamilton, Carol M.
 APPLICANT: Price, Jennifer L.
 APPLICANT: Raines, Tracy M.
 APPLICANT: Yu, Yang
 APPLICANT: Rameaka, Joshua G.
 APPLICANT: Page, Amy
 APPLICANT: Matthew, Abraham V.
 APPLICANT: Ledford, Brooke L.
 APPLICANT: Moesener, Jeffrey P.
 APPLICANT: Haas, William David
 APPLICANT: Garcia, Carlos A.
 APPLICANT: Kricke, Maya
 APPLICANT: Slader, Ted
 APPLICANT: David, Keith R.
 APPLICANT: Allen, Keith
 APPLICANT: Hoffman, Neil
 APPLICANT: Hurben, Patrick
 TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 TITLE OF INVENTION: thaliana
 FILE REFERENCE: 2027 (PARA-016PRV)
 CURRENT APPLICATION NUMBER: US/09/770,444
 CURRENT FILING DATE: 2001-01-26
 PRIOR APPLICATION NUMBER: 60/178,502
 PRIOR FILING DATE: 2000-01-27
 NUMBER OF SEQ ID NOS: 999
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 39
 LENGTH: 476
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1)..(476)
 OTHER INFORMATION: n = A,T,C or G
 US-09-770-444-39

Query Match 9.1%; Score 133.2; DB 9; Length 476;
 Best Local Similarity 55.4%; Pred. No. 1e-30;
 Matches 255; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 190 TAAATTTTGGCGGCAAGATGATGATGCTTCAATGCTTCAATCCTGGACGCTT 249
 Db 16 TCATATCTGTTGTTCAAGAGCTACCGATGCTTCAATCGATTTCAATCCGGAACGCTT 75
 QY 250 GGCATATCCTTGACAGATTTTACTGGGTACTAAGTCAAGTACTGCTGTGGA 309
 Db 76 GGCACATCTCGACATCTCTTCAACGCGTTACACATCAGAGATTTCAAGTCTCGAAG 135
 QY 310 TGTCAAGACTCAGAAAGGCTGCTCTGAGTTTCTAAGATGAGGTTGTTCAAGAC 369

Db 136 TCTACGCGATTAACCGTCTATAGCTGCCGAGTTTGTAACTCGCTCTTTCAAGACA 195
 QY 370 CAGGCAAGAGGGATCTACTGCTCAATCTTTTGTGTGTGTGTTGCTGTGAGTGT 429
 Db 196 AAGGTACGTTACTCTCTACCTTACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 255
 QY 430 ACGGTCTCTACTGCAAGACACCTGGGCTCATCTTGTGTGTGTGTGTGTGTGTGTGT 489
 Db 256 ACGGTCTTGT 315
 QY 490 TGTATGCTCAGAGT 549
 Db 316 TCTCTGATCCAGAGCGCTTACATAGGTCAGATTTGTGTGTGTGTGTGTGTGTGT 375
 QY 550 ACCGTAGCTTAATGCTCTTTTCAATATGACAGAAATGTGATGTGTGTGTGTGTGT 609
 Db 376 ACMAATCTTATACAGATTGCTCAGCTTCTTNNGTAACTGTCTCACCGGAATCTCA 435
 QY 610 TTGCATGTGGAAGTTGACATTAACACCCATCACTTGTG 649
 Db 436 TCGCGTGTGGAATGAGATCAACATGCTCATCATCTAGC 475

RESULT 6
 US-09-878-574-3260
 ; Sequence 3260, Application US/09878574
 ; Patent No. US20020110548A1
 ; GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Thompson, Michael D.
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 FILE REFERENCE: 38-21 (15401)B
 CURRENT APPLICATION NUMBER: US/09/878,574
 CURRENT FILING DATE: 2001-12-21
 PRIOR APPLICATION NUMBER: 09/333,535
 PRIOR FILING DATE: 1998-06-14
 NUMBER OF SEQ ID NOS: 15775
 SEQ ID NO 3260
 LENGTH: 287
 TYPE: DNA
 ORGANISM: Glycine max.
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)..(287)
 OTHER INFORMATION: unsure at all n locations
 OTHER INFORMATION: Clone ID: LIB3028-013-Q1-B1-H6
 US-09-878-574-3260

Query Match 8.0%; Score 117; DB 10; Length 287;
 Best Local Similarity 62.9%; Pred. No. 9e-26;
 Matches 180; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 921 TTCTGACTGTGATTTCTTACTCTCTTCTGCTTACCAATGCTGGAAGGGCTATG 980
 Db 2 TTTTGATTTGTCTCTCTTATGATCTATCTCTGCAATTTGGAGAAAGGGCTATG 61
 QY 981 TATTTACGCTCTGTTAGACGTGCGGGTTTCAACATGTGACAGTTGACTTGAATCAC 1040
 Db 62 TTTGTTTGGCAGTTTGT 121
 QY 1041 TTTGCTTAAATGTTTACATGTTTGTGCTTACCGGTATGATTTGTTTACACAGAC 1100
 Db 122 TTGCGACGAGATGTATGAGGGCCACCAATGTGCATGCTGTGGAAGCAAACT 181
 QY 1101 AAGGACGCTCAATACAGCTTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1160
 Db 182 GGTGCAATTTGACATCTCTTGTCTTACATGATGATGATGATGATGATGATGATGAT 241
 QY 1161 TTTCAATTTGACATCTCTTGTCTTACATGATGATGATGATGATGATGATGATGAT 1206
 Db 242 TTCAACTTTGACATCTTGTCTTACATGATGATGATGATGATGATGATGATGATGAT 287

Db 479 AGCACTACTCTACTACATCATGATGTTCCGCCGCTGAACCTTACCGTCTCGT 538
 QY 853 TTAAG 857
 Db 539 GGGAG 543

RESULT 10

US-09-923-876-5116
 ; Sequence 5116, Application US/09923876
 ; Patent No. US20020013958A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Laligudi, Raghunath V.
 ; APPLICANT: Kamigaki, Laura Y. (Ito)
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
 ; FILE REFERENCE: FL-0012-1 CON
 ; CURRENT APPLICATION NUMBER: US/09/923,876
 ; CURRENT FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: 09/298,329
 ; PRIOR FILING DATE: 1999-04-21
 ; PRIOR APPLICATION NUMBER: 60/085,331
 ; PRIOR FILING DATE: 1998-05-05
 ; NUMBER OF SEQ ID NOS: 6332
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 5116
 ; LENGTH: 265
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20020013958A1 700456385H1
 US-09-923-876-5116

Query Match 4.5%; Score 66.2; DB 9; Length 265;
 Best Local Similarity 55.4%; Pred. No. 7.2e-10;
 Matches 128; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 646 TTGCGCTTAATAGCGCAATCTGGATCTTGATTTAGACCTTCTATTAATGCAATAT 705
 Db 2 TGGCTGCAACAGCTTGGCAACATATGCTCTTCTTACACGCGGACCTTCTGTTGCT 61
 QY 706 CCCCCAATTTTTCACACTCCCTTACATCATATATCAACAATGACCTATGATC 765
 Db 62 CCCCCAAGCTTGTGGCAACATATGCTCTTCTTACACGCGGACCTTGGCTGAGC 121
 QY 766 GCGCTGCCAGTTTGTGTTAGCTTTCAGCACTGACATTTTATCTGCAATGTTAAGC 825
 Db 122 CCGCCTCGAATTCCTCATCAGCTACAGCACTGACCTTCTACCCGGTAATGTCATCG 181
 QY 826 TTAGCTCATCTTTTATTTCTCTTTTAAAGTGTGTTTTCACAACA 876
 Db 182 CCAGGATTAATCTTCTGCGGCGAGTCCGCTGTCTTCTCTGACCGAAGA 232

RESULT 11

US-09-923-876-5116
 ; Sequence 5116, Application US/09923876
 ; Patent No. US20020013958A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Laligudi, Raghunath V.
 ; APPLICANT: Kamigaki, Laura Y. (Ito)
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
 ; FILE REFERENCE: FL-0012-1 CON
 ; CURRENT APPLICATION NUMBER: US/09/923,876
 ; CURRENT FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: 09/298,329
 ; PRIOR FILING DATE: 1999-04-21
 ; PRIOR APPLICATION NUMBER: 60/085,331
 ; PRIOR FILING DATE: 1998-05-05
 ; NUMBER OF SEQ ID NOS: 6332
 ; SOFTWARE: PERL Program

; SEQ ID NO 5116
 ; LENGTH: 265
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20020013958A1 700456385H1
 US-09-923-876-5116

Query Match 4.5%; Score 66.2; DB 12; Length 265;
 Best Local Similarity 55.4%; Pred. No. 7.2e-10;
 Matches 128; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 646 TTGCGCTTAATAGCGCAATCTGGATCTTGATTTAGACCTTCTATTAATGCAATAT 705
 Db 2 TGGCTGCAACAGCTTGGCAACATATGCTCTTCTTACACGCGGACCTTCTGTTGCT 61
 QY 706 CCCCCAATTTTTCACACTCCCTTACATCATATATCAACAATGACCTATGATC 765
 Db 62 CCCCCAAGCTTGTGGCAACATATGCTCTTCTTACACGCGGACCTTGGCTGAGC 121
 QY 766 GCGCTGCCAGTTTGTGTTAGCTTTCAGCACTGACATTTTATCTGCAATGTTAAGC 825
 Db 122 CCGCCTCGAATTCCTCATCAGCTACAGCACTGACCTTCTTACCCGGTAATGTCATCG 181
 QY 826 TTAGCTCATCTTTTATTTCTCTTTTAAAGTGTGTTTTCACAACA 876
 Db 182 CCAGGATTAATCTTCTGCGGCGAGTCCGCTGTCTTCTCTGACCGAAGA 232

RESULT 12

US-09-938-842A-1200
 ; Sequence 1200, Application US/0993842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Krebs, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 1200
 ; LENGTH: 405
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-1200

Query Match 4.1%; Score 60.8; DB 10; Length 405;
 Best Local Similarity 59.1%; Pred. No. 4.7e-08;
 Matches 104; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 48 ATGGAAGACCCAAAGACATTTTGGCAAGACGACCTTGGCAAGATTAAGCAACAGAGA 107
 Db 1 ATGGAGAGAGAAAGCAAGATCTTCTTTAGAGATTTGAGACATATATCAAGCTCAT 60
 QY 108 GATTATGATCTCTATCAAGGAAGATTTCATATCTCAAGTGAAGTGAAGAGCAT 167
 Db 61 GACTGTGATTTCTCATCATGAAAGGTGACCAATGACCAAGTTTCTTGAAGACCAT 120
 QY 168 CCGGTGTGAGCTCCCATTTTGAAGTTTGGCGGCAAGATGTCATGATGCGTT 223
 Db 121 CCAGGTGGGAGAGATGTTCTTCTTCTTCAACAGGTAAGATGACCAAGATGATTT 176

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RESULT 13
US-10-278-391-3
; Sequence 3, Application US/10278391
; Publication No. US20030159164A1
; GENERAL INFORMATION:
; APPLICANT: KOPCHIK, JOHN J.
;            KELDER, BRUCE
;            HUANG, YUNG-SHENG
;            KIRCHNER, STEPHEN J.
;            MUKERJI, PRADIP
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;                   SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM
;                   PRODUCTS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/278,391
; FILING DATE: 23-Oct-2002
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,578
; FILING DATE: 29-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OHU-03348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1374 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-278-391-3

Query Match          4.0%; Score 58.6; DB 13; Length 1374;
Best Local Similarity 52.2%; Pred. No. 5, 1e-07;
Matches 130; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

453  ACCTGGGCTACTCTTGGCTCTGGTTGCTAAAGGGATGCTATGCTCCAGAGTGGTTGG 512
Db      ACCCTGGCAACGCTCTCGGCTGGCTTTGGGCTGTCTGTCTGTGAGAGAGCGGATG 507
448  ACCCTGGCAACGCTCTCGGCTGGCTTTGGGCTGTCTGTCTGTGAGAGAGCGGATG 507
453  GTGGGCGCATGATCTTTGTCTACTACCAAGTATGCTTACCGTAAAGCTTATGCTTTT 572
Db      TTGGTCTACGACTTTTGGATCACCAGGCTTCCAGACCGTTTCTGGGGTATCTTTTC 567
508  CAAATCATTTGACGAGAAATGTGATTCGTGGTGTAGTCTGCATGGAGGAAGTTGACCAT 632
Db      GGGCTTCTTTGGGGAGTGTCTGCGAGGGCTTCTGCTCTCGTGGGGAAGACAGCAC 627
568  AACACCCATCACTTTGGCTGTATAGCGCCAAATCTGATCTGTATTTACAGACCTTCT 692
Db      AACATCTACACAGCGCCGCCCAACGTCACAGCGGCGAGGATCCGACACTTACACCCACT 687
628  AATATGCTC 701

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Db      688 CTGTTGACC 696

RESULT 14
US-10-191-513A-37
; Sequence 37, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paridip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295. US. D3
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatsSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5) .. (5)
; OTHER INFORMATION: k = g or t/u at position 5
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6) _ (6)
; OTHER INFORMATION: m = a or c at position 6
US-10-191-513A-37

Query Match      3.9%; Score 57.4; DB 15; Length 449;
Best Local Similarity 58.5%; Pred. No. 5.9e-07;
Matches 100; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy      1080 GATTGGTTTCACGACGACAAAGGGCAGCTCAACATPACAGCTTCTGCTGTGGGAT 1139
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      167 GACTGGGTTTCACCCAGCTCCAGGACCATGACATGTCACAAAGTCGCTTCATGAC 226

Qy      1140 TGGTTTCATGCTGGCCCTGCACATTTTCAGATTTAGACATATCTGTTCCAAAGATGCTAAG 1199
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      227 TGGTTTCAGTGGACACCTTCACCTTCACATTTTCAGATTTAGACACCATCTTTTCCACATGCTTGA 286

Qy      1200 TGCATTTTCAGGAATATCTCACCCATTTGTAACAACTTTCCAGAAAGCAT 1250
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      287 CACAATTACCAACAAGTGGCTCCCTGCTGTGACATCTTGTGTGCCAAGCAT 337

RESULT 15
US-10-191-513A-3
; Sequence 3, Application US/10191513A
; Publication No. US20030104596A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paridip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Tapas, Das
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295. US. D3
; CURRENT APPLICATION NUMBER: US/10/191,513A
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08

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: PRIOR APPLICATION NUMBER: PCT/US98/07422
: PRIOR FILING DATE: 1998-04-10
: PRIOR APPLICATION NUMBER: US 08/833,610
: PRIOR FILING DATE: 1997-04-11
: NUMBER OF SEQ ID NOS: 54
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 3
: LENGTH: 655
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-191-513A-3

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Query Match	3.9%;	Score	57.4;	DB	15;	Length	655;
Best Local Similarity	58.5%;	Pred. No.	7.5e-07;				
Matches	100;	Conservative	0;	Mismatches	71;	Indels	0;
						Gaps	0;

QY 1080 GATTGGTTTACACGACGACAAAGGGGACGGCTCAACATGACAGCTTTCGTTGGGGAT 1139

Db 161 GACTGGGTTTCCACCCAGCTCCAGGCCACATGACATGTCACAGCTGCTTCAATATAC 220

QY 1140 TGGTTTTCATGGTGGGCTGCACTTTTCAGATTGATGATCATCTGTTTCCAAGATGGCTAAG 1199

Db 221 TGGTTTCACTGACACACTTCACTTCCAGATTGAGCACCATCTTTTCCACGATGGCTCGA 280

QY 1200 TGCCATTTTCAGAAAATCTCAACCCATTGTGAAACAAACTTTGGCAGAACAT 1250

Db 281 CACAAATTACCAAAAGTGGCTCCCTGGTGCAGTCTTGTGTGCCAAGCAT 331

Search completed: January 1, 2004, 05:18:54
Job time : 370.894 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 41.2461 Seconds
(without alignments)
1724.030 Million cell updates/sec

Title: US-09-857-524B-2
Perfect score: 2470
Sequence: 1 MESEPKHGHSQADLAKHKQPG.....KDYTKFVPRKMWMEANMTFG 448

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A.GeneSeq.19Jun03:*
2: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1980.DAT:*
3: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1981.DAT:*
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12: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1990.DAT:*
13: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1991.DAT:*
14: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1992.DAT:*
15: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1993.DAT:*
16: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1994.DAT:*
17: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1995.DAT:*
18: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1996.DAT:*
19: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1997.DAT:*
20: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1998.DAT:*
21: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1999.DAT:*
22: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT:*
23: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:*
24: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:*
25: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2470	100.0	448	21	AAV71551
2	1465.5	59.3	448	17	AA98455
3	1465.5	59.3	448	19	AAW67471
4	1465.5	59.3	448	20	AAW98130
5	1465.5	59.3	450	21	AAV71554
6	1463.5	59.3	448	21	AAV51349
7	1459.5	59.1	448	23	AAU79830
8	1459.5	59.1	448	24	ABG73095
9	1451.5	58.8	446	20	AAW85122

10	1446.5	58.6	448	24	ABG73417	Borage delta-6-des
11	1407.5	57.0	449	21	AAW29290	Arabidopsis thaila
12	1395.5	56.5	449	21	AAV51333	B. napus aldi prot
13	1391.5	56.3	458	21	AAV51348	Sphingolipid deat
14	1372.5	55.6	449	21	AAW07392	Arabidopsis thaila
15	1372.5	55.6	449	21	AAW53861	Arabidopsis thaila
16	1372.5	55.6	449	21	AAW51334	A. thailana aldi p
17	1372.5	55.6	417	21	AAW07391	Arabidopsis thaila
18	1314.5	53.2	452	23	AAU79851	Evening primrose d
19	1314.5	53.2	452	23	ABG73416	Evening primrose d
20	1301.5	52.7	450	24	ABG73418	Evening primrose d
21	1295.5	52.4	462	21	AAV71552	Corn sphingolipid
22	1294.5	52.4	469	21	AAV71555	Wheat sphingolipid
23	1030.5	41.7	353	21	AAW07393	Arabidopsis thaila
24	1030.5	41.7	353	21	AAW53862	Arabidopsis thaila
25	1017.5	41.2	326	21	AAW29291	Arabidopsis thaila
26	984	39.8	326	21	AAW53863	Arabidopsis thaila
27	831	33.6	284	21	AAV51351	Protein b51bo with
28	733.5	29.7	252	19	AAW84141	Desaturase enzyme
29	682.5	27.6	222	21	AAV51352	Protein d52pu with
30	676.5	27.4	224	21	AAV51350	Protein d52pu with
31	663.5	26.9	483	22	AAW46435	C. purpureus delta
32	663.5	26.9	483	22	AAW46436	C. purpureus delta
33	632	25.6	253	21	AAV71553	Soybean sphingolip
34	626	25.3	520	22	AAW46440	C. purpureus delta
35	560.5	22.7	459	23	AAW22063	Pythium irregulare
36	550	22.3	525	21	AAV51354	Protein b5pp with
37	550	22.3	525	22	AAW46810	P. patens delta6-d
38	550	22.3	525	23	ABG73602	P. patens D6 desat
39	550	22.3	525	23	ABG73607	P. patens delta6 d
40	550	22.3	525	23	ABG73609	P. patens delta6 d
41	550	22.3	525	23	ABW98277	Physcotrella pat
42	549	22.2	457	19	AAW84137	A delta-6 desatura
43	549	22.2	457	20	AAW95504	Mortierella alpina
44	549	22.2	457	21	AAV92599	M. alpina delta-6
45	549	22.2	457	21	AAV56045	Fungal delta6-deaa

ALIGNMENTS

RESULT 1	AAV71551	standard; Protein; 448 AA.
ID	AAV71551	
AC	AAV71551	
XX		
DT	12-OCT-2000	(first entry)
XX		
DE	Florida bitterbush delta-6 fatty acid desaturase.	
XX		
KW	Florida bitterbush; delta-6 fatty acid desaturase; tartaric acid;	
KW	transgenic plant; fatty acid; membrane-bound desaturase.	
XX		
OS	Picramnia pentandra.	
XX		
PN	WO200032790-A2.	
XX		
PD	08-JUN-2000.	
XX		
PF	02-DEC-1999; 99WO-US28589.	
XX		
PR	03-DEC-1998; 98US-0110784.	
XX		
PA	(DUPO) DU PONT DE NEMOURS & CO B I.	
XX		
PI	Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;	
XX	WPI, 2000-412336/35.	
DR	N-PSDB; AAD01349.	
XX		
PT	Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is	

PT useful for screening cDNA expression libraries -
 XX Claim 10; Page 40-41; 57pp; English.
 CC The present sequence is a delta-6 fatty acid desaturase protein sequence
 CC from clone pps-pk0011.d5:15 isolated from Florida bitterbush developing
 CC seed cDNA library, pps. The delta-6 desaturase enzyme catalyses the
 CC formation of tauric acid, a fatty acid that has a triple bond at the
 CC delta-6 carbon. The present sequence is useful for producing
 CC transgenic plants having altered levels of delta-6 desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is also useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
 XX
 SQ Sequence 448 AA;
 Query Match 100.0%; Score 2470; DB 21; Length 448;
 Best Local Similarity 100.0%; Pred. No. 3,4e-253;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEEPKKHSQADLAKHQPDLWISIKGYDISKMKRHPGGLPLSPAGQDVTDAFI 60
 DB 1 MEEPKKHSQADLAKHQPDLWISIKGYDISKMKRHPGGLPLSPAGQDVTDAFI 60
 QY 61 AHPGTAQYLDREFTGYVQDYVSSEMSKDYRLVSEFSKMGLEKTPGKGVCSIFPV 120
 DB 61 AHPGTAQYLDREFTGYVQDYVSSEMSKDYRLVSEFSKMGLEKTPGKGVCSIFPV 120
 QY 121 VLPLSYGVLYCKSTWVAHLCSGLMGMLVQSGVGHDSCHYQVMPNRKLNRLFOIIAG 180
 DB 121 VLPLSYGVLYCKSTWVAHLCSGLMGMLVQSGVGHDSCHYQVMPNRKLNRLFOIIAG 180
 QY 121 VLPLSYGVLYCKSTWVAHLCSGLMGMLVQSGVGHDSCHYQVMPNRKLNRLFOIIAG 180
 DB 121 VLPLSYGVLYCKSTWVAHLCSGLMGMLVQSGVGHDSCHYQVMPNRKLNRLFOIIAG 180
 QY 181 NVLAGSVVAMWKLDPNTHHFAKNSANLDPDIOHPLIAISPKFNSLTSTYHNCMTYDR 240
 DB 181 NVLAGSVVAMWKLDPNTHHFAKNSANLDPDIOHPLIAISPKFNSLTSTYHNCMTYDR 240
 QY 181 NVLAGSVVAMWKLDPNTHHFAKNSANLDPDIOHPLIAISPKFNSLTSTYHNCMTYDR 240
 DB 181 NVLAGSVVAMWKLDPNTHHFAKNSANLDPDIOHPLIAISPKFNSLTSTYHNCMTYDR 240
 QY 241 AARFVFSFOHMTFYPALLSVRLYFILSPKVFVSNRKYKRSQELIGVAAFLTWYSLL 300
 DB 241 AARFVFSFOHMTFYPALLSVRLYFILSPKVFVSNRKYKRSQELIGVAAFLTWYSLL 300
 QY 301 SRLPNNRMYFTSCLAVALGFOHMFSLNHFASNVYTGHPSGNDWFHOOTKGLNTTAS 360
 DB 301 SRLPNNRMYFTSCLAVALGFOHMFSLNHFASNVYTGHPSGNDWFHOOTKGLNTTAS 360
 QY 361 AAMDWFHGGHFOIENHLFPRMPKCHFRKISPIVNYKLCQKHNLSYETATWMEANKVYST 420
 DB 361 AAMDWFHGGHFOIENHLFPRMPKCHFRKISPIVNYKLCQKHNLSYETATWMEANKVYST 420
 QY 421 LRAVAMEAKDVTKVPKNNWMEANTFG 448
 DB 421 LRAVAMEAKDVTKVPKNNWMEANTFG 448

RESULT 2
 AAR98455 standard; Protein: 448 AA.
 AC AAR98455;
 DT 15-SEP-1996 (first entry)
 DE Borage delta-6-desaturase.
 XX
 XX Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;
 KM polyunsaturated fatty acid; octadecatetraenoic acid;
 KM chilling resistance; oilseed.
 XX
 OS Borage officinalis.
 XX
 FH Key Location/Qualifiers
 FT Region 156..163
 FT label= lipid_box

FT Region 196..200
 FT /label= Metal_box-1
 FT Region 372..377
 FT /label= Metal_box-2
 XX
 XX WO9621022-A2.
 XX
 PD 11-JUL-1996.
 XX
 XX 28-DEC-1995; 95MO-IB01167.
 XX
 PR 30-DEC-1994; 94US-0366779.
 XX
 PA (RHON) RHONE POULENC AGROCHIMIE.
 XX
 XX Freyssiuet GL, Nuccio M, Numberg AN, Reddy AS, Thomas TL;
 XX
 DR WPI; 1996-333997/33.
 DR N-PSDB; AAT30395.
 XX
 PT Transgenic plants comprising the borage delta-6-desaturase gene -
 PT show increased production of gamma linolenic acid and having
 PT increased resistance to chilling
 PS Claim 3; Page 52-53; 75pp; English.
 CC Borage delta-6-desaturase (AAR98455) catalyses the conversion of
 CC linoleic acid to gamma-linolenic acid (GLA). Its sequence was
 CC deduced from that of the delta-6-desaturase gene (AAT30395) isolated
 CC from a borage membrane-bound polyosomal library. The sequence is
 CC distinct from that of Synecocystis delta-6-desaturase (AAR98456).
 CC Expression of the desaturase in transgenic plants, esp. sunflower,
 CC soybean, maize, tobacco, peanut, carrot or oilseed rape, results in
 CC increased GLA prodn. Alteration of the plant membrane lipids as a
 CC result of expression of the desaturase may also result in increased
 CC resistance to chilling.
 XX
 SQ Sequence 448 AA;
 Query Match 59.3%; Score 1465.5; DB 17; Length 448;
 Best Local Similarity 55.4%; Pred. No. 1.7e-146;
 Matches 246; Conservative 90; Mismatches 107; Indels 1; Gaps 1;
 QY 5 KKHISQADLAKHQPDLWISIKGYDISKMKRHPGGLPLSPAGQDVTDAFIAYHP 64
 DB 6 KKHISQADLAKHQPDLWISIKGYDISKMKRHPGGLPLSPAGQDVTDAFIAYHP 64
 QY 65 GTAMQYLDREFTGYVQDYVSSEMSKDYRLVSEFSKMGLEKTPGKGVCSIFVSVLPA 124
 DB 65 GTAMQYLDREFTGYVQDYVSSEMSKDYRLVSEFSKMGLEKTPGKGVCSIFVSVLPA 124
 QY 66 ASYWKDLKRFETGYLYKDYVSSEMSKDYRLVSEFSKMGLEKTPGKGVCSIFVSVLPA 125
 DB 66 ASYWKDLKRFETGYLYKDYVSSEMSKDYRLVSEFSKMGLEKTPGKGVCSIFVSVLPA 125
 QY 125 LSYGVLYCKSTWVAHLCSGLMGMLVQSGVGHDSCHYQVMPNRKLNRLFOIIAGNYLA 184
 DB 125 LSYGVLYCKSTWVAHLCSGLMGMLVQSGVGHDSCHYQVMPNRKLNRLFOIIAGNYLA 184
 QY 126 MSYGVLYCKSTWVAHLCSGLMGMLVQSGVGHDSCHYQVMPNRKLNRLFOIIAGNYLA 185
 DB 126 MSYGVLYCKSTWVAHLCSGLMGMLVQSGVGHDSCHYQVMPNRKLNRLFOIIAGNYLA 185
 QY 185 GVSVAAMWKLDPNTHHFAKNSANLDPDIOHPLIAISPKFNSLTSTYHNCMTYDRARF 244
 DB 185 GVSVAAMWKLDPNTHHFAKNSANLDPDIOHPLIAISPKFNSLTSTYHNCMTYDRARF 244
 QY 245 FVSGHMTFYPALLSVRLYFILSPKVFVSNRKYKRSQELIGVAAFLTWYSLLSRP 304
 DB 245 FVSGHMTFYPALLSVRLYFILSPKVFVSNRKYKRSQELIGVAAFLTWYSLLSRP 304
 QY 305 NMPERVMYFTSCLAVALGFOHMFSLNHFASNVYTGHPSGNDWFHOOTKGLNTTASAWMD 364
 DB 305 NMPERVMYFTSCLAVALGFOHMFSLNHFASNVYTGHPSGNDWFHOOTKGLNTTASAWMD 364
 QY 365 WFRGGLFOIENHLFPRMPKCHFRKISPIVNYKLCQKHNLSYETATWMEANKVYSTLRAV 424
 DB 365 WFRGGLFOIENHLFPRMPKCHFRKISPIVNYKLCQKHNLSYETATWMEANKVYSTLRAV 424
 QY 425 AMEAKDVTKVPKNNWMEANTFG 448
 DB 425 AMEAKDVTKVPKNNWMEANTFG 448

Db 425 ALQARDITKPLPKNLVWEALHTHG 448

RESULT 3
AAM67471
ID AAM67471 standard; Protein; 448 AA.
XX
AC AAM67471;
XX
DT 02-MAR-1999 (first entry)
XX
DE Borage delta-6 desaturase protein.
XX
KM Upstream region; regulatory region; sunflower; albumin; seed; expression;
lipoic metabolism; delta-6 desaturase; transgenic plant.
XX
OS Borage officinalis.
XX
FH Key Location/Qualifiers
FT 40..44
FT /note="cytochrome b5 haem-binding motif"
FT Domain 156..163
FT /note="His-rich metal binding motif"
FT Domain 196..200
FT /note="His-rich metal binding motif"
FT Domain 373..377
FT /note="His-rich metal binding motif"
XX
PN WO9845460-A1.
XX
PD 15-OCT-1998.
XX
PF 09-APR-1998; 98WO-US07178.
XX
PR 09-APR-1997; 97US-0831570.
XX
PA (RHON) RHONE-POULENC AGROCHIMIE.
PI Beremand PD, Nunberg AN, Thomas TL;
XX
DR WPI; 1998-583201/49.
XX
CC N-PSDB; AAV34398.
XX
PT New sunflower albumin 5' regulatory region - useful for directing
PT altered lipid metabolism in plant seeds
XX
PS Example 2; Fig 1; 38pp; English.
XX
CC This sequence corresponds to the borage (Borage officinalis) delta-6
CC desaturase enzyme. The encoding lipid metabolism gene is an example
CC of a heterologous gene which can be expressed at high levels in a
CC seed-specific manner in transgenic plants, when placed under control
CC of the sunflower albumin gene 5' regulatory region (AAV34397).
XX
SQ Sequence 448 AA;
XX
Query Match 59.3%; Score 1465.5; DB 19; Length 448;
Best Local Similarity 55.4%; Pred. No. 1.7e-146;
Matches 246; Conservative 90; Mismatches 107; Indels 1; Gaps 1;
XX
QY 5 KKHISQADIAKHKOPDLMWISIKGVYDLSKWKHPGGGLPLSPAGODVTPAFIAYHP 64
DB 6 KKITIDELKNDKPDGLWISIQKAYDVSDWKDHPGGSFPLKSLAGQEVTDAPVAFHP 65
QY 65 GTAMQYLDREFTGYVQDVSVSEMSKDYRLVSEFSKMGLEFKTPGKGVCSIFVSVLPA 124
DB 66 AATWKULDFEFTGYLKDYSVSEVSKDYRLVSEFSKMGLEFKTPGKGVCSIFVSVLPA 125
QY 125 LSYVGLYCKSTAHKCSGLMGLMOSGVVGHDSCHYVMMNRKLNRLFOIIAGNVIA 184
DB 126 MSYVGLYFCBGVYVHLFSGCLMGLMOSGVVGHDSCHYVMMNRKLNRLFOIIAGNVIA 185
QY 185 GVSVAWMLKDHNTHHFAKNSANLDPDIOHLPILAISPFPNSLTSYHNCKMTYDRAAR 244

Db 186 GISIGWKKNNHNAHIAKNSLEYDPLQYIPELVVSKFEFSLTSHFYERKLPFDSLSRP 245

QY 245 FVSPQHTFYPALLSLRLYLFLISFKVVSNNRKYKROELGYAFLTWISLLSRP 304
DB 246 FVSQHTFYPALLSLRLYLFLISFKVVSNNRKYKROELGYAFLTWISLLSRP 304
QY 305 NMPERVMTFSCIAVAGFQMOFSLNHPASNVYGLPSGNDPFOOTKTLNTASAMWD 364
DB 305 NMGERIMFYIASLSVGMQOVQFSLNHPASNVYGLPSGNDPFOOTKTLNTASAMWD 364
QY 365 WFGGLHFOIEHLLFPRMPKCHFRKISPIVNLKQKHNTSYETATWEMANKVYSTLRV 424
DB 365 WFGGLHFOIEHLLFPRMPKCHFRKISPIVNLKQKHNTSYETATWEMANKVYSTLRV 424
QY 425 AMBAKDVTKPVPKNNWEMANTFG 448
DB 425 ALQARDITKPLPKNLVWEALHTHG 448

RESULT 4
AAM98130
ID AAM98130 standard; Protein; 448 AA.
XX
AC AAM98130;
XX
DT 21-JUN-1999 (first entry)
XX
DE Borage delta-6 desaturase.
XX
KM Delta-6 desaturase; borage; oleosin; Acs21; promoter;
KM transgenic plant; seed; lipid; fatty acid; oilseed; vegetable oil;
KM gamma-linolenic acid; octadecatretenic acid.
XX
OS Borage officinalis.
XX
FH Key Location/Qualifiers
FT 40..44
FT /note="cytochrome b5 haem-binding motif"
FT Binding-site 156..163
FT /note="metal binding, histidine-rich motif"
FT Binding-site 196..200
FT /note="metal binding, histidine-rich motif"
FT Binding-site 373..377
FT /note="metal binding, histidine-rich motif"
XX
PN WO9845461-A1.
XX
PD 15-OCT-1998.
XX
PF 09-APR-1998; 98WO-US07179.
XX
PR 09-APR-1997; 97US-0831575.
XX
PA (RHON) RHONE-POULENC AGROCHIMIE.
PI Li Z, Thomas TL;
XX
DR WPI; 1999-180333/15.
XX
CC N-PSDB; AAX24917.
XX
PT Nucleic acid containing oleosin 5'-regulatory region - useful for
PT modulating fatty acid synthesis and lipid metabolism in plants,
PT particularly to increase content of gamma-linolenic acid
XX
PS Example 2; Page 61; 101pp; English.
XX
CC The present sequence is borage delta-6 desaturase, an enzyme that
CC catalyzes the conversion of linoleic acid to gamma-linolenic acid
CC (GLA). Delta-6 desaturase cDNA (see AAX24917) was isolated from a
CC borage membrane-bound polyosomal cDNA library using a partial clone,
CC obtained from an EST database search, as probe. The borage delta-6
CC desaturase nucleic acid can be operably linked to the seed-specific

CC 5' regulatory region (see AAX24916) of the Arabidopsis thaliana
CC oleosin At5g1 gene in claimed expression cassettes of the invention.
CC Transgenic plants, e.g. sunflower, soybean, maize, tobacco, cotton,
CC peanut, oilseed rape or Arabidopsis are obtained that show increased
CC levels of GUA or octadecatetraenoic acid. The levels of desirable
CC fatty acids in oilseed crops can be manipulated to provide seed
CC oils of use in human health and industrial applications.

XX Sequence 448 AA;

Query Match 59.3%; Score 1465.5; DB 20; Length 448;
Best Local Similarity 55.4%; Pred. No. 1,7e-146;
Matches 246; Conservative 90; Mismatches 107; Indels 1; Gaps 1;

QY 5 KKHISQADLAKHQPQDLMISIKGKYDISEKTKHFGGELPLSPAGQDVTDAFI 64
DB 6 KKITDEKKNHDPDLWISIQKAYDSDWKDHGSGFPLKSLAGQEVTAFAVAFHP 65
QY 65 GTAMQYLDREFTGYVODYSVSEMSKDYRLVSEFSKMGLEFKTPGKGVCSIFSVLFA 124
DB 66 ASYWKALDRFTGYVLYKDYSEVSKDYRLVSEFSKMGLEFKTHMFAITLCFIAMLFA 125
QY 125 LSVYGYLYCKSTWANHCSGLMGMLWLGSGWGHDSCHYQVWPNKRLPLFQIAGNVIA 184
DB 126 MSYGYVLPFGGVVHLFSGCLMGFLWLGSGWGHDSCHYQVWPNKRLPLFQIAGNVIA 185
QY 185 GUSVAMWKLDPHNTNHPACNSANLDPDIOHPIAISPKNFNSITSYHNCKMYDRAARF 244
DB 186 GSGIGWKNHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAH 245
QY 245 FVSFOHMTFYPALLSVRLYLFIISFKVFSNNKRYKRSQELIGYAAFLTWYSLLSRLP 304
DB 246 FVSFOHMTFYPALLSVRLYLFIISFKVFSNNKRYKRSQELIGYAAFLTWYSLLSRLP 304
QY 305 NMEPERVMTFTSCLAVAGFOHMFSLNHPASNVYTGLPSCNDWFRHOQTKTLNTASAMWD 364
DB 305 NMEPERVMTFTSCLAVAGFOHMFSLNHPASNVYTGLPSCNDWFRHOQTKTLNTASAMWD 364
QY 365 WFRGGLHFOLEHNLFRPMKCHFRKISPIVNLCKOKNLSYETATWEMANKMYSTLRAY 424
DB 365 WFRGGLHFOLEHNLFRPMKCHFRKISPIVNLCKOKNLSYETATWEMANKMYSTLRAY 424
QY 425 AMEAKDVTKVPKNNWMEAMNTFG 448
DB 425 ALQARDITKPLPKNLMEALHTHG 448

RESULT 5
AAY71554

ID AAY71554 standard; Protein; 450 AA.

AC AAY71554;

DT 12-OCT-2000 (first entry)

DE Soybean sphingolipid desaturase #2.

KW Soybean sphingolipid desaturase; membrane-bound desaturase;
KM transgenic plant; fatty acid.

OS Glycine max.

PN WO200032790-A2.

PD 08-JUN-2000.

PF 02-DEC-1999; 99MO-US28589.

PR 03-DEC-1998; 98US-0110784.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;

XX WPI: 2000-412336/35.
DR N-PSDB; AAD01352.

XX Polynucleotide encoding delta-6 desaturase enzyme useful for producing
XX transgenic plants and for producing antibodies specific to which is
XX useful for screening cDNA expression libraries

PS Claim 10; Page 47-48; 57pp; English.

CC The present sequence is a sphingolipid desaturase
CC from clone sgl.pk0017.b4.15 isolated from soybean seedling cDNA
CC library, sel. The present sequence is useful for producing
CC transgenic plants having altered levels of sphingolipid desaturase which
CC in turn would alter the fatty acid composition. The enzyme is also useful
CC for producing polyclonal or monoclonal antibodies. The polynucleotide
CC is useful as primer or probe for screening cDNA libraries to
CC isolate desired full-length cDNA clones.

XX Sequence 450 AA;

Query Match 59.3%; Score 1465.5; DB 21; Length 450;
Best Local Similarity 55.4%; Pred. No. 1.8e-146;
Matches 248; Conservative 90; Mismatches 109; Indels 1; Gaps 1;

QY 1 MEEPRKHISQADLAKHQPQDLMISIKGKYDISEKTKHFGGELPLSPAGQDVTDAFI 60
DB 4 VEKEKKTITSSEELKGNKGGDLWISIQKAYNSDWKHPGQDVISNLAGQDVTDAFI 63
QY 61 AYHPTAMQYLDREFTGYVODYSVSEMSKDYRLVSEFSKMGLEFKTPGKGVCSIFVYS 120
DB 64 AYHPTAMQYLDREFTGYVODYSVSEMSKDYRLVSEFSKMGLEFKTPGKGVCSIFVYS 123
QY 121 VLFALSVGYLYCKSTWANHCSGLMGMLWLGSGWGHDSCHYQVWPNKRLPLFQIAG 180
DB 124 VLFALSVGYLYCKSTWANHCSGLMGMLWLGSGWGHDSCHYQVWPNKRLPLFQIAG 183
QY 181 NVIAGSVAMWKLDPHNTNHPACNSANLDPDIOHPIAISPKNFNSITSYHNCKMYDRAARF 240
DB 184 NVIAGSVAMWKLDPHNTNHPACNSANLDPDIOHPIAISPKNFNSITSYHNCKMYDRAARF 243
QY 241 AARFVSFOHMTFYPALLSVRLYLFIISFKVFSNNKRYKRSQELIGYAAFLTWYSLLS 300
DB 244 IARFLCYQHFFTPYPCVAVNLVYQITLLFESRRK-VQDRALNMGILVFTWPEPLV 302
QY 301 SRIENPERVMTFTSCLAVAGFOHMFSLNHPASNVYTGLPSCNDWFRHOQTKTLNTAS 360
DB 303 SRIENPERVMTFTSCLAVAGFOHMFSLNHPASNVYTGLPSCNDWFRHOQTKTLNTAS 362
QY 361 AMWDWFRHGLHFOLEHNLFRPMKCHFRKISPIVNLCKOKNLSYETATWEMANKMYST 420
DB 363 SSMDWFRHGLHFOLEHNLFRPMKCHFRKISPIVNLCKOKNLSYETATWEMANKMYST 422
QY 421 LRAVAMEAKDVTKVPKNNWMEAMNTFG 448
DB 423 LRTALQARDITKPLPKNLMEALHTHG 450

RESULT 6
AAY51349

ID AAY51349 standard; Protein; 448 AA.

AC AAY51349;

DT 27-APR-2000 (first entry)

DE Sunflower HADES protein.

KW Sphingolipid desaturase, sld1; sphingobase; ceramide; capnoid;
KM transgenic plant; crop plant; delta-8-unsaturated long-chain base;
KM tolerance; resistance; soil salinity; ion stress; toxicity; drought;
KM cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
KM pharmaceutical; food; chemical raw material.

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XX Helianthus annuus.
XX DE19828850-A1.
PN XX
XX 30-DEC-1999.
PD XX
PF 27-JUN-1998; 98DE-1028850.
PR XX
XX 27-JUN-1998; 98DE-1028850.
PA (GVSE-) GVS GRS ERWERB & VERW LANDWIRTSCHAFTLICH.
PI Heinz E, Zaehring U, Schmidt H, Sperling P;
DR WPI; 2000-12/7549/12.
XX
XX New sphingolipid desaturase that selectively introduces double bond
PT into sphingolipids and capnoids -
XX Disclosure; Page 33-34; 62pp; German.
XX
XX This invention describes a novel sphingolipid desaturase that selectively
CC introduces a double bond into the sphingosine of the ceramide residue of
CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
CC desaturase, or a vector containing the DNA sequence, can be used to
CC produce transgenic plants, especially crop plants, with an increased or
CC decreased delta-8-unsaturated long-chain base content or an altered
CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
CC compensate for a delta-8-unsaturated long-chain base deficiency, to
CC exclude production of delta-8-unsaturated bases, to increase tolerance
CC or resistance to soil salinity, ion stress or toxicity, drought, wet
CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
CC alter size growth and flowering time. Cells, transgenic organisms or
CC plants containing the DNA sequence can be used to produce sphingolipids
CC and capnoids with unsaturated sphingosines. The sphingolipids or capnoids
CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
CC materials. This sequence represents a desaturase protein, HADES, isolated
CC from Helianthus annuus (sunflower) which is used in the method of the
CC invention.
SQ Sequence 448 AA;
Query Match 59.3%; Score 1463.5; DB 21; Length 448;
Best Local Similarity 55.4%; Pred. No. 2.9e-146;
Matches 246; Conservative 90; Mismatches 107; Indels 1; Gaps 1
QY KKHISQADLAHKRGKGDLMISKGYVDISKMTKEHPGELPLLSFAGODVTDAPFAVHP 64
DB 6 KKYYTSDKLKNDDPKFDMLISTIGKAYDVSDWKDHPPGSFPFKSLAGEVDAFAAHP 65
QY 65 GTAMQVLDRFPTYGVVQDYSVESSKDYRLVSEFSKMGLFTPTKGKVCSIFVSVLPA 124
DB 66 ASTWMGNLDKFFGYLLKYDYSVESESKDYRLVSEFSKMGLYDKGHIMATLCFIAMLRA 125
QY 125 LSYGVLYCKSTMAHLCSGLMGMLMLOS GWYGHDSCHYQVMENRKLNLFOIIAGNVIA 184
DB 126 MSYGVLYCEGVLYHLPFGCLGMFLIWOGMWIGHDAGHTMYVSDSLNKFMGIPANCIS 185
QY 185 GVSVAWMLDHTTHPACNSALDPDIQLPLIILSPKFNLSITYNHCKMTYDRAAF 244
DB 186 GISISMWKKNNHAHHAIACSLEYPDLOQTIPFLVUSCKFFGSTSHFYEKRLTFPSLSRF 245
QY 245 FVSFOHMFYRPALTLVRLYLFTLSFVVNSNNKRIVYKSGOELLGYAAFLTWLILSRP 304
DB 246 FVSYOHMFYRPMCARLMMYQS-LIMLTTRNNYSYRQEBLLCGLVFSTWIPLVSCIP 304
QY 305 NWPERVMTFTSCLAVALGFQHMOPSLNHFAANNYTGLPSGNDWFHQOTKTGLINTASAWMD 364
DB 305 NMGERIMEFVIASLTSTMGOVOFSLNHFESSVYGKPKNNMEPEKOTDGTDLIDSCPAMD 364
QY 365 WPHGGHLOIEHNLPMPMKCFPKRKSLPVNKLCOQHNLSTETATWEMAKNYSTLRAY 424

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DB      365 WFHGGLGFQIEBHLEFPKMPRCKLRISPYVIELCKKNLPPYNAVSFSKANEMTLRTLTANT 424
OY      425 AMEAKDVTKPYPKMVMWEANMTFG 448
       |::|::|::|::|::|::|::|::|
Db      425 ALQARDITKPLPKNLVWEALHTHG 448

RESULT 7
AAU79830 AAU79830 standard; Protein; 448 AA.
XX AC AAU79830;
XX DT 15-JUL-2002 (first entry)
DE Borage officinalis delta6-desaturase.
XX KX delta6-desaturase; sunflower; soybean; maize; tobacco;
KM peanut; carrot; oil seed rape; gamma linolenic acid; GLA;
XX chilling tolerance; borage.
OS Borage officinalis.
FH Key Location/Qualifiers
FT Region 156..163
FT /label=Lipid_box
FT 196..200
FT /label=Metal_box_1
FT 372..377
FT Region /label=Metal_box_2
XX XX US6355861-B1.
PN 12-MAR-2002.
PD 19-SEP-1997; 97US-0934254.
PF 13-OCT-1992; 92US-0959952.
PR 10-OCT-1991; 91US-0774475.
PR 08-JAN-1992; 92US-0817919.
PR 14-SEP-1994; 94US-0307382.
PR 28-JAN-1997; 97US-0789936.
PA (RHON ) RHONE-POULENC AGROCHIMIE.
PI Thomas TL;
DR N-PSDB; ABEK49502.
XX WP1: 2002-380944/41.
PT Novel nucleic acid encoding evening primrose delta6-desaturase which
PT converts linoleic acid to gamma linolenic acid useful for producing
PT gamma linolenic acid in transgenic plant or bacteria -
XX Example 9; Column 31-34; 53pp; English.
XX PS The invention describes an isolated nucleic acid encoding an evening
CC primrose Delta6-desaturase. The nucleic acid and a vector expressing the
CC nucleic acid are useful for producing a plant such as sunflower, soybean,
CC maize, tobacco, peanut, carrot or oil seed rape plant, with increased
CC gamma linolenic acid (GLA) content, and also for inducing or increasing
CC production of GLA in a bacteria or plant deficient, lacking in or
CC producing low levels of GLA. The nucleic acid is also useful for inducing
CC chilling tolerance in plants. This is the amino acid sequence of the
CC borage delta6 desaturase involved in the production of gamma linoleic
CC acid.
XX SQ Sequence 448 AA;
XX Query Match 59.1%; Score 1459.5; DB 23; Length 448;
XX Best Local Similarity 55.2%; Pred. No. 7.6e-146;
XX Matches 245; Conservative 90; Mismatches 108; Indels 1; Gaps 1;
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Qy	5	KKHSIADALAKHNPQDLMISIKGKAYDISKMTXKHPPGDELPLSPFAODVTDFAIYHP	64
	6	KKIITSDELKMDKPDLMISTIQKRAYDSBVYKHPPGSPFLKSLAQEYTDFAVAFHP	65
Qy	65	GTAMQYLDLRFPTGYVYVDYSVSEMSKDYRLVSEFSXKGLFEKTPGKYCSIFPVSLFA	124
Db	66	ASTWKMULDKEFTGYLKYDYSSEVSXDYRKLFEESSKGLDYDKKHIMFATLCEIAMLFA	125
Qy	125	LSYGYVLVYCKSTWANHCSGLLMGMLTOSGMVGHDSCHYQWMPRKINRLQIIAGVIA	184
Db	126	MSYGYVLPFCGVLVHLPSCGLMGFLMTIQSGMIGHAGHMYVSDRLKMPGIFPAACLS	185
Qy	185	GVSVAWAKLDHNTHTFHFCNSANLDPDIQHLPIIATSPREFNSLTSYHANCWATYDRAAF	244
Db	186	GISIGMWMKNHNHAIHACNSLEVDPLQYIIPLVYSSKFPQSLISHFEKRLTJDSLSRF	245
Qy	245	FVSEFQWHTYRPLLSTRVLFTLSFEVWFSENNKRYKKSQELGYAAFLTWYSLLSLRLP	304
Db	246	FVSYQHTETPIMICARLMMYVQSL-IMLLTTRNYSYRAOBLGCLVFSIYPLVSLCP	304
Qy	305	NMBERVWYFSCLAVALPQHMOPSLNHFASNYVTGLPSCNDWFHOQTGTLNTITASAMWD	364
Db	305	NMBERLMFVYASLSVGMQOVQPSLNHFSSSYVYQKPKGNWFEKQDTGTIDISCPHMD	364
Qy	365	WFFGSLHFOIENHLPFPMPCHEFRKISPIVNTLCOJANLSEYATATWMEANKMYSTILRAV	424
Db	365	WFFGSGQFOIENHLPFPMPCRNLRKISPYVIELCKKHNLPLYVYASFSAKANEMLTJRLNLT	424
Qy	425	AMEAKDVTPKPVKNWYMEAMNTFG	448
Db	425	ALQARDITKPLPKNLWEMELNTHG	448

	RESULT 8
ID	ABG73095
AC	ABG73095 standard; Protein; 448 AA.
DT	17-APR-2003 (first entry)
DE	Borage delta-6-desaturase #1.
KW	Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower; soybean; maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA, octadecatetraenoic acid, alpha-linolenic acid; delta-15-desaturase;
KM	borage.
OS	Borago officinalis.
XX	
FH	Key
FT	Misc-difference 370
PN	/note= "Encoded by TTG"
XX	
PD	US2002108147-AI.
XX	
PD	08-AUG-2002.
XX	
PF	21-DEC-2001; 2001US-0029756.
XX	
PR	13-OCT-1992; 92US-0959952.
PR	19-SEP-1997; 97US-0934254.
PR	10-OCT-1991; 91US-0774475.
PR	08-JAN-1992; 92US-0817919.
PR	14-SEP-1994; 94US-0307382.
PR	28-JAN-1997; 97US-0789936.
PA	(THOM) THOMAS T L.
PI	Thomas TL;
XX	
XX	
DR	WPI, 2003-066659/06.
NR	N-PSDB; ABX15366.

XX Novel nucleic acid encoding eventing primrose delta-6-desaturase, useful
 PT for producing plant with increased gamma linolenic acid content, and
 PT for inducing octadecatetraenoic acid production in plant -
 XX
 PS
 PV Example 9, Fig 5B; 55pp; English.

CC The invention relates to a nucleic acid encoding an evening primrose
CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
CC for producing a plant (such as sunflower, soybean, maize, tobacco,
CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
CC acid (GLA) content by transforming a plant cell with the nucleic acid or
CC vector and regenerating a plant with increased GLA content from the plant
CC cell, for inducing or increasing production of GLA in an organism lacking
CC in or producing low levels of GLA and for inducing production of
CC octadecatretraenoic acid in at least one of a plant deficient or lacking
CC in or producing low levels of octadecatretraenoic acid, a bacterium which
CC produces alpha-linolenic acid or a bacterium which exhibits a
CC delta-15-desaturase activity on a GLA substrate. This sequence represents
CC a boraga delta-6-desaturase polypeptide.

Sequence 448 AA;

Query Match	59.1%	Score 1459.5	DB 24	Length 448
Best Local Similarity	55.2%	Pred. No. 7.6e-14		
Matches 245		Conservative 90	Mismatches 108	Indels 1
				Gaps 1

0y 5 KKHISQADLAKHKQPGDLMWISIKGVYDISKTKENPGGELPLLSFAGQDVTDAFIAYNH 64

Db 6 KKYTSDDELKNHDKPGDLMWISIQKAYDSWVKDHPGGSFLPLSLAGQEVTDFAVAFNR 65

65 GTAWQYLDREFTGYVQDYSVSEMSKDYRLVSEFSKMGLEKTPGKGVYCSIFVSVLFA 12

Db 66 ASTWKNLDFKFTGYLLKDYSSVSEVSKDYRKLVEEFSKMGLYDKKGHIMFATLCFIAMLFA 12

QY 125 LSVYGVLYCKSTWAHLCSGLMGLWLOSGWVGHDSCHYQVMPNPKLNLRLFOIIAGNVIA 18

Db 126 MSVYGVLFCEGLVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSLNKKFMGIFAANCL 18

185 GVSVAWWKLDHNTTHFACNSANLDPDIQHLPIAISPKFNSLTSYYHNCKMTYDRARF 24

Db 186 GISIGWKKNNHAIACNSLEYDPLQYIPFLVSSKFFGSLTSHFYEKRLTFDSLRF 24

245 FVSFOHWTYPALSVRLYLEILSEKVFESNNKRVYKRSQEIIGYAAFLTWYSLLSRLP 30

Db 246 FVSYQHWTFFYPIMCARLNMVQSL-IMLLTKRNVSYRAQELGCLVFSIWYPLLVSCLP 30

305 NWPERVMYFTSCLAVAGFQHWQFSLNHFAASNVTGLPSGNDWEFHQOTKGTINITASAWWD 36

Db 305 NWGERIMFVIA^{SL}SVTGMQOVQ^{FS}LNHFSSSVYVGKPKGNWFEKQ^{TD}GLDISCPWMD 36

QY 365 WFHGGLHFOIEHHLPFRMPKCHFRKISPIVNKLCQKINLSYETATMWEANKMVSJLRAY 42

Db 365 WFHGGSQFQIEHHLFPMPCNLRKISPYVIELCKGHLPNYASFSSKANEMTLRTLRLNT 42

QY 425 AMEAKDVTKPVPKNMWEAMNTFG 448

Db 425 ALQARDITKPLPKNLVWEALHTHG 448

CONCLUSION

AAW85122

5
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XX
XX

22 XX

XX

KW malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis;

[illegible]

Db	246	FVSIQHTFFPYIMCARLAMYQSL-IMLTGRNVSYPAGELLGCLVFISWPLVLSCLP	304
Qy	305	NWPERVMYFTSCLAVAGFQHWQFSLNHFPASVNYTGLPSGNDWFHOQTKCTLNITASAMWD	364
Db	305	NWGERIMEVIASLSVTGMQOVQFSLNHFSSSVYVGKPKGNMFEKQTDGLDISCPMWD	364
Qy	365	WFHGGMLHQLIEHHLFPRPMKCHKFRKISPLVNLCKGNLSYETATMWEANKVYSLTRAV	424
Db	365	WFHGGLOPQIHHHLPFKMPCRCNLRKISPYVIELCKGNLPYNYASPSKANEMTLRTLRYNT	424
Qy	425	AMEAKDVTKPVKNNVMEAMNT	446
Db	425	ALQARDITKPLPKNLWMEALHT	446
RESULT 10			
ABG73417			
ID	ABG73417	standard; Protein; 448 AA.	
AC	ABG73417;		
XX			
DT	16-APR-2003	(first entry)	
XX			
DE	Borage delta-6-desaturase #2.		
XX			
KW	Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower; soybean;		
KW	maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid;		
KW	octadecatetraenoic acid; alpha-linolenic acid; delta-15-desaturase;		
KW	borage.		
OS	Borago officinalis.		
XX			
PN	US2002108147-A1.		
XX			
PD	08-AUG-2002.		
XX			
PF	21-DEC-2001; 2001US-0029756.		
XX			
PR	13-OCT-1992; 92US-0959952.		
PR	19-SEP-1997; 97US-0934254.		
PR	10-OCT-1991; 91US-0774475.		
PR	08-JAN-1992; 92US-0817919.		
PR	14-SEP-1994; 94US-0307382.		
PR	28-JAN-1997; 97US-0789936.		
XX			
PA	(THOM/) THOMAS T L.		
XX			
P1	Thomas TL;		
XX			
DR	WPI; 2003-066659/06.		
XX			
PT	Novel nucleic acid encoding evening primrose delta-6-desaturase, useful		
PT	for producing plant with increased gamma linolenic acid content, and		
PT	for inducing octadecatetraenoic acid production in plant		
XX			
PS	Example 15; Fig 11; 55pp; English.		
XX			
CC	The invention relates to a nucleic acid encoding an evening primrose		
CC	delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the		
CC	nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful		
CC	for producing a plant (such as sunflower, soybean, maize, tobacco,		
CC	peanut, carrot or oil seed rape plant) with increased gamma-linolenic		
CC	acid (GLA) content by transforming a plant cell with the nucleic acid or		
CC	vector and regenerating a plant with increased GLA content from the plant		
CC	cell, for inducing or increasing production of GLA in an organism lacking		
CC	in or producing low levels of GLA and for inducing production of		
CC	octadecatetraenoic acid in at least one of a plant deficient or lacking		
CC	in or producing low levels of octadecatetraenoic acid, a bacterium which		
CC	produces alpha-linolenic acid or a bacterium which exhibits a		
CC	delta-15-desaturase activity on a GLA substrate. This sequence represents		
CC	a borage delta-6-desaturase polypeptide.		
XX			

SQ Sequence 448 AA;
Query Match 58 64; Score 1446.5; DB 24; Length 448;
Best Local Similarity 54.38; Pred. No. 1.0e-144;
Matches 241; Conservative 94; Mismatches 108; Indels 1; Gaps 1;
QY 5 KKHISADLAKHQPGLMISIKGVYDISEKTEHFGELPLISFAGQVDTAFIAYHP 64
D 6 KKITDELKHNHKKPGLMISIQKAYDSDWKDHGSGFPLKSLAGQVDTAFVAFHP 65
QY 65 GTAMQYIDRFPTGYVODIVSENSKDYRLVSEFSMGLFKTPGKGVCSIFPVYLFA 124
D 66 ASTMKNLDEKFFGTGYLLKDYDVSSEVSKDYRLVSEFSMGLFKTPGKGVCSIFPVYLFA 125
QY 125 LSYGVYLCKSTMAHLCSGLMGLWLSQGVGHDSCHYQVMPKRNLFQIAGVIA 164
D 126 MSYGVYLCFGVYLHPSGCLMGLWLSQGVGHDSCHYQVMPKRNLFQIAGVIA 165
QY 185 GVSVAWMLDHNTHFACNSANLDPDIQHPITAIKPFNSLTSYYHNCMTYDRAARF 244
D 186 GIGIGWKKMNNHNLACNLEYPDQIYPLVSSKFFGSLTSHFEKRLIFDSLSRF 245
QY 245 FVSGQHWTFYPALLSVRLYFILSKVYFSNNKRVYRSGEILGYAFLTWYSLLSRLP 304
D 246 FVSGQHWTFYPALLSVRLYFILSKVYFSNNKRVYRSGEILGYAFLTWYSLLSRLP 304
QY 305 NMPERWVYFSCLAIVGFGHMOSSLNHFASNVYTGLEPSGDMFHQCKTGLNTASAWMD 364
D 305 NMPERWVYFSCLAIVGFGHMOSSLNHFASNVYTGLEPSGDMFHQCKTGLNTASAWMD 364
QY 365 WFGGHLFOIEHLLFPPMPKCHFRKISPIYVNLCKQKNLSYETATWMEANKVYSTRAV 424
D 365 WFGGHLFOIEHLLFPPMPKCHFRKISPIYVNLCKQKNLSYETATWMEANKVYSTRAV 424
QY 425 AMEAKDVTXVPKXMTWEANNTFG 448
D 425 ALQARDITKPLPKLVMEALHTHG 448

RESULT 11
AAG29290
ID AAG29290 standard; Protein; 449 AA.
XX
AC AAG29290;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 34824.
XX
KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPL033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
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PR 07-MAY-1999; 99US-0132863.
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 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
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 PR 15-SEP-1999; 99US-0154018.
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 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
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 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
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 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160880.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 57.0%; Score 1407.5; DB 21; Length 449;
 Best Local Similarity 54.5%; Pred. No. 2,5e-140;
 Matches 242; Conservative 82; Mismatches 119; Indels 1; Gaps 1;

QY 5 KKHISQADLAKHKQPDLMISIKGVYDISKMTKEHPGEBLPLSPAGDVTDAFLAYHP 64
 DB 7 KRYVTSDDLKKNKPPDLMISIQKYYDVSDWKSHPGGEAAILNLAGDVTDAFLAYHP 66
 QY 65 GTAMQYLDREFFGYVYQDVSGSEMSKDYRRLVSEPSKMLFKTRPGKGYCSIFVGLPA 124
 DB 67 GTAMHHLERLHNGYHVRDHSVDSDYRRLLAEFSKRGFLPKKGVTLLYTLTCVGMLA 126
 QY 125 LSYVGYLYCKSTWAMHLCISGLMGLMLQSGWYGHDSCHYQVMPNRKLNRLFOIIAGNVIA 184
 DB 127 AVLYGVLACTSIWAMHLSAVILGLMIQSAVYGHDSGHYTVISTKCNKLIQLSGNCUT 186
 QY 185 GVSVAWKKLDHNTTHPACNSANLDPDIQHLPTIALSPKFPNSLTSYHNCKMTYDPAARF 244
 DB 187 GISIAWKKWTHNAHNLACNSLDHDPDLOHPIPIFAVSTKFPNSWTSRFGKLTFFDPLARF 246
 QY 245 FVSPQHTFEPYALLSVRLYLFILSPKVPNSNKKRYKRSOELIGYAPLITWYSLLSRLP 304
 DB 247 LLSYQHTFYPWCVCGRINLFTQTFLLPS-KKHVDRDLNLAGILVFTWFLVSLP 305
 QY 305 NMPERVMYFTSCLAVAGFOHMOFSLNHPASNYVTGLPSGNDWFHQOTKGLNTITASAMWD 364
 DB 306 NMQERFIYFVSPFAVYALQHVQFCNLHFAADYVTGPPNGDNDFEKOTAGTLDISCRSFM 365
 QY 365 WPHGGLHFOIEHLFPRMKCHFRKISPIYVVKLCQKHNLSEYETATWEMANKWYSTLRAY 424
 DB 366 WFFGGLQFQLEHNLFPRLPRCHLRTVSPVKEICKKHNLPRSLSWEMANWMTIRLKN 425
 QY 425 AMEAKDVTKEPVRKNWMEAMNTFG 448
 DB 426 AIQARDATNPVLDKNLMEAVNTHG 449

RESULT 12
 ID AAY51333 standard; Protein; 449 AA.
 AC AAY51333;
 XX
 XX
 DT 27-APR-2000 (first entry)
 XX
 XX
 DE B. napus sidi protein.
 XX
 KW Sphingolipid desaturase; sidi; sphingobase; ceramide; capnoid;
 KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;

Db 16 KKIYTSKELKKANNNDLWISILGKYVNTWMAKEHPGDAPLNLINAGDVDAFLAFHP 75
Qy 65 GFAWOYLDPEFTGYVODYSVSEMSKDYRLVSEFSKMGLEKTRGKYVCSIFPVSULRA 124
Db 76 GTRMKHLDKLFCTYHKLKDQVSDISRDKLASEFPAKAGFEKKGVLYSLCFVSLUS 135
Qy 125 LSVYGVLYCKSTWAHLCSGLMLMWLQSGVGHDSCHYQVMBRKLNLRFQIIAGNVIA 184
Db 136 ACYGVGLVSGSFPIHMLSGAILGLAMWQJALYGHDAIGHQVMAIRGMNKPAGIFIGNCT 195
Qy 185 GYSVAMWKLDHNTHTFACNSANIDPDIQHLPIAISPKFPNSLTSYHNCKMTYDPAAR 244
Db 196 GISIAWKKWTHNAHHTACNSLDYDPLOHPLMAVSSKLFNSITSVFYGQLFDFDLARF 255
Qy 245 FVSFOHTYPPALSLRVLVFLISFKVPSNNKRYKRSSEILGYAFLTWYSLLSRP 304
Db 256 FVSIOYLYVPIPCVARNVLYLTITLLYSKRR-IPDRGINLTGLIPMTWFLVSRLP 314
Qy 305 NMPERVMTFTSCLAVAGFOHMOFSLNHFASNVYTGHPSGNDMPFOOTKGLNTITASAWMD 364
Db 315 NMPERAVFLVSPFCVGIQIHOITLNFSGDYVGPFGDNWFEKOTRGIDJACSSWMD 374
Qy 365 WTHGGIHFQIETHLFPFPMCKHFRKISPIYVKLCQKHNLSEFATWMAANKWYSTLRAY 424
Db 375 WFGGGLQFQLEHHLFPLRPRCHRISISPICRELCKKYNLPYVLSFYDANVTLTKTLART 434
Qy 425 AMEAKDVTKPVKPMWMEANNTFG 448
Db 435 ALQARDLTNPAPONLAMEANNTFG 458

RESULT 14
AAG07392 standard; Protein: 449 AA.
AAG07392;
17-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 4528.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4528.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
hybridization assay; genetic mapping; gene expression control; promoter;
termination sequence.
KM
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
PF 25-FEB-2000; 2000EP-030139.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.

PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 14-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 22-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 26-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.

	Query Match	55.6%;	Score 1372.5;	DB 21;	Length 449;
	Best Local Similarity	51.7%;	Pred. No. 1.3e-136;		
	Matches 231;	Conservative 95;	Mismatches 120;	Indels 1;	Gaps 1
PR	21-OCT-1999;	99US-0160815.			
PR	22-OCT-1999;	99US-0160980.			
PR	22-OCT-1999;	99US-0160981.			
PR	22-OCT-1999;	99US-0160989.			
PR	25-OCT-1999;	99US-0161404.			
PR	25-OCT-1999;	99US-0161405.			
PR	25-OCT-1999;	99US-0161406.			
PR	26-OCT-1999;	99US-0161359.			
PR	26-OCT-1999;	99US-0161360.			
PR	26-OCT-1999;	99US-0161361.			
PR	28-OCT-1999;	99US-0161920.			
PR	28-OCT-1999;	99US-0161922.			
PR	28-OCT-1999;	99US-0161993.			
PR	29-OCT-1999;	99US-0162142.			
QY	2 EEPKHHISQADLAKGKQPGDWMISKGVYDYSKTKTKHPPGELPLLSFAGQDYDAFPA 61				
DB	4 ETEKKYLTNEBLCXKGNKSGDLMIAIGQGVYVSDMIKTHPGDVTILNLVGDVDPAFPA 63				
QY	62 YHPGAMQYLRPFYGVYVODYSVSEMSKDYRRLVSEPSKQGLFKTPGKGVYCSIFVSV 121				
DB	64 FHPGTAMHHLHLFTGHIHIDFQVSEVSRDYRRMAAEFRKGLGFENKGVHTLYTLAFVPA 123				
QY	122 LFLSVYGVLYCKSTWAKHCSGLMLGMLLQSGWVGHDSCHYQVMPNRKLNRLFOIIAGN 181				
DB	124 MFLNVLGVGLACTSVFAHQIAAALLGLLMIQSAVIGHDSGHVIMSNKSYNRFALLSGN 183				
QY	182 VIAGVSAVAMKLDINHTTHFACNSANLDPDIOHLPILAIISPKFNSLTSYHNCNTTYDRA 241				
DB	184 CLTGISIMVMTNTHAHLACNSLDYDDLOHIIPVFAVSTKFFSSLSFHYDRKLTDPDV 243				
QY	242 ARFVYSFQHTFFYFALLSVRLYFLTSLKGVFNNKRYVKSQELIGYAAFLTWYSLILS 301				
DB	244 ARFLVSYHFFYFVPMCFGRINLFLQTLILFS-KREVPDRALNFAGLLVFWMFEPILVS 302				
QY	302 RLPMWPERVMTFSCLAVAGFQHWQFSLNHFASNYTGLPSGNDWPHOOTKGTINLTASA 361				
DB	303 CLPWPDEPFVFFVFGFTYTLAQHOFTLNHPADYVVPPTGSDMFEKQAGTIDISCRS 362				
QY	362 WMDWFGGLHFOIEHHILPRMPKCHFKRISPIVNLCKQHNLSYETATWENAKMYSTL 421				
DB	363 YMDVFFGGLQFQLEHHILPRRLPRCLTRKVSYPVQELCRKHNLPYRSMGWFANVLINTL 422				
QY	422 RAVAMEADYTKRPVKNNVMEAMNTPG 448				
DB	423 KTAAYQARDVANPVKNLWELALNTHG 449				
RESULT 15					
AAAG53861	standard; Protein; 449 AA.				
ID	AAAG53861 standard; Protein; 449 AA.				
XX	AAAG53861;				
XX	18-OCT-2000 (first entry)				
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 68613.				
DE	Protein identification; signal transduction pathway; metabolic pathway;				
KW	hybridisation assay; genetic mapping; gene expression control; promoter;				
KM	termination sequence.				
XX	Arabidopsis thaliana.				
OS	EP1033405-A2.				
PN	06-SEP-2000.				
XX	25-FEB-2000; 2000EP-0301439.				
PF					

XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134570.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135529.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
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PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 21-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139817.
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PR 24-JUN-1999; 99US-0140655.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140823.
PR 30-JUN-1999; 99US-0140991.
PR 01-JUL-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142055.
PR 08-JUL-1999; 99US-0142390.
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PR 12-JUL-1999; 99US-0142977.
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PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
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PR 20-JUL-1999; 99US-0144352.
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PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145813.
PR 27-JUL-1999; 99US-0145819.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
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PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147392.
PR 06-AUG-1999; 99US-0147600.
PR 06-AUG-1999; 99US-0147803.
PR 06-AUG-1999; 99US-0147816.
PR 09-AUG-1999; 99US-0147933.
PR 09-AUG-1999; 99US-0147935.
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PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
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PR 23-AUG-1999; 99US-0149902.
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PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
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PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.

Search completed: January 1, 2004, 06:36:51
 Job time : 43.2461 secs

PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
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 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 55.6%; Score 1372.5; DB 21; Length 449;
 Best Local Similarity 51.7%; Pred. No. 1.3e-136;
 Matches 231; Conservative 95; Mismatches 120; Indels 1; Gaps 1;

QY 2 EEPKKHISQADLAKHOPGDLMTISIKGVYDISKWKTEHPGELPLISFAGDVTDAFIA 61
 DB 4 ETEKKYITNEDLKXKNSGDLMTIAIQGKYVNSDWMKTHPGDVTIILVIGDVTDAFIA 63
 QY 62 YHGTAMQVYDRFPTGYVODYSVSEMSKDYRRLVSEFSKMGPKTPGKGVYCSIFPVSV 121
 DB 64 FHPGTAMHLDHLFTGTHIRDFOVSEVSRDYRRMAAEFRKLGLENKGAVTLTYTLAFVAA 123
 QY 122 LFAISYGVLYCKSTWHLCSGLMGLMTQSGWGHDSCHYOVMPRKLNRLFOIAGN 181
 DB 124 MFLGVLYGVLAGTSVFAHQIAAALLGLMTQSAVIGHDSGHYVIMSKSYNRFAGLLSGN 183
 QY 182 VIAGSVAAWKKLDHNTTHFAKNSANLDDPDIOHLPIAISPKFNSLTSYHNCCKMTYDRA 241
 DB 184 CLTGISIAWKKMTHNAHLACNSLDYDPDQHPVFAVSTKFFSLSLTSFYDRKLTDPDV 243
 QY 242 ARPFVFOHWTFFPALSLVLYPIISFKVPSNNKRVYRSOEIIGYAAFLTWYSLLS 301
 DB 244 ARFLVSIQHFTYYPVPCFGRINLFIQTFLLFS-KREVDPRLNPAIGILVFWTWPFLVS 302
 QY 302 RLBNWBERVVMYFTSCLAIVAGFOHMFSLNHFASNVYTGSLPSGNDWFHOQTKTLNITASA 361
 DB 303 CLBNWBERFFVFTSFTVTALQHIQFTLNFPADVYGPPTGSDWPEKOAAGTIDISCRS 362
 QY 362 WMDWFGHGLFQIEHHIFPPMPKCHFRKISPIYNKLCQKINLSYETATWMEANKMYVSTL 421
 DB 363 YMDWFGGLQFOLEHHIFPRLPRCHLRKVSPPVQELCKKINLPIYSMSWFEAVVLTINTL 422
 QY 422 RAVAMEAKDYTKRVPKMWMEANMTFG 448
 DB 423 KTAAYQARDVANPVXNLVWEALNTHG 449

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 16.8616 Seconds
(without alignments)
255.128 Million cell updates/sec

Title: US-09-857-524B-2
Perfect score: 2470
Sequence: 1 MESEPKGHISQADLAKHKQPG.....KDYTKPVPKMWMEANNTFG 448

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1407.5	57.0	449	2 A84900	hypothetical prote
2	1395.5	56.5	449	2 T50555	delta-8 sphingolip
3	1391.5	56.3	458	2 S68358	delta-8 sphingolip
4	1372.5	55.6	449	2 T47950	delta-8 sphingolip
5	622	25.2	523	2 JC7556	linoleoyl-CoA desa
6	454	18.4	444	2 T13155	linoleoyl-CoA desa
7	449	18.2	444	2 UG0180	delta-6 fatty acid
8	449	18.2	473	1 T26280	linoleoyl-CoA desa
9	385	15.6	447	1 T43319	delta-5 fatty acid
10	371.5	15.0	454	2 H88791	protein T13P2.1 f
11	257	10.4	345	2 T36617	probable Delta6 fa
12	220	8.9	359	2 S35157	Delta6 fatty acid
13	183	7.4	368	2 S54609	linoleoyl-CoA desa
14	173	7.0	359	2 S52650	omega-3 fatty acid
15	166.5	6.7	384	1 S54484	probable fatty aci
16	161	6.5	387	2 T07687	omega-6 desaturase
17	159.5	6.5	135	2 A86390	hypothetical prote
18	157	6.4	137	2 T52469	cytochrome b5 (imp
19	152.5	6.2	134	2 T52469	cytochrome b5 (imp
20	152.5	6.2	147	2 S67453	probable heme bind
21	152	6.2	438	2 T15039	omega-3 fatty acid
22	151	6.1	370	2 B83034	conserved hypochet
23	148.5	6.0	120	2 S63052	cytochrome b5 - ye
24	148	6.0	139	2 S46306	cytochrome b5 - co
25	146.5	5.9	134	2 T00796	cytochrome b5 At2g
26	145	5.9	121	2 H96631	probable Cytochrom
27	144.5	5.9	140	2 T52468	cytochrome b5 (imp
28	143	5.8	427	2 G70590	probable deaA3 pro
29	142.5	5.8	135	2 T09946	cytochrome b5 - 80

30	142.5	5.8	890	2 T11805	nitrate reductase
31	142.5	5.8	900	2 S47029	nitrate reductase
32	142	5.7	881	2 S25445	nitrate reductase
33	141.5	5.7	352	2 B69901	fatty-acid desatur
34	141.5	5.7	453	1 JQ2339	omega-3 fatty acid
35	141.5	5.7	904	1 RDNTNT	nitrate reductase
36	140.5	5.7	446	1 JQ2336	omega-3 fatty acid
37	140.5	5.7	591	1 CBBY2	L-lactate dehydrog
38	140.5	5.7	904	1 RDNTNS	nitrate reductase
39	139.5	5.6	134	2 T14454	cytochrome b5 - w1
40	139.5	5.6	135	2 S49200	cytochrome b5 - co
41	139	5.6	132	2 E84905	probable cytochrom
42	139	5.6	380	2 JQ2338	omega-3 fatty acid
43	138.5	5.6	359	2 AG2005	omega-3 fatty acid
44	137.5	5.6	129	2 T41083	probable cytochrom
45	137.5	5.6	431	2 T07685	omega-3 fatty acid

ALIGNMENTS

RESULT 1
A84900
hypothetical protein At2g46210 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #ext_change 02-Feb-2001
C/Accession: A84900
R/In, X.; Kaul, S.; Rounsley, S.D.; Shua, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MID:20083487; PMID:10617197
A/Accession: A84900
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-449 <80>
A/Cross-references: GB:AF002093; NID:g3702328; PIDN:AAC6885.1; GSPDB:GN00139
C/Genes:
A/Gene: At2g46210
A/Map position: 2

Query Match	57.0%	Score 1407.5:	DB 2:	Length 449:
Best Local Similarity	54.5%	Pred. No. 1.2e-110:		
Matches 242:	Conservative 82:	Mismatches 119:	Indels 1:	Gaps 1:
Qy	5	KKHISQADLAKHKQPGDLWISIKGVYDISKTKHSGGELPLSPAGQVTDFAIAYHP	64	
Db	7	KRYVTSEDLKKNKPGDLWISIQGVYDVSMDVKSHRGEAAILNLAGQVTDFAIAYHP	66	
Qy	65	GTAMQYLDKFPFGYVQDYVSSEMSKDYRLVSEPSKMGLPFTGKGVYCSIFPVSVLPA	124	
Db	67	GTAMHLEKLNHGYVRDHSVDVSRRLAEFSKRGLPDKGCHVTLYTLTCVGMVLA	126	
Qy	125	LSVYGVLYCKSTMAHLCGSLMGMLGSGVGHDSCHYQVWPNRKLNLFOILANVIA	184	
Db	127	AVLYGVLYCTSIWAHLISAVLLGLMTQSAVYGHDSGHTVYTSKPCNKLQILSNCLT	186	
Qy	185	GVSVAWMLKDHNTTHPACNSANLDDPDIOHLPILAIASPKFNSLTSYHNCMKVYDPAARF	244	
Db	187	GSIAWMLKWNHNAHIAAGNSLDHDPDLOHPIPIFAVSTKFFNSMTSFRGKRLTFDPLARF	246	
Qy	245	FVSGHWTYTPALLSVRLYFLTSLFKVNVSNKRVKRSQELIGVAFPLTWYSSLSLRP	304	
Db	247	LISYQHWTYTPVPCVGRINLFIQTFLLRS-KRHVPDRALNTAGLIVFTWTFPLVSVLP	305	
Qy	305	NMPERVMTSCLAAVGFQHWQFSLNHPASVYTGIPSGNDWPHQOTKGTNLNTASAMWD	364	
Db	306	NMOGRFIFVFSFAVYALDHVQCLNHPADAVYTGPNNDWPEKQTAGLIDISCRSPMD	365	
Qy	365	WFGHGLHFOIEHNLFRPMKPKCHFRKISPIVNLKCOGNLSYETATWMEANKVYSTLRVAV	424	
Db	366	WFGGLHFOIEHNLFRPLRCHLRITVSPVVKELCKKNLPYRSLSWMEANVTIRTLKNA	425	

Qy 425 AMEAKDVTKEPVKMMWEAMNTFG 448
 Db 426 AIQARDTNPVLLKMLMEAVNTHG 449

RESULT 2

delta-8 sphingolipid desaturase [imported] - rape

C/Species: Brassica napus (rape)
 C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 15-Sep-2000
 C/Accession: T50555

R/Speering, P.; Zaehneringer, U.; Heinz, E.

J. Biol. Chem. 273, 28590-28596, 1998

A/Title: A sphingolipid desaturase from higher plants. Identification of a new cytochrome

A/Reference number: Z22986; MUID:99003197; PMID:9786850

A/Accession: T50555

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-449 <SPE>

A/Cross-references: EMBL:AJ224160; PIDN:CA11857.1

A/Experimental source: cultivar Drakkar

C/Genetics:

Query Match 56.5%; Score 1395.5; DB 2; Length 449;
 Best Local Similarity 54.1%; Pred. No. 1.2e-109;
 Matches 240; Conservative 85; Mismatches 118; Indels 1; Gaps 1;

Qy 5 KKHISOADLAKHKOPGDLWISIKGKYDYSKMTKEHPGGLPLLSFAGODVDTAFIAYHP 64
 Db 7 KRFTSDLLKKNHNGPDLWISIKGKYDYSKMTKEHPGGLPLLSFAGODVDTAFIAYHP 66

Qy 65 GTAMQVLDREFTGYVVDYVSSEMSKDYRLVSEFSKMGLEFKTPGKGVYCSIFVSVLFA 124
 Db 67 GTAMRHLENNHNGYHVDHVDSDYRRLAERFSKRGLEFKKGHVTLYTLTCVAAMLA 126

Qy 125 LSYVGVLYCKSTVAHLCSGILMGMLQSGVGVHDSCHYOVMRNKLNRLFOIAGNVIA 184
 Db 127 AVAYGVVACTSIYAHLSAVILGLMIOASVGVHDSCHYVNTSTKPKCKLVQLSGNCIT 186

Qy 185 GVSVAWMLKLDHNTTHFACNSANLDPDIQHLPIAISPKFNSLTSYHNCMTYDRAARF 244
 Db 187 GISIAWKKMTHNAHNSLSDHDPDQHLPLVLSKFKFSMTSRYSRGLTFDPLARF 246

Qy 245 FVSGQHTFYPALISVRLYLFIISFKVFSNNKRYRSGEILGYAFLTWYSLLSRLP 304
 Db 247 LLSYQHSFYPIMCVGRINLFIQTLILFSS-RRVPPRALNIGILVFWTFPLVSEFLP 305

Qy 305 NMPERVVYFTSCLAVAGFQHMQFSLNHPASVNYTGLSGNDWPHQOTKGLTINTASAMWD 364
 Db 306 NMQERITFVFLSNVAVYAIQHVQFLNHPADVTPGPRGNDWFEKQTAGTLDISCRSYMD 365

Qy 365 WFGHGLFQIEHNLFPMPKCHFRKISPIYVKLCOKHNSYETATWMEANMYSTLRAY 424
 Db 366 WFEGLQFQIEHNLFPRLPRCHLRGSPVYQELCKKGNLPRSLSWMEANVTLRTIRKA 425

Qy 425 AMEAKDVTKEPVKMMWEAMNTFG 448

Db 426 AVQARDVNTNPVLLKMLMEAVNTHG 449

RESULT 3

delta-8 sphingolipid desaturase (EC 1.14.99.-) [similarity] - common sunflower

C/Species: Helianthus annuus (common sunflower)

C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000

C/Accession: S68358

R/Speering, P.; Schmidt, H.; Heinz, E.

Eur. J. Biochem. 232, 798-805, 1995

A/Title: A cytochrome-b(5)-containing fusion protein similar to plant acyl lipid desaturase

A/Reference number: S68358; MUID:96028121; PMID:7588718

A/Accession: S68358

A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-458 <SPE>

A/Cross-references: EMBL:X87143; NID:g1040728; PIDN:CAA60621.1; PID:g1040729

C/Superfamily: cytochrome b5 core homology

C/Keywords: heme; iron; metalloprotein; oxidoreductase

F16-90/Domain: cytochrome b5 core homology <CB5>

F51,74/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 56.3%; Score 1391.5; DB 2; Length 458;
 Best Local Similarity 52.7%; Pred. No. 2.7e-109;
 Matches 234; Conservative 90; Mismatches 119; Indels 1; Gaps 1;

Qy 5 KKHISOADLAKHKOPGDLWISIKGKYDYSKMTKEHPGGLPLLSFAGODVDTAFIAYHP 64
 Db 16 KKITSELKKNHNPDLWISIKGKYDYSKMTKEHPGGLPLLSFAGODVDTAFIAYHP 75

Qy 65 GTAMQVLDREFTGYVVDYVSSEMSKDYRLVSEFSKMGLEFKTPGKGVYCSIFVSVLFA 124
 Db 76 GTAMKHLDKLFTHYHLDYVSDISRDYRLASEPAKAGFEKKGHVTLYTLTCVAAMLA 135

Qy 125 LSYVGVLYCKSTVAHLCSGILMGMLQSGVGVHDSCHYOVMRNKLNRLFOIAGNVIA 184
 Db 136 ACYVGVLYSGSFVHMLSGAILGLAMWQIAYLGDHGHYQMMATRMNNKPFAGIFGNCIT 195

Qy 185 GVSVAWMLKLDHNTTHFACNSANLDPDIQHLPIAISPKFNSLTSYHNCMTYDRAARF 244
 Db 196 GISIAWKKMTHNAHNSLSDHDPDQHLPLVLSKFKFSMTSRYSRGLTFDPLARF 255

Qy 245 FVSGQHTFYPALISVRLYLFIISFKVFSNNKRYRSGEILGYAFLTWYSLLSRLP 304
 Db 256 FVSGYHLYVYPIVCARVNLVYQTLITLLISKR-IDRGNILGTLIFWTWPLVLSRLP 314

Qy 305 NMPERVVYFTSCLAVAGFQHMQFSLNHPASVNYTGLSGNDWPHQOTKGLTINTASAMWD 364
 Db 315 NMPERAVFVLSVPCVGIQIIOPTLNHFSGDYVGVGPKGNWFEKQTAGTLDISCRSYMD 374

Qy 365 WFGHGLFQIEHNLFPMPKCHFRKISPIYVKLCOKHNSYETATWMEANMYSTLRAY 424
 Db 375 WFEGLQFQIEHNLFPRLPRCHLRGSPVYQELCKKGNLPRSLSWMEANVTLRTIRKA 454

Qy 425 AMEAKDVTKEPVKMMWEAMNTFG 448
 Db 435 AIQARDTNPAPQNLMEAVNTHG 458

RESULT 4

delta-8 sphingolipid desaturase (EC 1.14.99.-) [validated] - Arabidopsis thaliana

N/Alternate names: protein F2A19.180

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000

C/Accession: T47950; T51848

R/De Haan, M.; Maarse, A.C.; Grievell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quec

A/Title: A sphingolipid desaturase from higher plants. Identification of a new cytochrome

A/Reference number: Z22986; MUID:99003197; PMID:9786850

A/Accession: T51848

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-449 <DEH>

A/Cross-references: EMBL:AJ32962; PIDN:CA81088.1

A/Experimental source: cultivar Columbia; BAC clone F2A19

R/Speering, P.; Zaehneringer, U.; Heinz, E.

J. Biol. Chem. 273, 28590-28596, 1998

A/Title: A sphingolipid desaturase from higher plants. Identification of a new cytochrome

A/Reference number: Z22986; MUID:99003197; PMID:9786850

A/Accession: T51848

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-449 <SPE>

A/Cross-references: EMBL:AJ224161; PIDN:CA11858.1

A/Experimental source: cultivar Columbia; mainly green parts, some flowers, few roots

C/Genetics:

A:Gene: sld1
 A:Map position: 3
 A:Note: P2A19.180
 C:Function:
 A:Description: (EC 1.14.99.-); delta-8 sphingolipid desaturase [validated, PMID:99003197]
 C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 55.6%; Score 1372.5; DB 2; Length 449;
 Best Local Similarity 51.7%; Pred. No. 1e-107;
 Matches 221; Conservative 95; Mismatches 120; Indels 1; Gaps 1;

QY 2 EEPKRIISQADLAKHOPGDLWISIKKYVYDISKWKTEHGEGLPLLSFAGQDVDTAFIA 61
 DB 4 ETEKRIITNEDLKKHKSGLMIAIQOKYVNSDWIKTHPGDVTILNLVGQVDTAFIA 63
 QY 62 YHGTAMQVLDLRFPGTYVODYSVSEMSKDYRLVSEFSMGKFKTPGKGVCSIFVSV 121
 DB 64 FHGTAMHLDHLEFTYHNRDFQVSEVSRDVRMAAEFRGLGFENKGHVTLTYTLAFVA 123
 QY 122 LFLATSYGVLYCKSTWAAHCSGLMGMLQSGWGHDSCHYOVNPNRKLNLFOIAGN 181
 DB 124 MFLGVLYGVLYCTSVAAHQIAALLGLMIQSAVIGHDSGHVYMSKSYNRPQDLN 183
 QY 182 VIAGSVAAWKLDPNTHHFAANSANLDPDIOHLPIIASPFNSLTSYYHNCMTYDA 241
 DB 184 CLGISIAWKKWTHNAHLAANSLDVDPDQHPVFAVSTKFPSSLTSRFRDKLTFDPV 243
 QY 242 ARPFVSFOHMTFYPALLSVRLYLFIISFKVVSNNKRVYKRSOELLGYAFLTWYSLIS 301
 DB 244 ARFLVSYOHFTYYPVWCFGRIINLFIOFLFLFS-KREVDPALNFGILVFWTFPLVS 302
 QY 302 RLDPNPERVWYFPTSCLAVAGFQHMOPSLNHPASNVYTGLPSGNDWFHQTKGLNTASA 361
 DB 303 CLPNWERPFVFTSTVTAHQIOTLNFADYVGPSTGDMWEKQAGTIDISCBS 362
 QY 362 WMDWFGHLPFOIENHLPFRMPKCHFRKISPIVNLCKQKHLSEYETATWEANKVYSTL 421
 DB 363 YMDWFGHLPFOIENHLPFRMPKCHFRKISPIVNLCKQKHLSEYETATWEANKVYSTL 422
 QY 422 RAVAMEAKDVTYKVPKQWMEANMTG 448
 DB 423 KTAAYQARDVANPVNKLWEALNTHG 449

RESULT 5

JCT556
 l1no1eoyl1-CoA desaturase (EC 1.14.19.3) - Mucor rouxii
 N:Alternate names: delta6-desaturase
 C:Species: Mucor rouxii
 C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Jun-2002
 C:Accession: JCT556
 R:Laoteng, K.; Manontarat, R.; Tanticharoen, M.; Cheevadhanarak, S.
 Biochem. Biophys. Res. Commun. 279, 17-22, 2000
 A:Title: Delta6-desaturase of Mucor rouxii with high similarity to plant delta6-desaturase
 A:Reference number: JCT556; PMID: 20563795; PMID:11112411
 A:Accession: JCT556
 A:Molecule type: DNA
 A:Residues: 1-523 <LAO>
 A:Cross-references: GB:AF290983
 A:Experimental source: strain ATCC 24905
 C:Keywords: This enzyme, a membrane-bound key enzyme, is responsible for the transformation of oxidoreductase; transformation

Query Match 25.2%; Score 622; DB 2; Length 523;
 Best Local Similarity 29.7%; Pred. No. 1.9e-44;
 Matches 146; Conservative 76; Mismatches 191; Indels 78; Gaps 9;

QY 20 GDLWISIKGVYDISKWKTEHGEGLPLLSFAGQDVDTAFIAHPRGAWYL----- 71
 DB 34 GDSVLYEQKVVYNNFMAGPGSEALRSALGRDVTDEIRTMHPQVVEKLLNLYCTGD 93
 QY 72 -----DRPFT-----GYVQDYSVS-----EMSKD-- 91

DB 94 YMPDVIRPASKMOHTFTKPKEDKPYLTATWEGGFTVQAYDDAIDLHKHSHDLIKAV 153
 QY 92 -----YRLVSEFSKMGLEKTPGKGVCSIF-----FVSLPALSYGVY 131
 DB 154 LQKDLNGDOIRNAVRLAEALYAKGLF-----CNWKYARREGCRYTLILFLSLMFTL 206
 QY 132 YCKSTWAAHCSGLMGMLQSGWGHDSCHYOVNPNRKLNLFOIAGNVIAGVSAWV 191
 DB 207 KQETHTWMAAGAFMAFMHQVLVTAHDAGHNEITKSIDHIVIGIYIANFGLSLGWW 246
 QY 192 KLDNTHHFAANSANLDPDIOHLPIIASPFNSLTSYYHNCMTYDAARFVSFOH 251
 DB 267 KQNHVHNLVTHNPRHNDPDIQHPFMAITTKFPNNYTSYYKRVLPFDAARFVHQQY 326
 QY 252 TFPYALLSVRLYLFIISFKVVSNNKRVYKRSOELLGYAFLTWYSLISRLPNPERVW 311
 DB 327 LYLLISFGFNLHLSFAYLUT-CNVVTRITLVLGTFYVWFGSLSLTLPMTMIRIA 385
 QY 312 YFTSCLAVAGFQHMOPSLNHPASNVYTGLPSGNDWFHQTKGLNTASAWMDFHGLH 371
 DB 386 YIMVSYMLFPRLHVOQTLTSHFGMSTEDRGP-BPPAKMLRTTMDVDCPEMDHMFHGLQ 444
 QY 372 FOIENHLPFRMPKCHFRKISPIVNLCKQKHLSEYETATWEANKVYSTLRAVAMEAKDV 431
 DB 445 YQAVHNLFPRLHRLRQCVPYKFKCDEVGLHYVWYNSFGVYLGTLKSVADQVFM 504
 QY 432 TKPVPKQW-VW 441
 DB 505 NEVAKSNAEIW 515

RESULT 6

T13155
 l1no1eoyl1-CoA desaturase (EC 1.14.19.3) [validated] - human
 N:Alternate names: Delta6 fatty acid desaturase; protein DKFZp586C201.1
 C:Species: Homo sapiens (man)
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 03-Jun-2002
 C:Accession: T13155; T08765
 R:Cho, H.P.; Nakamura, M.T.; Clarke, S.D.
 J. Biol. Chem. 274, 471-477, 1999
 A:Title: Cloning, expression, and nutritional regulation of the mammalian Delta-6 desaturase
 A:Reference number: Z17612; PMID:99085046; PMID:9867867
 A:Accession: T13155
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-444 <CHO>
 A:Cross-references: EMBL:AF126799; NID:94406527; PID:94406528; PIDN:AAD20018.1
 R:Mambutti, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, March 1999
 A:Reference number: Z16471
 A:Accession: T08765
 A:Molecule type: mRNA
 A:Residues: 'RTG', 138-428, 'D', 430, 'W', 432-444 <WAM>
 A:Cross-references: EMBL:AL050118
 A:Experimental source: adult uterus; clone DKFZp586C201
 C:Genetics: GDB:PADSD6
 A:Gene: GDB:PADSD6
 A:Cross-references: GDB:9956652
 A:Note: DKFZp586C201.1
 C:Superfamily: cytochrome b5 core homology
 C:Keywords: cytochrome; heme; iron; metalloprotein; oxidoreductase; unsaturated fatty
 F;18-94/Domain: cytochrome b5 core homology <CB5>
 F;53/76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 18.4%; Score 454; DB 2; Length 444;
 Best Local Similarity 28.7%; Pred. No. 2.1e-30;
 Matches 124; Conservative 65; Mismatches 185; Indels 58; Gaps 13;

QY 9 SQADLAKHOPGDLWISIKKYVYDISKWKTEHGEGLPLLSFAGQDVDTAFIAHPRGAWYL 68
 DB 22 SWEIEQKHNLRTRDRLVLDKRYNITTKMSIOHPGGGRVIGHVAGBATATAFRAFH----- 77
 QY 69 QYLDLRFPGTYV-----QDYSV-SEMSKDYRLVSEFSKMGLEKTPGKGVY 113

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Db      78 ---DLFVGKFLRLIGELAPBEPBQDHGKSKITFEDPALKRTAEDMLFRTN----- 129
Qy      114 CSIFF-----VSVLFALSYVGLYCKSTV-AHLCSGLMGMLOSQVNGHSCHYQM 166
Db      130 -HVFLLLLAHITALESIAMFTVFPNGMIFPLITAFVLTATSOAQGWLOHBYGHLSYV 188
Qy      167 PNRKRLRLFOIAGNVIAQSVAMWKLDPHTHHPACNSANLDDPDQHLPIAISPKFENS 226
Db      189 RRPKNHLVHKPFIYGHKGSANMNNRHFQHAKRPIFKDDVNNLHVFLUG----EW 244
Qy      227 LTSYHNCIMTYDRAARFVVSFOHMTFY----PALLSVRLYLFLSKVFSN-NKRVYK 281
Db      245 QPIREYKXKLLKY-----LPYNHQBHFYFLGIPPLIPMYQYQIIMTMIVHKMVDLAWA 299
Qy      282 RSGEILIGYAFLTWYSLLSLRLPNRBPVWYFTSCAVAGFQHWQSLNHPASVYTGLP 341
Db      300 VSYIIFFTYIIPFYGLGLML-----FLNFRFLFESHMFV-WYQWNIHIMEI--DOE 350
Qy      342 SGNDWFHOQTKFTLNTASAMWDPHGGHFOIENHLPMPKCHPRKISPIVNLCKQH 401
Db      351 AYRDMSSQITATCNVBOSEFFNDMFGHLMFOLEHLPMPKHNHKLAPLVKSLCANK 410
Qy      402 NLSYETATWMEA 413
Db      411 GIEYQKPLLR 422

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RESULT 7

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JG0180
Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
C/Accession: JG0180
R/Aki, T.; Shimada, Y.; Inagaki, K.; Hishashimoto, H.; Kawamoto, S.; Shigeta, S.; Ono, K.
Biochem. Biophys. Res. Commun. 255, 575-579, 1999
A/Title: Molecular cloning and functional characterization of rat delta-6 fatty acid des
A/Reference number: JG0180, PMID:99160394, PMID:10049752
A/Accession: JG0180
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-444 <AKI>
A/Cross-references: DDBJ:AB021980; NID:94514721; PIDN:BAW5496.1; PID:94514722
C/Superfamily: cytochrome b5 core homology
C/Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid biosynthe
F:18-94/Domain: cytochrome b5 core homology <C85>
F:53/76/Binding site: heme iron (His) (axial ligands) #status predicted

```

Query Match 18.2%; Score 449; DB 2; Length 444;

Best Local Similarity 26.1%; Pred. No. 5.7e-30;

```

Matches 120; Conservative 75; Mismatches 186; Indels 78; Gaps 13;
Qy      1 MEEPKHISQADLAKHKGPDLMISIKGYDISKWTKEHPGELPLSPAGQVTDAPL 60
Db      14 LQAPMPTFMWESIQKINLRTDRWLVIDRKYVNTKMSQRHPGHRVIGHYSGEADTAPR 73
Qy      61 AHNPGANQYLDREFFGYVQDYV-----SEMSKYRLVSEFSKMGLP 105
Db      74 AFH-----LDLDFGKFLKPLLIGELAPBEPBLSDRGSSQITTEDFRLAKKTAEDMNLF 126
Qy      106 KTPGKGVCSIFVSVLPAISVGLVYCKSTW-AHLCGGLMGMLOSQVNGHSDCHQ 164
Db      127 KTNHLEFLLLSHIIYMEISAWFISYFGNGMIPYITAFVLTATSOAQGWLOHBYGHLS 186
Qy      165 VMPNRKRLRLFOIAGNVIAQSVAMWKLDPHTHHPACNSANLDDPDQHLPIAISPKKF 224
Db      187 VYKKSIMNHIIVHKFVIGHKGSANMNNRHFQHAKRPIFKDDVNNLHVFLUG--W 244
Qy      225 NSLTSTYHNCKMTYDAARFVVSFOHMTFY--PALLSVRLYLFLSKVFSNNKR--- 278
Db      245 QPLE--YGRKKLKY-----LPYNHQBHFYFLGIPPLIPMY--FOYQIIMTIRRRRW 293
Qy      279 -----YKRSQELIGYAFLTWYSLLSLRLPNRBPVWYFTSCAVAGFQ 323

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Db      294 VDLAMASVYARFYTIIIPFYGLGLVFLNFRFLFESH-----WFLV----- 335
Qy      324 HMOFSLNHPASVYTGLPBGNDWFHOQTKGTANTITASAMWDPHGGHFOIENHLPMP 363
Db      336 -WYQWNIHIMEI--DLDPYRDMFSSQALATCNVBOSEFFNDMFGHLMFOLEHLPPTMP 392
Qy      384 KCHFRKISPIVNLCKQHLSYETATWMEANKNVYETLR 422
Db      393 RHNHKLAPLVKSLCANKHGIYQKPLLRALLDIYSSLK 431

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RESULT 8

linoleoyl-CoA desaturase (EC 1.14.19.3) W08D2.4 - Caenorhabditis elegans

```

N/Alternate names: Delta6 fatty acid desaturase
C/Species: Caenorhabditis elegans
C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 03-Jun-2002
C/Accession: T26280; T37238
R/Swinburne, J.; Alnough, R.
submitted to the EMBL Data Library, March 1996
A/Reference number: Z20188
A/Accession: T26280
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-473 <WIL>
A/Cross-references: EMBL:Z70271; PIDN:CA94233.1; GSPDB:GN00022; CESP:W08D2.4
A/Experimental source: clone W08D2
R/Napier, J.A.; Hey, S.J.; Lacey, D.J.; Shewry, P.R.
Biochem. J. 330, 611-614, 1998
A/Title: Identification of a caenorhabditis elegans Delta6-fatty-acid-desaturase by he-er
A/Reference number: Z21637, PMID:98149727, PMID:9480865
A/Accession: T37238
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-38,69-430,'V',432-473 <NAP>
A/Cross-references: EMBL:AF031477; NID:93088519; PIDN:AA015586.1; PID:93088520
C/Genetics:
A/Gene: CESP:W08D2.4
A/Map position: 4
A/Intons: 13/3; 39/2; 234/3; 277/3; 378/1; 413/3
C/Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C/Keywords: alternative splicing; oxidoreductase; unsaturated fatty acid biosynthesis

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Query Match 18.2%; Score 449; DB 1; Length 473;

Best Local Similarity 28.2%; Pred. No. 6.1e-30;

```

Matches 138; Conservative 65; Mismatches 187; Indels 100; Gaps 18;
Qy      17 KQGDLMISIKG-VYDISKWTKEHPG-----ELPLS----- 49
Db      5 KNASGLRMKVDGKMLYSELVYKKGAVIEOYSIPLANKIETRGITTRGSSNALDI 64
Qy      50 ---FAGQVTDAPFAYHPGTANQY-----LDRFRTGYVQDY 83
Db      65 LVFYRNSDATTHIFAHHEGSSQAYKQDLCLKGHEHDEFLKQLEKRLDKVDINVSAYDV 124
Qy      84 SYSEMSKDYRLVSEFSK-----GLFKTEGKGYGCSIFPVSUVPALSYVC-VLYKCS 135
Db      125 SVAQERK---WVESPEKRLKLDHDKLAKNE-----TYFLPKAISTJISIMAFAYLOY 175
Qy      136 TNAHLCGGLMGMLOSQVNGHSDCHYOVMPNRKRLRLFOIAGNVIAQSVAMWKLDPH 195
Db      176 LGMYITISACLLALAQGFQFGLTHFCHQPTKRLPLNDTISLFGNFGLOGFSRDWKKDG 235
Qy      196 NTHHFAQNSANLDDPDQHLPIAISPKFNSLTSYHNCIMTYDRAARFVVSFOHMTFY 255
Db      236 NTHHAATNVIDHDGIDLAPLAFIP---GDLCKY---KASFEKALIKIVPYOHLYFTA 288
Qy      256 ALLSVRLYLFLSKVFSNNKRVYKRSOE-----ILGTAAPLTWYSLLSLRLPNMP 307
Db      289 MLEPMLRFSWTGOSVQVQFKENQMEYKYORANFWEQATIVGHAWV-FYQLFL--LPTWP 345
Qy      308 ERMVMTYTSCLAVAG--FQHWQPSLNHPASVYTGLPBG-----NDWHDQTKGTANTITASA 361

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Db      346 LRAVAYIISQMGGLIAH-VTFNNNSVDKY---PANSRLINFAALDILFTTRNMTSPSP 401
Qy      362 MWDMFHGSLHFOIEHLLFPMRPMCKHPRKXSPIYNKLCQKHNLSYERATWMEANKMYSTLU 421
Db      402 FIDMLMGSLNYQIEHLLFTMPRCNLNACMKYKWKCKENNLPLYLVDYFDGYANMLQOL 461
Qy      422 RAVA--MEAK 429
Db      462 KMAHEHIQAK 471

RESULT 9
T43319
Deltas fatty acid desaturase (EC 1.14.99.-) T13F2.1 [validated] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C:Accession: T43319; T24875
R:Michaelson, L.V.; Napier, J.A.; Lewis, M.; Griffiths, G.; Lazarus, C.M.; Stobart, A.K.
FEBS Lett. 439, 215-218, 1998
A:Title: Functional identification of a fatty acid deltas desaturase gene from Caenorhab
A:Reference number: Z22422; MUID:99059458; PMID:9845325
A:Accession: T43319
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-447 <MIC>
A:Cross-references: EMBL:AF078796; NID:94003522; PIDN:AA095143.1; PID:94003523
R:Swindburne, J.
Submitted to the EMBL Data Library, October 1996
A:Reference number: Z19947
A:Accession: T24875
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-197; VSHFNN, 198-447 <MII>
A:Cross-references: EMBL:281122; PIDN:CA03352.1; GSPDB:GN00022; CESP:T13F2.1
C:Genetics:
A:Experimental source: clone T13F2
A:Gene: CESP:T13F2.1; des-5
A:Map position: 4
A:Map position: 4
A:Introns: 43/3; 80/3; 197/3; 295/3; 318/2; 349/1; 384/3
C:Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match      15.6%; Score 385; DB 1; Length 447;
Best Local Similarity 25.0%; Pred. No. 1.4e-24;
Matches 115; Conservative 74; Mismatches 199; Indels 72; Gaps 14;

Qy      23 WISIKGVYDISKMT-KEHGGELPLLSFAGODVTDALFAYHPT--AMQYLDREFFTGY 79
Db      12 FIKIDKMGQIDDAVLRSHPGGS-ATTYKNDATVFTHTFGSKKAYQWLTELKKECP 70
Qy      80 VQDYSVSEMSKDYRLVSEFSKGLF-----KTPKGVY--CSIFP 118
Db      71 TQEPPEIPDKDPIDKIDVNV-MGTFNISEKSAQINKSFDTLRMRVRAEGLMDGSPLEY 129
Qy      119 V-----SVLFALSVGVLYCKSTWMLCSGLMGLMLQSGWGHDSCHYQVMPNPK 170
Db      130 IKKILETITLIFA-----FLQYHTYLLPSAILMGVAMQOLGWIHFAHQLPKNXY 183
Qy      171 LNRLFOIAGNVIAVAVAMWKLDNTHHFAFNSANLDPDIQHLPIAISPKFNSLTGY 230
Db      184 YNDLASVFGNPLQSGSSGKWEQHNVAHAAATVVRDGDLDLP-----FYATVAH 236
Qy      231 YHNCKMTYRRAARFVFSQ---HMTFYALLSVRLYLFIISFKVVSNNKRVYKRSQEI 286
Db      237 LNN---YSQDSVWVTLFRMOHVHTFMPLFRLISWLLQSIIFVSQMPHYDYUYNAT 292
Qy      287 ---LGYAFLTWYSLLSRLPMPRERVYFTSCLAVAG-----FOHWQPSLNHFAFN 335
Db      293 YEOVGSLHMANSLGQLYFLPDSTIMFVLVSHLVGGLSHVTFNNYSVEKPAISN 352
Qy      336 VYTGLPFGNDWPHQQTGTLNITASAMWDFHGLHFOIEHLLFPMRPMCKHPRKXSPIYN 395

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Db      353 IM-----SNVACIQIMTTRNNRPGRFIDMLWGLNYQIEHLLFTMPRRNLNTVMPLVK 406
Qy      396 KLCQKHNLSYERATWMEANKMYSTLRAVAMEAKDYTKPV 435
Db      407 EFAAANGLPYWDYFTGFWLEIEQRFNIAVAAKLTCKI 446

RESULT 10
H88791
protein T13F2.1 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: H88791
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_eleg
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: H88791
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-454 <STO>
A:Cross-references: GB:chr_IV; PIDN:CA03352.1; PID:93879828; GSPDB:GN00022; CESP:T13F2.1
C:Genetics:
A:Gene: T13F2.1
A:Map position: 4
C:Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase

Query Match      15.0%; Score 371.5; DB 2; Length 454;
Best Local Similarity 24.6%; Pred. No. 1.9e-23;
Matches 115; Conservative 74; Mismatches 199; Indels 79; Gaps 15;

Qy      23 WISIKGVYDISKMT-KEHGGELPLLSFAGODVTDALFAYHPT--AMQYLDREFFTGY 79
Db      12 FIKIDKMGQIDDAVLRSHPGGS-ATTYKNDATVFTHTFGSKKAYQWLTELKKECP 70
Qy      80 VQDYSVSEMSKDYRLVSEFSKGLF-----KTPKGVY--CSIFP 118
Db      71 TQEPPEIPDKDPIDKIDVNV-MGTFNISEKSAQINKSFDTLRMRVRAEGLMDGSPLEY 129
Qy      119 V-----SVLFALSVGVLYCKSTWMLCSGLMGLMLQSGWGHDSCHYQVMPNPK 170
Db      130 IKKILETITLIFA-----FLQYHTYLLPSAILMGVAMQOLGWIHFAHQLPKNXY 183
Qy      171 LNRLFOIAGNVIA-----GVSVAWMLDNTHHFAFNSANLDPDIQHLPIAISPKF 223
Db      184 YNDLASVFGNPLQVSHIFNNGFSSGKWEQHNVAHAAATVVRDGDLDLP-----F 236
Qy      224 FNSLSYHNCKMTYDRARFVFSQ---HMTFYALLSVRLYLFIISFKVVSNNKRV 279
Db      237 YATVMEHLNN---YSQDSVWVTLFRMOHVHTFMPLFRLISWLLQSIIFVSQMPHYD 292
Qy      280 YKRSQEI---LGYAFLTWYSLLSRLPMPRERVYFTSCLAVAG-----FOHWQPS 328
Db      293 YRNRATIEQVGLSLHMANSLGQLYFLPDKSTRIMFVLVSHLVGGLSHVTFNNYSVE 352
Qy      329 LNHFASNYVTGLPSGNDWPHQQTGTLNITASAMWDFHGLHFOIEHLLFPMRPMCKHPR 388
Db      353 KPALSSNIM-----SNVACIQIMTTRNNRPGRFIDMLWGLNYQIEHLLFTMPRRNLN 406
Qy      389 KSPIVNLQCKHNSYERATWMEANKMYSTLRAVAMEAKDYTKPV 435
Db      407 TMLPVKPEFAAANGLPYWDYFTGFWLEIEQRFNIAVAAKLTCKI 453

RESULT 11
T36617
probable Delta6 fatty acid desaturase (EC 1.14.99.-) SCH35.42c [similarity] - Streptomyces
C:Species: Streptomyces coelicolor
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C:Accession: T36617
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.

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submitted to the EMBL Data Library, June 1999

A:Reference number: Z21610

A:Accession: T36617

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-345 <OLI>

A:Cross-references: EMBL:AL078610; PIDN:CA844385.1; GSPDB:GN0070; SCOEDB:SCH35.42c

A:Experimental source: strain A3 (2)

C:Genetics:

A:Gene: SCOEDB:SCH35.42c

C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 10.4%; Score 257; DB 2; Length 345;

Best Local Similarity 26.0%; Pred. No. 6, 1e-14;

Matches 94; Conservative 62; Mismatches 161; Indels 44; Gaps 14;

Qy 91 DYRLVSESKGLF-KTPGKYVCISIFVSV--LFLASYGVLYCKSTVAHLCSGLMG 147
 Db 16 DFARLSKRVADAGLGRPG---YTLRTAVTGLVAGMAAFVLVAGASWMTLAIAPLA 72

Qy 148 MMLQSGWVGDSCHVOVMNRKLNRLFOIAGVIVAGSVAMWKLDHNTHFACNSANL 207
 Db 73 VMQGVQVAVHDAHARQVFRRRRSELSGRIAGAST-GMSGWWQDHTTHANPTEDL 131

Qy 208 DPDIQHLPIAISPKFNSLTSYHNCMTYDRAARFVSPQHTFPALLSVRLYFIL 267
 Db 132 DPDIQF-DLIVSPDQARATG-----LPLRGWQAFPLPDLTLEGFNLHVA 179

Qy 268 SFKRVPSNNKRVYKRSQE--ILGYAFLTWYSLLSRLPMPBRVMTSCLAAGFQH 324
 Db 180 SGRAM--ANRLKRRALDGLALLHACA--VYLTALFVVLV--PGMAIAF--LAVHQCIF 230

Qy 325 WQSLNHFANVNTGLP-----SGNDWFHOOTKGLNTITASAWMDWHGHLHQIEHHLF 379
 Db 231 GVLGSAFAFN-HKGMPIITLADRPDPLRQVLTLSRVNGCLFDLALGGLNHQIEHHLF 289

Qy 380 PRAPKCHFRKISPIVNLCKOHNLSYETATMWEAKVYVTLVAAMEADVTKPVPKM 439
 Db 290 PSMPSPLRLKARAIKVRRCYCDLGVDAFETGLVASYRLALSLH-----DAGTPLRRT 342

Qy 440 V 440
 Db 343 V 343

Qy 440 V 440
 Db 343 V 343

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Qy 440 V 440
 Db 343 V 343

Qy 440 V 440
 Db 343 V 343

C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 8.9%; Score 220; DB 2; Length 359;

Best Local Similarity 24.0%; Pred. No. 8, 3e-11;

Matches 96; Conservative 54; Mismatches 148; Indels 102; Gaps 20;

Qy 90 KQYRRLVSE-----FSKMGFKTPGKYVCISIFVSVLRLASYGVLYCKSTVAHLCSG- 143
 Db 13 RGRFRVLNQRVADYFAHEHGLTQRDNPSMTLKLII-----VLMFSAWAFVLPAP 62

Qy 144 ----LIMGMLIQ-----SCVGHDSCHVOVMNRKLNRLFOIAGVIVAGSVAMWK 192
 Db 63 VIFPVALLSCVYALALAAFSFVNGHDANMNVSSPNHNRKLVGMTYDFV--GLSSFLR 120

Qy 193 LDHN--THHACNSANLDPDIQHLPIAISPKFNSLTSYHNCMTYDRAARFVSPQHT 251
 Db 121 YRHNVLHHYTNLIGHDVEIHGDGAVKSP--QEHVGIYR-----FOQFYTW 166

Qy 252 TFPYALLSVRLYFILSPKRVPSNNKRVYKRSQ-----ELGYAFLTW-----YS 297
 Db 167 GLY---LFIPIFWFLDYVLV--NKGXHDHKKIPFQPLBLASLIGIK--LMLGTVFG 219

Qy 298 LILSLRPNPPE-----RMYFTSCLAAGFQHMQPSLNPASVNTGLPDSG-----NDM 346
 Db 220 LPLALGFSIPEVLIGASVYTMVYGIYVCTI---FMLAVLSTETFLTPDGSGLAIDEM 275

Qy 347 FHOOTKGLNTI--TASAMWDFHGGHFOIEHHLFRMPKCHFRKISPIVNLCKOHNLSY 405
 Db 276 ALCQITTFANFANNNPFMMPCGGLNHQVTHLHFNICHHIHPQLENTIKDVCQEGVER 335

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

Qy 406 EPTATMEANKVYSTLRVAVAMEAKDVTKPVPKMNV--EAM 444
 Db 336 K-----YPTFKAA-----IASVYRLLEAM 355

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 9.85756 Seconds
(without alignments)
2137.240 Million cell updates/sec

Title: US-09-857-524B-2
Perfect score: 2470
Sequence: 1 MEPPKRGHSQADLAKHKQPG.....KDVTKRPVKMVMKANTFG 448

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	444	18.0	444	1	PADS_BRARE
2	220	8.9	444	1	Q9dex7 brachydanio
3	166.5	6.7	384	1	008871 synchocyst
4	161	6.5	387	1	003529 saccharomyc
5	157	6.4	387	1	FD61_SOYBN
6	153	6.2	137	1	CYB5_ORISA
7	152.5	6.2	131	1	CYB5_RHIST
8	152.5	6.2	134	1	CYB5_ARATH
9	151.5	6.1	132	1	YDAA_SCHPO
10	148.5	6.0	130	1	CYB5_BOROF
11	148	6.0	136	1	CYB5_YEAST
12	146.5	5.9	134	1	CYB5_TOBAC
13	142.5	5.8	135	1	CYB5_CUSRE
14	142.5	5.8	890	1	NIA2_PHAVU
15	142.5	5.8	900	1	NIA1_LORVA
16	142	5.7	881	1	NIA1_PHAVU
17	141.5	5.7	453	1	FD3C_SOYBN
18	141.5	5.7	904	1	NIA1_TOBAC
19	140.5	5.7	446	1	FD3C_ARATH
20	140.5	5.7	591	1	CYB2_YEAST
21	140.5	5.7	904	1	NIA2_TOBAC
22	139.5	5.6	134	1	CYB5_BRACOL
23	139.5	5.6	135	1	CYB5_TOBAC
24	139	5.6	380	1	FD3E_SOYBN
25	138	5.6	129	1	CYB5_NEUCR
26	137.5	5.6	139	1	CYB2_SCHPO
27	137.5	5.6	146	1	CYB5_HUMAN
28	137	5.5	911	1	NIA1_LYCES
29	136.5	5.5	146	1	CYB5_RAT
30	136.5	5.5	383	1	FD62_SOYBN
31	136	5.5	902	1	NIA1_PHYIN
32	135.5	5.5	886	1	NIA1_SOYBN
33	135	5.5	911	1	NIA1_BRANA

34	135	5.5	911	1	NIA2_BRANA	P39868 brassica na
35	134.5	5.4	980	1	NIA2_SOYBN	P39870 glycine max
36	134.5	5.4	918	1	NIA1_CUCMA	P17569 cucurbita m
37	134.5	5.4	926	1	NIA1_SPIOL	P23312 spinacia ol
38	134	5.4	379	1	FD3E_TOBAC	P48626 nicotiana t
39	134	5.4	621	1	NIA1_MAIZE	P17571 zea mays (m
40	134	5.4	909	1	NIA1_PETRY	P36859 petunia hyb
41	133.5	5.4	447	1	FD6C_SPIOL	P48629 spinacia ol
42	133.5	5.4	573	1	CYB2_HANAN	P09437 hananula a
43	132.5	5.4	130	1	CYB5_MORAP	O9Y706 mortierella
44	131.5	5.3	134	1	CYB5_DROME	O9V4N3 drosophila
45	131.5	5.3	898	1	NIA1_BETVE	P27783 betula verr

ALIGNMENTS

RESULT 1	ID	FAVS_BRARE	STANDARD;	PRT;	444 AA.
AC	Q9dex7;				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DE	Delta-5/delta-6 fatty acid desaturase (EC 1.14.19.-).				
GN	FADS2 OR FADS6C				
OS	Brachydanio rerio (Zebrafish) (Danio rerio).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;				
OC	Cyprinidae; Danio.				
ON	NCBI_TaxID=7955;				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RX	MEDLINE=21592990; PubMed=11724940;				
RA	Haestinge N., Agaba M., Tocher D.R., Leaver M.J., Dick J.R.,				
RT	"A vertebrate fatty acid desaturase with deltas and deltas				
RT	activities";				
RL	Proc. Natl. Acad. Sci. U.S.A. 98:14304-14309(2001).				
CC	-1- FUNCTION: Fatty acid desaturase with both delta-5 and delta-6				
CC	activities. May represent a component of the polyunsaturated fatty				
CC	acid biosynthesis pathway.				
CC	-1- PATHWAY: Polyunsaturated fatty acid biosynthesis.				
CC	-1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.				
CC	-1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.				
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CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch)				
DR	EMBL: AR309556; ANG25710.1; -.				
DR	HSSP: P00173; JUEX.				
DR	ZFIN: ZDB-GENE-011212-1; fads2.				
DR	InterPro: IPR001199; Cyt b5.				
DR	InterPro: IPR005804; FA desat fam.				
DR	Pfam: PF00487; FA desaturase; 1.				
DR	Pfam: PF00173; heme_1; 1.				
DR	ProDom: PD000612; Cyt b5; 1.				
DR	ProDom: PD001081; FA desat fam; 2.				
DR	PROSITE: PS00191; CYTOCHROME B5_1; FALSE_NEG.				
DR	PROSITE: PS02055; CYTOCHROME B5_2; 1.				
KW	Fatty acid biosynthesis; Oxidoreductase; Heme.				
FT	DOMAIN 18 95				
FT	FT				
FT	METAL 53 53				
FT	METAL 76 76				
SQ	SEQUENCE 444 AA; 52032 MW; 6AA25A1DC1C0F65 CRC64;				

Query Match 18.0%; Score 444; DB 1; Length 444;

RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=9820296; PubMed=9559540;
 RA Dunn T.M., Haak D., Monaghan E., Beeler T.J.;
 RT "Synthesis of monohydroxylated inositolphosphorylceramide (IPC-C) in
 RT Saccharomyces cerevisiae requires Scs7p, a protein with both a
 RT cytochrome b5-like domain and a hydroxylase/desaturase domain.";
 RL Yeast 14:311-321(1998).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=98019193; PubMed=9353282;
 RA Mitchell A.G., Martin C.E.;
 RT "Fahp, a Saccharomyces cerevisiae cytochrome b5 fusion protein, and
 RT its Arabidopsis thaliana homolog that lacks the cytochrome b5 domain
 RT both function in the alpha-hydroxylation of sphingolipid-associated
 RT very long chain fatty acids.";
 RL J. Biol. Chem. 272:28281-28288(1997).
 CC -1- FUNCTION: INVOLVED IN THE ALPHA-HYDROXYLATION OF SPHINGOLIPID-
 CC ASSOCIATED VERY LONG CHAIN FATTY ACIDS. HYDROXYLATES THE C26-FATTY
 CC ACID OF INOSITOLPHOSPHORYLCERAMIDE-B (IPC-B) TO FORM IPC-C.
 CC -1- COPACTOR: IRON (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
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 CC
 CC EMBL: Z49260; CA89255.1; -.
 DR PIR: S54484; S54484.
 DR HSSP: P04166; 1EUE.
 DR SGD: S0004885; SC57.
 DR GO: GO:0005783; C:endoplasmic reticulum; IMP.
 DR GO: GO:0016491; F:oxidoreductase activity; IMP.
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR006087; Sterol_desat.
 DR Pfam: PF04116; FA_hydroxylase; 1.
 DR Pfam: PF00173; heme 1; 1.
 DR PRINTS: PRO0363; CYTOCHROMEBS.
 DR PRODOM: PD000612; Cyt_B5; 1.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KM Oxidoreductase; Fatty acid biosynthesis; Iron; Electron transport;
 KM Transmembrane; Endoplasmic reticulum; Heme.
 FT DOMAIN 1 90
 FT TRANSMEM 197 217 HEME-BINDING.
 FT TRANSMEM 223 243 POTENTIAL.
 FT TRANSMEM 298 318 POTENTIAL.
 FT TRANSMEM 353 373 POTENTIAL.
 FT METAL 45 45 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 70 70 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 384 AA; 44881 MW; DF4BA5F2E0BA2218 CRC64;
 Query Match 6.7%; Score 166.5; DB 1; Length 384;
 Best Local Similarity 21.2%; Pred. No. 3e-06;
 Matches 96; Conservative 67; Mismatches 141; Indels 149; Gaps 25;
 QY 9 SQADLAHKQPGDLWISIKG-KVYDISKWKKEHGGELPLLSFAGQDVT---DAFLAVH 63
 DB 13 SKTVQEHNTANDCWVTVYQNRKITYDVRFLSEHGGESILDYAGKDITIMQSDVHEH 72
 QY 64 PGTAMQVL-DRFTGYVVDYVSSEMSKDYRLVSESKGKFKTEGKGYCIFVSVL 122
 DB 73 SDSAVLELDEYVILGIYATDEEA-----RLITNKKHKEVQLSDGTEFDSTTVKEL 126
 QY 123 FA---LSV---YGVLYCKSTWALHCSGLMGML---WLGSGWVG--HDSCHYQVMPNRKL 171

DB 127 PAEEKSLATDYSDNYKKHFLDLNRLMLQILRSDPKDFVVDQIHRRHY----GKGS 182
 QY 172 NNLFOILAGNVAGVS-VAMWKLIDNTHHFAQNSANLDPDIGHLPIT---AISPKEFNS 226
 DB 183 ADPLF---GNLEPLIKTAMWV-----VAMLPVVTYHMGVALKNMQ 222
 QY 227 LTSYHNCMTVDRAARFVSFOHWTFFPALISVRLYLFLSFKVVFSSNNKRYKRSOI 286
 DB 223 LFACLFLC-----GVFWVT---LEYGHRFLRFLP----- 250
 QY 287 LGYAAFLTWYSLLSLRLPWA-PEVWYFTSCIAVAFQWQPSLNLHNASVYTGPSGND 345
 DB 278 KRLVMPFLFVILCAPFYKLVALLPLTWAAAGFAGVFGYCYDECHP-----LHHS 332
 QY 389 KISPIVNLK-----CQGNLSYE-----TATWME 412
 DB 333 KLPPFRKTKKXHLNHHYKNYQLGFGVTSWPFND 365
 RESULT 4
 ID PD61 SOYBN STANDARD; PRT; 387 AA.
 AC P48630;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 1
 DE (EC 1.14.19.-).
 GN PAD2-1.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxId=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Seed;
 RX MEDLINE=96151506; PubMed=8587990;
 RA Heppard E.P., Kinney A.J., Stecca K.L., Miao G.H.;
 RT "Developmental and growth temperature regulation of two different
 RT microsomal omega-6 desaturase genes in soybeans.";
 RL Plant Physiol. 110:311-319(1996).
 CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
 CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
 CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN DEVELOPING SEEDS.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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 CC
 CC EMBL: L43920; AAB00859.1; -.
 DR PIR: T07687; T07687.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR PRODOM: PD01081; FA_desat_fam; 2.
 KM Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;

KM Transmembrane.
 FT TRANSMEM 54 74 POTENTIAL.
 FT TRANSMEM 87 107 POTENTIAL.
 FT TRANSMEM 121 141 POTENTIAL.
 FT TRANSMEM 183 203 POTENTIAL.
 FT TRANSMEM 227 247 POTENTIAL.
 FT TRANSMEM 251 271 POTENTIAL.
 FT DOMAIN 109 113 HISTIDINE BOX-1.
 FT DOMAIN 145 149 HISTIDINE BOX-2.
 FT DOMAIN 319 323 HISTIDINE BOX-3.
 SQ SEQUENCE 387 AA; 44662 MW; 49068505C21A1C31 CRC64;
 Query Match 6.5%; Score 161; DB 1; Length 387;
 Best Local Similarity 25.4%; Pred. No. 8.4e-06;
 Matches 86; Conservative 48; Mismatches 139; Indels 66; Gaps 19;
 QY 118 FSVYVYDLSFAFIYIATYFHLPPFSLIAMPYVWLGCLLTGVVIAHECGHAFS 117
 DB 167 PNRLNLPOLIAGNVAGSVAMWKDHTHFCANSALDPDIOHLPILAIKPFNS 226
 DB 118 KYQWVDVVGGLTHSTLLVPYFSWKSHRRH--SVTGLDRDVEVP---KPKSKVA 170
 QY 227 LTSYHNCMTYDRAAFVFSQ--HMTFYPAL--LSVLYLFIIS---PKVFSNKKRY 280
 DB 171 WFSKYLNNPL--GRAVSLVLTITGCMYLAFNVSGRPYDSFASHYHPAPIYNNRRL 228
 QY 281 KRSEILGYAFLTWYSLLSLRLPNRERV---MYFTSLAVAGF-----QHWQFSL 329
 DB 229 IYVSDV---ALFSTVYSLY--RVATLKGVLWLCVYGVPLIIVGVLTITVYLTHTHFA 283
 QY 330 NHRFSNVTGLPSCNDFPHOQTKTLNITASAMWD-----FHGSLHPOLEHLPFRMP 383
 DB 284 PHYDSSSEW-----DWL---KGL---ATMDRYSGLINKVFHITDTVAHHLFSTMP 329
 QY 384 KCHFRK----ISPIVNLCKQKHLSEYETATWMEANKMY 418
 DB 330 HYHMEATNAIKPILEGVYQPDPTFYKALMREARECLY 368
 RESULT 5
 CYBS ORYSA STANDARD; PRT; 137 AA.
 AC PA9100;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriactoidae; Oryzaceae; Oryza.
 NC EMBL TaxID=4530;
 NC NCBI TaxID=4530;
 RN SEQUENCE FROM N.A.
 RP TISSUE=Callus;
 RC MEDLINE=94325476; PubMed=8049375;
 RA Smith M.A., Stohart A.K., Shewry P.R., Napier J.A.;
 RT "Tobacco cytochrome b5: cDNA isolation, expression analysis and in
 RT vitro protein targeting."
 RL Plant Mol. Biol. 25:527-537 (1994).
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases (By similarity).
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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 CC -----
 CC EMBL: X75670; CAA53366.1; --
 CC FIR; S46307; S46307.
 CC HSP; P00171; IEHB.
 CC Gramene; P49100; --
 CC Interpro; IPR001199; Cyt B5.
 CC Pfam; PF00173; heme 1; 1.
 CC Prodom; PD000612; Cyt B5; 1.
 CC PROSITE; PS00191; CYTOCHROME_B5_1; 1.
 CC PROSITE; PS0255; CYTOCHROME_B5_2; 1.
 CC KX Electon transport; Transmembrane; Heme; Iron; Microsome.
 FT TRANSMEM 108 128 POTENTIAL.
 FT METAL 41 41 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 65 65 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 137 AA; 15296 MW; 4260C90633B60FDA CRC64;
 Query Match 6.4%; Score 157; DB 1; Length 137;
 Best Local Similarity 32.1%; Pred. No. 5.5e-06;
 Matches 45; Conservative 22; Mismatches 53; Indels 20; Gaps 5;
 QY 5 KKHISQADLAKHKQPDLMISIKGYDISKMTKEHSGELPLSPAGDVTDAF-IAVH 63
 DB 6 KKYTLEEVAKHNSKDDCWLLIGKYYNYSKFLSDHPGDDVLLSSTGKDADTFEDVGH 65
 QY 64 PGFAMGYLDRFTFGYVVDYVSSEMSKDYRLVSEBSKNGLFETPKGYGSAIFSV-- 121
 DB 66 TTTARMMDBE---YVVGIDITSTIPARTKVPKPPHYNDKTPF-----FIKKIQ 114
 QY 122 -LFALSVGV-----LYCKS 135
 DB 115 FLVPLAIIGLAIVAIRYTKS 134
 RESULT 6
 CYBS RHIST STANDARD; PRT; 131 AA.
 AC 09HFLV;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5.
 OS Rhizopus stolonifer (Rhizopus nigricans).
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
 OC Rhizopus.
 NC EMBL TaxID=4846;
 NC NCBI TaxID=4846;
 RN SEQUENCE FROM N.A.
 RP MEDLINE=21414663; PubMed=11523811;
 RA Kunic B., Tuan G., Brekvar K., Pompon D.;
 RT "Functional cloning, based on acrole resistance in Saccharomyces
 RT cerevisiae, and characterization of Rhizopus nigricans redox carriers
 RT that are differentially involved in the P450-dependent response to
 RT progesterone stress."
 RL Mol. Genet. Genomics 265:930-940 (2001).
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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 CC -----
 CC EMBL: AF290427; AAC23835.1; --
 CC HSP; P04166; IEUE.
 CC Interpro; IPR001199; Cyt B5.
 CC Pfam; PF00173; heme 1; 1.
 CC PRINTS; PR00363; CYTOCHROME B5.

RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Berto J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Uesery D., Barrell B.G., Nure P.,
 RT "The genome sequence of *Schizosaccharomyces pombe*."
 RL Nature 415:871-980(2002).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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 CC -----
 CC EMBL: 269944; CAA93814.1; -
 DR PIR: S67453; S67453.
 DR HSSP: P00175; 1LTD.
 DR GeneDB: Spombe: SPAC1F12.10C; -
 DR InterPro: IPR001199; Cyt_B5.
 DR Pfam: PF00173; heme_1; 1.
 DR PRINTS: PR00363; CYTOCHROME_B5.
 DR ProDom: PD000612; Cyt B5; 1.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Hypothetical protein; Heme.
 FT METAL 106 106 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 129 129 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 147 AA; 16667 MW; E874859F52E1AF1D CRC64;
 Query Match 6.2%; Score 152.5; DB 1; Length 147;
 Best Local Similarity 39.0%; Pred. No. 1.4e-05;
 Matches 30; Conservative 16; Mismatches 24; Indels 7; Gaps 2;
 QY 8 ISQADLAKHQPGDLMISIKGVYDLSKMTKEHPGGLPLSPAGQDVTAFIYHPTA 67
 DB 74 VTKELAKHKTKEDCWAIKGVYNSAVLYPHNAGCKRLIDVGRATVYFMKFF--A 130
 QY 68 W---QYLDREFPTGYV 80
 DB 131 WVNEDALKTSFVGFLV 147
 RESULT 9:
 CYB5_BOROF STANDARD; PRT; 132 AA.
 ID CYB5_BOROF STANDARD; PRT; 132 AA.
 AC 004354;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5.
 OS *Borago officinalis* (Bourrache) (Borage).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Jamids; Boraginaceae; Borage.
 NC NCBI_TaxID=13363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97268723; PubMed=9108131;
 RA Savanova O., Smith M.A., Lapinskas P.A., Stobart K., Dobson G.,
 RA Christie W.W., Sherry P.R., Napier J.A.;
 RT "Expression of a borage desaturase cDNA containing an N-terminal
 RT cytochrome b5 domain results in the accumulation of high levels of
 RT delta-desaturated fatty acids in transgenic tobacco."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases (By similarity).
 CC -1- SUBCELLULAR LOCATION: MICROSOAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -----

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 CC -----
 CC EMBL: U79011; AAC49701.1; -
 DR HSSP: P00171; 1CYO.
 DR InterPro: IPR001199; Cyt_B5.
 DR Pfam: PF00173; heme_1; 1.
 DR PRINTS: PR00363; CYTOCHROME_B5.
 DR ProDom: PD000612; Cyt B5; 1.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Electron transport; Transmembrane; Heme; Iron; Microsome.
 FT TRANSMEM 104 124 POTENTIAL.
 FT METAL 37 37 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 61 61 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 132 AA; 14556 MW; 96EF72A06F2E8C5B CRC64;
 Query Match 6.1%; Score 151.5; DB 1; Length 132;
 Best Local Similarity 41.1%; Pred. No. 1.5e-05;
 Matches 30; Conservative 15; Mismatches 27; Indels 1; Gaps 1;
 QY 6 KHISQADLAKHQPGDLMISIKGVYDLSKMTKEHPGGLPLSPAGQDVTAFIY-HP 64
 DB 3 KFTLLEVAQHNNSKQCMILINKGVYDTKFDHPGSDVLSTATGKADITDFEDIGHS 62
 QY 65 GTAWQYLDREFPTGY 77
 DB 63 SSKAKMLDEYYVG 75
 RESULT 10:
 CYB5_YEAST STANDARD; PRT; 120 AA.
 ID CYB5_YEAST STANDARD; PRT; 120 AA.
 AC P40312;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5.
 GN CYB5 OR YNL11C OR N1949.
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 NC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FL100.
 RX MEDLINE=94237477; PubMed=8181746;
 RA Tuan G., Eginat J.-C., Rougeulle C., Cullin C., Pompon D.,
 RT "Cloning and characterization of a yeast cytochrome b5-encoding gene
 RT which suppresses ketoconazole hypersensitivity in a NADPH-P-450
 RT reductase-deficient strain."
 RL Gene 142:123-127(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97245296; PubMed=9090055;
 RA de Antoni A., D'Angelo M., Dal Pero F., Sartorello F., Pandolfo D.,
 RA Pallavicini A., Lanfranchi G., Valle G.;
 RT "The DNA sequence of cosmid 14-13b from chromosome XIV of
 RT *Saccharomyces cerevisiae* reveals an unusually high number of
 RT overlapping open reading frames."
 RL Yeast 13:261-266(1997).
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases. It plays a role in
 CC fatty-acid desaturation and is also involved in several steps of
 CC the sterol biosynthesis pathway, particularly in the 4-
 CC demethylation of the 4,4'-dimethyl zymosterol.
 CC -1- SUBCELLULAR LOCATION: MICROSOAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -----

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -----
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 CC -----
 DR EMBL: L22494; AAA67468.1; -
 DR EMBL: Z69382; CAA93396.1; -
 DR EMBL: Z71387; CAA93990.1; -
 DR PIR: S63052; S63052.
 DR HSSP: P04166; 1EUE.
 DR SGD: S0005055; CYB5.
 DR GO: G0:0005792; C:microsome; IDA.
 DR GO: G0:0016126; P:sterol biosynthesis; IDA.
 DR InterPro: IPR001199; Cyt_B5.
 DR Pfam: PF00173; heme_1; 1.
 DR PRINTS: PR00363; CYTOCHROMEBS.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 DR KEGG: K01199; Cytochrome b5; Heme; Iron; Microsome.
 FT TRANSMEM 98 118
 FT METAL 37 37 POTENTIAL.
 FT METAL 61 61 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT CONFLICT 17 17 E -> Q (IN REF. 1).
 SQ SEQUENCE 120 AA; 13297 MW; 598EP2A6730CA019 CRC64;
 Query Match 6.0%; Score 148.5; DB 1; Length 120;
 Best Local Similarity 30.8%; Pred. No. 2.3e-05;
 Matches 40; Conservative 23; Mismatches 50; Indels 17; Gaps 5;
 QY 4 PKKHISQADLAKHKOPGDLWISIKGVYDISKWTKEHPGELPLISFAGQDVTDAFIAY- 62
 DB 2 PKKY-SYGEVAENHNGENFWIILDDKVVYDSQPKDEHPGDELIMLGQDATESFVDIG 60
 QY 63 HPGTAQVYLDPRFTGYVQDYSVSEMSKDYRLVSEPSKMKGLFKTPGKGVYCSIFPVSVL 122
 DB 61 HSDEAL-----RLKGLGYIGD-----VDKTSERVSVEKVSSTSEMSKSGST-----LVVYL 105
 QY 123 FALSYGVGLY 132
 DB 106 LALLMLGVAY 115
 RESULT 11
 CYB5_TOBAC STANDARD; PRT; 136 AA.
 ID ID
 AC P49058;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
 OC NCBI_TaxId=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=leaf;
 RA MEDLINE=94325476; PubMed=8049375;
 RA Smith M.A., Stobart A.K., Shewry P.R., Napier J.A.;
 RT "Tobacco cytochrome b5: cDNA isolation, expression analysis and in
 RT vitro protein targeting";
 RL Plant Mol. Biol. 25:527-537(1994).
 CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
 CC OXYGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY
 CC DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH IN

CC THE DEVELOPING SEED IS UTILIZED FOR MEMBRANE SYNTHESIS AND IN THE
 CC DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE
 CC LIPIDS. IS INVOLVED IN THE REDUCTION OF CYTOCHROME P-450 AND
 CC MAY THEREFORE BE INVOLVED IN FLAVONOID BIOSYNTHESIS IN THE PETALS.
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC TISSUE SPECIFICITY: IS HIGHLY EXPRESSED IN DEVELOPING SEEDS,
 CC MODERATELY EXPRESSED IN FLOWERS, AND IS EXPRESSED AT LOW
 CC LEVELS IN THE LEAF.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X71441; CAA50575.1; ALT_INIT.
 DR EMBL: X68140; CAA48240.1; -
 DR HSSP: P04166; 1BSM.
 DR InterPro: IPR001199; Cyt_B5.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 DR KEGG: K01199; Cytochrome b5; Heme; Iron; Microsome;
 FT TRANSMEM 107 127
 FT METAL 40 40 POTENTIAL.
 FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT CONFLICT 10 11 LA -> EF (IN REF. 1; CAA48240).
 FT CONFLICT 105 105 MISSING (IN REF. 1; CAA48240).
 SQ SEQUENCE 136 AA; 14979 MW; DAC9E2A695B2835F CRC64;
 Query Match 6.0%; Score 148; DB 1; Length 136;
 Best Local Similarity 28.5%; Pred. No. 2.9e-05;
 Matches 41; Conservative 21; Mismatches 42; Indels 40; Gaps 5;
 QY 6 KHISQADLAKHKOPGDLWISIKGVYDISKWTKEHPGELPLISFAGQDVTDAFIAYHP 64
 DB 6 KYFTLAIVSQHNNADQWLVISGVYDVTKFLPDHHRGDBVLLSATGKATDDFEBVGH 65
 QY 65 GTRWQYLDPRFTG-----YYVDYSVSEMSKDYRLVSEF-SKMKL 104
 DB 66 SSRARMLDEYVYVDDISATIPRTKTYTPPNOPHYNDKT-----SEFVVKLLQ 113
 QY 105 FKTPGKGVYCSIFPVSVLPALSY 128
 DB 114 FLVP-----LIIIGVAFGIRFY 130
 RESULT 12
 CY52_ARATH STANDARD; PRT; 134 AA.
 ID ID
 AC Q48845;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable cytochrome b5 isoform 2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Rounsaey S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,

RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhagen G.P., Preuss D.,
 RA Niernan W.C., White O., Bisen J.A., Salzberg S.L., Frazer C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 402:761-768(1999).
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases (By similarity).
 CC -1- SUBCELLULAR LOCATION: Mitochondrion. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -----
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 CC -----
 CC EMBL: AC003974; AAC04491.1; -
 CC PIR: T00796; T00796.
 CC HSSP: P04166; 1B5M.
 CC InterPro: IPR001199; Cyt_B5.
 CC Pfam: PF00173; heme_1.1.
 CC PRINTS: PR00363; CYTOCHROME_B5.
 CC ProDom: PD000612; Cyt_B5; 1.
 CC PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 CC PROSITE: PS0255; CYTOCHROME_B5_2; 1.
 CC KEGG: Electron transport; Transmembrane; Heme; Iron; Microsome;
 CC Multigene family.
 CC TRANSMEM: 107 127 POTENTIAL.
 CC FT METAL 40 40 IRON (HEME AXIAL LIGAND) (By similarity).
 CC FT METAL 64 64 IRON (HEME AXIAL LIGAND) (By similarity).
 CC SQ SEQUENCE 134 AA; 15016 MW; B405F5430F5716C1 CRC64;
 CC -----
 CC Query Match 5.9%; Score 146.5; DB 1; Length 134;
 CC Best Local Similarity 35.9%; Pred. No. 3.8e-05;
 CC Matches 28; Conservative 22; Mismatches 27; Indels 1; Gaps 1;
 CC
 CC QY 1 MESPKNHISQADLAKKPGDLMISIKGVYDISKTKHPGELPLSPAGDVTDAF-59
 CC DB 1 MDEBAKIFITSEVSEHQAHCWIVNGKYVNTKFLDPHGGADVLSTGQDAIDDFE 60
 CC QY 60 IAYHPGTAMQYLDREFTG 77
 CC DB 61 DVGHSESAREMEQYVVG 78
 CC
 CC RESULT 13
 CC CYB5_CUSRE STANDARD; PRT; 135 AA.
 CC ID CYB5_CUSRE STANDARD; PRT; 135 AA.
 CC AC P49097;
 CC DT 01-FEB-1996 (Rel. 33, Created)
 CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Cytochrome b5.
 CC OS Cuscuta reflexa (Southern Asian dodder).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; lamiales; Solanales; Convolvulaceae; Cuscuta.
 CC NCBI_TaxID=4129;
 CC (1)
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=95047507; PubMed=7959021;
 CC RA Subramaniam K., Manadevan S.;
 CC RT "The cDNA sequence of cytochrome b5 associated with cytokinin-induced
 CC haustoria formation in Cuscuta reflexa.";
 CC RL Gene 149:375-376(1994).
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron

CC carrier for several membrane bound oxygenases.
 CC -1- SUBCELLULAR LOCATION: Mitochondrion. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -----
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 CC -----
 CC EMBL: L22209; AAA62621.1; -
 CC PIR: T09946; T09946.
 CC HSSP: P04166; 1EUR.
 CC InterPro: IPR001199; Cyt_B5.
 CC Pfam: PF00173; heme_1.1.
 CC ProDom: PD000612; Cyt_B5; 1.
 CC PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 CC PROSITE: PS0255; CYTOCHROME_B5_2; 1.
 CC KEGG: Electron transport; Transmembrane; Heme; Iron; Microsome;
 CC Multigene family.
 CC TRANSMEM: 106 126 POTENTIAL.
 CC FT METAL 39 39 IRON (HEME AXIAL LIGAND) (By similarity).
 CC FT METAL 63 63 IRON (HEME AXIAL LIGAND) (By similarity).
 CC SQ SEQUENCE 135 AA; 14745 MW; CFF21C952981F5DA CRC64;
 CC -----
 CC Query Match 5.8%; Score 142.5; DB 1; Length 135;
 CC Best Local Similarity 41.1%; Pred. No. 8.2e-05;
 CC Matches 30; Conservative 12; Mismatches 30; Indels 1; Gaps 1;
 CC
 CC QY 6 KHISQADLAKKPGDLMISIKGVYDISKTKHPGELPLSPAGDVTDAF-HP 64
 CC DB 5 KYTSLAEVSEHQAHCWIVNGKYVNTKFLDPHGGADVLSTGQDAIDDFEIGHS 64
 CC QY 65 GTAMQYLDREFTG 77
 CC DB 65 SSARAMDMEMCVG 77
 CC
 CC RESULT 14
 CC NIA2_PHAVU STANDARD; PRT; 890 AA.
 CC ID NIA2_PHAVU STANDARD; PRT; 890 AA.
 CC AC P39866;
 CC DT 01-FEB-1995 (Rel. 31, Created)
 CC DT 01-FEB-1995 (Rel. 31, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Nitrate reductase [NADH] 2 (EC 1.7.1.1) (NR-2).
 CC GN NIA2 OR NR2.
 CC OS Phaseolus vulgaris (Kidney bean) (French bean).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolae; Phaseolus.
 CC NCBI_TaxID=1885;
 CC (1)
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=cv. Saxa;
 CC RA Jensen P.E., Hoff T., Stummann B.M., Henningsen K.W.;
 CC RA Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
 CC step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
 CC -1- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
 CC AND ONE MOLYBDENUM ATOM.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 CC N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
 CC C-TERMINAL DOMAIN.
 CC -----
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 CC -----
 DR EMBL; U01029; AAA95940.1; -
 DR PIR; T11805; T11805.
 DR HSSP; P17571; 2CND.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR001834; Cyt_B5_reductase.
 DR InterPro; IPR000572; Euk_Mb_oxred.
 DR InterPro; IPR001709; FPN_cyt_reductase.
 DR InterPro; IPR005066; Mo-co_dimer.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR Pfam; PF03404; Mo-co_dimer; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR Pfam; PF00174; oxidored_mol_yb; 1.
 DR PRINTS; PR00406; CYTB5RDASE.
 DR PRINTS; PR00363; CYTOCHROME B5.
 DR PRINTS; PR00407; EUMOPTERIN.
 DR PRINTS; PR00371; FPNCR.
 DR ProDom; PD000612; Cyt B5; 1.
 DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS0255; CYTOCHROME B5_2; 1.
 DR PROSITE; PS00559; MOLYBDOTERIN_EUK; 1.
 DR PROSITE; PS00559; MOLYBDOTERIN_EUK; 1.
 DR Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
 DR Nitrate assimilation; Multigene family.
 DR METAL 165 165 MOLYBDENUM-PTERIN (POTENTIAL).
 DR METAL 219 219 MOLYBDENUM-PTERIN (POTENTIAL).
 DR DISULFID 404 404 INTERCHAIN (POTENTIAL).
 DR METAL 548 548 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 DR METAL 571 571 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 DR SEQUENCE 890 AA; 99995 MW; FC0B96F0139DE1E CRC64;
 SQ
 Query Match 5.8%; Score 142.5; DB 1; Length 890;
 Best Local Similarity 34.1%; Pred. No. 0.00068;
 Matches 30; Conservative 14; Mismatches 35; Indels 9; Gaps 1;
 QY 1 MEEPKHISQADLAKKOPGDLWISIKGVYDISKWTKEHPGGLPLSLFAGQDVDAFI 60
 DB 509 NMTASCMFSEVSEKKSPPDSAMIIYHGVIYDCTRFLKHHPGGLDILNAGDCTEERD 568
 QY 61 AYHPTGMOYLDRFFGYVQDYSVSEM 88
 DB 569 AIHSDKAKIML-----EDYRIGEL 587
 RESULT 15
 ID NIA LOTJA STANDARD; PRT; 900 AA.
 AC P39869;
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR).
 GN NIA.
 OS Lotus japonicus.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosid 1; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.
 OC NCBI_TaxId=34305;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Gifu / B-129;
 RA Waterhouse R.N., Smyth A.J., Prosser I.M., Forde B.G., Clarkson D.T.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBD databases.
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
 CC step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
 CC -1- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)

CC AND ONE MOLYBDENUM ATOM.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOTERIN OXIDOREDUCTASES IN THE
 CC N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
 CC C-TERMINAL DOMAIN.
 CC -----
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 CC -----
 DR EMBL; X80670; CA56696.1; -
 DR PIR; S47029; S47029.
 DR HSSP; P17571; 2CND.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR001834; Cyt_B5_reductase.
 DR InterPro; IPR000572; Euk_Mb_oxred.
 DR InterPro; IPR001709; FPN_cyt_reductase.
 DR InterPro; IPR005066; Mo-co_dimer.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR Pfam; PF03404; Mo-co_dimer; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR Pfam; PF00174; oxidored_mol_yb; 1.
 DR PRINTS; PR00406; CYTB5RDASE.
 DR PRINTS; PR00363; CYTOCHROME B5.
 DR PRINTS; PR00407; EUMOPTERIN.
 DR PRINTS; PR00371; FPNCR.
 DR ProDom; PD000612; Cyt B5; 1.
 DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS0255; CYTOCHROME B5_2; 1.
 DR PROSITE; PS00559; MOLYBDOTERIN_EUK; 1.
 DR Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
 DR Nitrate assimilation.
 DR METAL 172 172 MOLYBDENUM-PTERIN (POTENTIAL).
 DR METAL 226 226 MOLYBDENUM-PTERIN (POTENTIAL).
 DR DISULFID 411 411 INTERCHAIN (POTENTIAL).
 DR METAL 556 556 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 DR METAL 579 579 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 DR SEQUENCE 900 AA; 101420 MW; 547C25388DD13535 CRC64;
 SQ
 Query Match 5.8%; Score 142.5; DB 1; Length 900;
 Best Local Similarity 31.4%; Pred. No. 0.00069;
 Matches 37; Conservative 19; Mismatches 51; Indels 11; Gaps 3;
 QY 6 KHISQADLAKKOPGDLWISIKGVYDISKWTKEHPGGLPLSLFAGQDVDAFI 65
 DB 522 KMYSLSEVSEKKSPPDSAMIIYHGVIYDCTRFLKHHPGGLDILNAGDCTEERDAI 581
 QY 66 TAYQVLDRFFGY-----YVQDYSVSEM-----KQYRL--VSESKGLFTTPGKV 112
 DB 582 KAKKMLEYRVGELITTYGTSDDSSPNSLHNSSEFKHLAPIKEITTWLPLPRKV 639

Search completed: January 1, 2004, 06:30:53
 Job time : 10.8576 secs

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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 40.2085 Seconds
(without alignments)
2875.205 Million cell updates/sec

Title: US-09-857-524B-2
Perfect score: 2470
Sequence: 1 MEEPKGHSQADLAKKQPG.....KDYTKPVPKNWWEANNTFG 448

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_rvrius:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	62.5	446	10 Q9ZTY9	Q9ZTY9 ricinus com
2	1519.5	61.5	448	10 Q8VZ22	Q8VZ22 echium gent
3	1509.5	61.1	448	10 Q8VZ21	Q8VZ21 echium pita
4	1465.5	59.3	448	10 Q9SAU5	Q9SAU5 borago offi
5	1461	59.1	446	10 Q8LID7	Q8LID7 aquilegia v
6	1460.5	59.1	448	10 Q04353	Q04353 borago offi
7	1405.5	56.9	448	10 Q8L177	Q8L177 argania spi
8	1395.5	56.5	449	10 Q9ZRP8	Q9ZRP8 brassica na
9	1391.5	56.3	448	10 Q43469	Q43469 helianthus
10	1372.5	55.6	449	10 Q8LB96	Q8LB96 arabidopsis
11	1372.5	55.6	449	10 Q9ZRP7	Q9ZRP7 arabidopsis
12	1325	53.6	446	10 Q9FR82	Q9FR82 borago offi
13	1293.5	52.4	469	10 Q9ZT08	Q9ZT08 trititum ae
14	663.5	26.9	483	10 Q9LENO	Q9LENO ceratodon p
15	626	25.3	520	10 Q9LEMG	Q9LEMG ceratodon p
16	620	25.1	523	3 Q9HDC8	Q9HDC8 mucor rouxi

17	560.5	22.7	459	10 Q944W4	Q944W4 pythium irr
18	550	22.3	525	10 Q9ZNM2	Q9ZNM2 physcomitre
19	549	22.2	457	3 Q9UVV3	Q9UVV3 mortierella
20	542	21.9	457	3 Q9HEV4	Q9HEV4 mortierella
21	540	21.9	457	3 Q8X173	Q8X173 mortierella
22	539	21.8	457	3 Q9UVY3	Q9UVY3 mortierella
23	528	21.4	457	3 Q9HEV1	Q9HEV1 mortierella
24	528	21.4	457	3 Q8X174	Q8X174 mortierella
25	521.5	21.1	467	3 Q9VCV3	Q9VCV3 mucor circi
26	520.5	21.1	477	10 Q8RXB0	Q8RXB0 phaeodactyl
27	514	20.8	568	3 Q8NKG9	Q8NKG9 saccharomyc
28	502	20.3	573	3 Q8NKG8	Q8NKG8 kluyveromyc
29	461	18.7	443	5 Q23221	Q23221 caenorhabdi
30	460	18.6	443	5 Q61387	Q61387 caenorhabdi
31	458	18.5	454	13 Q9BSW7	Q9BSW7 oncorhynch
32	455.5	18.4	501	4 Q8NCG0	Q8NCG0 homo sapien
33	454	18.4	444	4 Q9S864	Q9S864 homo sapien
34	453.5	18.4	444	4 Q9NRP8	Q9NRP8 homo sapien
35	453.5	18.4	444	4 Q60427	Q60427 homo sapien
36	450.5	18.2	444	4 Q96139	Q96139 homo sapien
37	449	18.2	444	11 Q92122	Q92122 rattus norv
38	449	18.2	452	13 Q8UMM5	Q8UMM5 oncorhynch
39	448	18.1	444	11 Q920R9	Q920R9 mus musculu
40	447.5	18.1	444	4 Q96T10	Q96T10 homo sapien
41	444.5	18.0	501	4 Q8NCC7	Q8NCC7 homo sapien
42	442.5	17.9	444	4 Q9NVX1	Q9NVX1 homo sapien
43	442	17.9	445	13 Q8AY64	Q8AY64 sparus aupa
44	441	17.9	454	13 Q8QGE2	Q8QGE2 salmo salar
45	439.5	17.8	444	4 Q96SV3	Q96SV3 homo sapien

ALIGNMENTS

RESULT 1	ID	Q9ZTY9	PRELIMINARY;	PRT;	446 AA.
AC	Q9ZTY9				
DT	01-MAY-1999 (TRENBLREL. 10, Created)				
DT	01-MAY-1999 (TRENBLREL. 10, Last sequence update)				
DT	01-OCT-2002 (TRENBLREL. 22, Last annotation update)				
DE	Desaturase/cytochrome b5 protein.				
OS	Ricinus communis (Castor bean).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	Euroside 1; Malpighiales; Euphorbiaceae; Ricinus.				
OX	NCBI_TaxID=3986;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Seed endosperm;				
RX	MEDLINE=97268723; PubMed=9108131;				
RA	Sayanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,				
RA	Christie W.W., Shewry P.R., Napier J.A.;				
RT	"Expression of a borage desaturase cDNA containing an N-terminal				
RT	cytochrome b5 domain results in the accumulation of high levels of				
RT	delta6-desaturated fatty acids in transgenic tobacco."				
RL	Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).				
CC	-1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.				
DR	EMBL; AF005096; AAD01240.1; -				
DR	HSSP; P00171; 115U.				
DR	InterPro: IPR001199; Cyt B5.				
DR	InterPro: IPR005804; FA_desat_fam.				
DR	Pfam; PF00487; FA_desaturase; 1.				
DR	Pfam; PF00173; heme_1; 1.				
DR	ProDom; PD000612; Cyt B5; 1.				
DR	ProDom; PD001081; FA_desat_fam; 1.				
DR	PROSITE; PS50255; CYTOCHROME_B5_2; 1.				
KW	Heme				
SQ	SEQUENCE	446 AA;	51418 MW;	A1954FDB2DDB600F CRC64;	
Query Match	62.5%;	Score 1543;	DB 10;	Length 446;	
Best Local Similarity	59.8%;	Pred. No. 3.9e-129;			
Matches 268;	Conservative 77;	Mismatches 101;	Indels 2;	Gaps 2;	

QY 1 MEEPKHIIISOADLAKHKOPOGLMWSIKGYDYSKMTKEHFGELPLLSFAGODVTDAPFI 60
 DB 1 MAETKATYTEDLEKKNHFGDLMSIOGKIYNTDMSKDHGVSPLHLAAGODVTDAPFV 60
 QY 61 AHHPTAMQYLDREFTGYVYVODYSVSEMSKDYRLVSEFSKMGLEFKTPGKGVCSIFVFS 120
 DB 61 AHHPTAMQYLDREFTGYVYVODYSVSEMSKDYRLVSEFSKMGLEFKTPGKGVCSIFVFS 119
 QY 121 VLPAISYVGLYCKSTVAHLCSGLMGMLVQSQWVGHDSCHYQVMPNRLKRLFOIAG 180
 DB 120 MLALSYVGLYCKSTVAHLCSGLMGMLVQSQWVGHDSCHYQVMPNRLKRLFOIAG 179
 QY 181 NVLAGSVAMKLDHNTTHHACNSANLDPDLOHPLIAISPKFNSLTSTYHNCMTYDAA 240
 DB 180 NVLAGSVAMKLDHNTTHHACNSANLDPDLOHPLIAISPKFNSLTSTYHNCMTYDAA 239
 QY 241 AAEFFVSFOHMTFYPALLSVRLYLFIISFKVVSNNKRYKRSOELIGYAAFLTWYSL 300
 DB 240 AAEFFVSFOHMTFYPALLSVRLYLFIISFKVVSNNKRYKRSOELIGYAAFLTWYSL 298
 QY 301 SRIPNMEERVYFSCIAVAGFOHMOFSLNHFASNYTGLPSGNDWPHOOTKTGLNTAS 360
 DB 299 SRIPNMEERVYFSCIAVAGFOHMOFSLNHFASNYTGLPSGNDWPHOOTKTGLNTAS 358
 QY 361 AAMDWFFHGLHFOIEHNLPRMPKCHFRKISPIYVKLCOKHNSYETATWMEANKMYST 420
 DB 359 AAMDWFFHGLHFOIEHNLPRMPKCHFRKISPIYVKLCOKHNSYETATWMEANKMYST 418
 QY 421 LRAVAMEAKDVTKEPKNWMEANTFG 448
 DB 419 LRAVAMEAKDVTKEPKNWMEANTFG 446

RESULT 2

Q8VZ22 PRELIMINARY; PRT; 448 AA.
 AC Q8VZ22; 08VZ22;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta-6-desaturase.
 GN D6DES.
 OS Echium gentianoideae.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Boraginaceae; Echium.
 OX NCBI_TaxID=173991;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maroto F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz J.R.;
 RT "Cloning and Molecular Characterization of the D6-Desaturase from
 RT Echium: Functional Expression in Yeast and Tobacco."
 RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AY055117; AL23580.1; -
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PSS0255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 448 AA; 51428 MW; CZA937951B87C183 CRC64;

Query Match 61.5%; Score 1519.5; DB 10; Length 448;
 Best Local Similarity 57.4%; Pred. No. 4.8e-127;
 Matches 255; Conservative 90; Mismatches 98; Indels 1; Gaps 1;

QY 5 KKHISOADLAKHKOPOGLMWSIKGYDYSKMTKEHFGELPLLSFAGODVTDAPFI 64
 DB 6 KKHISOADLAKHKOPOGLMWSIKGYDYSKMTKEHFGELPLLSFAGODVTDAPFI 65

QY 65 GTAMQYLDREFTGYVYVODYSVSEMSKDYRLVSEFSKMGLEFKTPGKGVCSIFVSVLFA 124
 DB 66 GTAMQYLDREFTGYVYVODYSVSEMSKDYRLVSEFSKMGLEFKTPGKGVCSIFVSVLFA 125
 QY 125 LSVYVGLYCKSTVAHLCSGLMGMLVQSQWVGHDSCHYQVMPNRLKRLFOIAGNVIA 184
 DB 126 LSVYVGLYCKSTVAHLCSGLMGMLVQSQWVGHDSCHYQVMPNRLKRLFOIAGNVIA 185
 QY 185 GVSVAAMKLDHNTTHHACNSANLDPDLOHPLIAISPKFNSLTSTYHNCMTYDAA 244
 DB 186 GVSVAAMKLDHNTTHHACNSANLDPDLOHPLIAISPKFNSLTSTYHNCMTYDAA 245
 QY 245 FVFOHMTFYPALLSVRLYLFIISFKVVSNNKRYKRSOELIGYAAFLTWYSLRLP 304
 DB 246 FVFOHMTFYPALLSVRLYLFIISFKVVSNNKRYKRSOELIGYAAFLTWYSLRLP 304
 QY 305 NMEERVYFSCIAVAGFOHMOFSLNHFASNYTGLPSGNDWPHOOTKTGLNTASAMD 364
 DB 305 NMEERVYFSCIAVAGFOHMOFSLNHFASNYTGLPSGNDWPHOOTKTGLNTASAMD 364
 QY 365 WFFHGLHFOIEHNLPRMPKCHFRKISPIYVKLCOKHNSYETATWMEANKMYSTLRAV 424
 DB 365 WFFHGLHFOIEHNLPRMPKCHFRKISPIYVKLCOKHNSYETATWMEANKMYSTLRAV 424
 QY 425 AAMEAKDVTKEPKNWMEANTFG 448
 DB 425 AAMEAKDVTKEPKNWMEANTFG 448

RESULT 3

Q8VZ21 PRELIMINARY; PRT; 448 AA.
 AC Q8VZ21; 08VZ21;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta-6-desaturase.
 GN D6DES.
 OS Echium pitardii var. pitardii.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Boraginaceae; Echium.
 OX NCBI_TaxID=174255;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maroto F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz J.R.;
 RT "Cloning and Molecular Characterization of the D6-Desaturase from
 RT Echium: Functional Expression in Yeast and Tobacco."
 RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AY055118; AL23581.1; -
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PSS0255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 448 AA; 51394 MW; 4B6D6EA4905DE263 CRC64;

Query Match 61.1%; Score 1509.5; DB 10; Length 448;
 Best Local Similarity 57.4%; Pred. No. 3.8e-126;
 Matches 255; Conservative 88; Mismatches 100; Indels 1; Gaps 1;

QY 5 KKHISOADLAKHKOPOGLMWSIKGYDYSKMTKEHFGELPLLSFAGODVTDAPFI 64
 DB 6 KKHISOADLAKHKOPOGLMWSIKGYDYSKMTKEHFGELPLLSFAGODVTDAPFI 65
 QY 65 GTAMQYLDREFTGYVYVODYSVSEMSKDYRLVSEFSKMGLEFKTPGKGVCSIFVSVLFA 124
 DB 66 GTAMQYLDREFTGYVYVODYSVSEMSKDYRLVSEFSKMGLEFKTPGKGVCSIFVSVLFA 125

Qy	125	LSVYGLVLCXSKSWAHLCSELMLGMWMLYOSGWGJHDSCHYQWVNEKRLNLTLPQIACNVA	184
Db	126	MSYVGLVLCCEGLVHLLIAGLGMFGWVIOGCMGHDXGHTIIVWPNPKLNTLMGIIVASNCIS	185
Qy	185	GVSVAMKLLDHTNTHFACNSANLDPDIOHLPILAISPKFENSITSYHNCXMTYDRAARF	244
Db	186	GISIGMWKMNHAHHIACNSLDYDPLQYIPLVYSSKLFSSLTSHFEKULTFDDLSRF	245
Qy	245	FVSFOHMTFFPALISVRLYFLTLSFKVFPSSNKRKYKRSQELIGYAPLTWYSLLSRLP	304
Db	246	FVSHQHTMFYFVWCASRVNMFVQSL-IMLTKRNVFYSRQELGLVFWIMWYELVLSCLP	304
Qy	305	NWPEVWVYFTSCLTAAVAGFOHMOFSLNHPASNNYTGCLPSGNDWFHOOTKGTLNTASAMWD	364
Db	305	NWGEIIMEFVAVSLSTYGLQOVFSLNHPAASYVVGPKGIWPEKOTCGTLIDSCPSMWD	364
Qy	365	WPHGLHFOIEHHLFPRMPKCHFRKSPILVNKLCOQHNLSEYFATYMWENAKWYSLTRAV	424
Db	365	WPHGLQFOVEHHLFPPKLRCHLRKISPFVMELOCKHNLSTNCASSQANEMTLRPLRDT	424
Qy	425	AMEAKDYTKPVPKNNVWEAMNTFG	448
Db	425	ALQARDLTKEPLPKULVWEALNTHG	448

Q9SAUS	PRELIMINARY;	PRT;	448 AA.
01-MAY-2000 (TREMBLrel. 13, Created)			
01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
Delta 6-desaturase.			
Borago officinalis (Bourrache) (Borage).			
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;			
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;			
Asteridae, lamids, Boraginaceae, Borago.			
NCBI_TaxID=13363;			
[1]			
SEQUENCE FROM N.A.			
TISSUE=Seed;			
Number A.N., Beremand P.D., Thomas T.L.;			
"Engineering of Plant Seed Oils to Produce Gamma Linolenic Acid			
(GLA).";			
Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.			
-1 SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.			
EMBL; AF007561; AAD01410.1; -			
InterPro; IPR001199; Cyt B5.			
InterPro; IPR005804; FA_desat_fam.			
Pfam; PF00487; FA_desaturase; 1.			
Pfam; PF00173; heme_1; 1.			
Prodrom; PD000612; Cyt B5; 1.			
Prodrom; PD001081; FA_desat_fam; 1.			
PROSITE; PS0255; CYTOCHROME_B5_2; 1.			
Heme			
SEQUENCE 448 AA; 51626 MW; EAC3FDBF22E0DE00 CRC64;			
Query Match 59.3%; Score 1465.5; DB 10; length 448;			
Best Local Similarity 55.4%; Pred. No. 3.2e-122;			
Matches 246; Conservative 90; Mismatches 107; Indels 1; Gaps 1.			
5 KKHISQADLAHKQKGDLMISIKGVNYDISKMTKEHPSGELRLPSFAQDVTDAFIATHP 64			
6 KKIYISDELKKNHDKGDMISIQGAAYVSDVWVKDHPGSGFPLKSLAQDEVDATVAENR 65			
65 GTAMQYIDRFFTGYVQDYSVSEMSKDYRRILVSEFSKMGLEFETPKSGKYVCSIFFYSLFA 124			
66 ASYWKNLDRKFFGYLLKDYKDYVSVEVSKDYRKLVFEEFSKGLYDKKHIMFATLCFIAMLFA 125			
125 LSYVGVLYCKSTWALCSGLMGMLWDSGVNGHNSCHYQVMPNKKRLRPIQINGVIA 184			
126 MSYGVLRCEGVLYLHFGSCGLMGFLMISGWHGADGAYMVVSDSLRINKFNGIFPANCIS 185			

Qy	185	GVSVAAMMLDINTHHFACNSANLPDIOHLPITAIISPKEFNSLSYHNCKMITYBAAAF	24
	186	GISTGMKKMNNNAHHIACNSLEYBPDIOYIIFPLVASSKFPGSLTHFYEKRLTFPDSLSRF	245
Db	245	FVFSQOHTFYFALLSVRLYLFLISEKVVFSNNKRYKKSQETLGYAFLTWYSLLSRLP	304
Qy	246	FVFSQOHTFYFYMCAARLMMYQSI-IMLLTKRNVSYAQLGLGLVSIWYPLVASC	304
Db	305	NMPERVMYFTSCIAVAGFOHQOFSLNHFASNVYTGLP&GNDWFHOOTKTLNITASAMD	364
Qy	305	NMGRIHFVILASLSVYGMQOVQFSLNHSSSVYQKPKGNMWFELQTDGTLDISCP&WD	364
Db	365	WFHGGHFOIEBHLLFPRMPKCHF&KISIPYVKLCOXNLSYETATMWEANKNVYSTLR&V	424
Qy	365	WFHGGHFOIEBHLLFPRMPKCH&KISIPYVKLCOXNLSYETATMWEANKNVYSTLR&V	424
Db	425	AME&KDVTKP&VKNNVME&MMTFFG	448
Qy	425	ALQ&RDITKPLPKULVME&LHTHG	448

ID	QBLDD7	PRELIMINARY;	PRT;	446 AA.
AC	QBLDD7;			
DT	01-OCT-2002 (TREMBLrel, 22, Created)			
DT	01-OCT-2002 (TREMBLrel, 22, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel, 23, Last annotation update)			
DS	Sphingolipid long chain base delta 8 desaturase.			
OS	Aquilegia vulgaris.			
OC	Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;			
OC	Spermatophytes; Magnoliophyta; eudicotyledons; Ranunculales;			
OC	Ranunculaceae; Aquilegia.			
OX	NCBI_TaxID=3451;			
XX	[1]			
RP	SEQUENCE FROM N.A.			
RA	Longman A.J., Michaelson L.V., Napier J.A.;			
RT	"Isolation and characterization of a cDNA encoding a delta 8			
RT	sphingolipid desaturase from Aquilegia vulgaris."			
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.			
DR	EMBL, AF406816; AAC03619.1; -.			
DR	InterPro: IPR001199; Cyt_B5.			
DR	InterPro: IPR005804; FA_desat fam.			
DR	Pfam: PF00487; FA_desaturase; 1.			
DR	Pfam: PF00173; heme 1; 1.			
DR	PRINTS: PR00363; CYTOCHROMEBS.			
DR	ProDom: PD000612; Cyt_B5; 1.			
DR	ProDom: PD001081; FA_desat fam; 1.			
DR	PROSITE: PSS0255; CYTOCHROME_B5_2; 1.			
KW	Heme.			
SO	SEQUENCE	446 AA;	51273 MW;	76366DDB08956D09 CRC64;
Query Match		59.1%;	Score 1461;	DB 10; Length 446;
Best Local Similarity		56.0%;	Pred. No. 7.9e-122;	
Matches	251;	Conservative 82;	Mismatches 113;	Indels 2; Gaps 2;
QY	1 MEEPKKHSIQADLAKHQPDWLWISIGKYDYSKTKKHPGSGSLPLSPAGQVDTAFI	60		
DB	1 MTEGRREITSEELKQKHNKHDWISIGKTYDSEWKDHPGSGAPPLNLTAGDVTAFAV	60		
QY	61 AYHNGTAMQVLDLRFPTGYVQDYVSSEMSKDYRLVSEFSGMGLFPTPGKGVCSIFPV	120		
DB	61 AFRHGSAMKTLDRKFTG-YLKDITYTISEVSKDYRLVAEFSAGLYDKKGHIIIESLTFTV	119		
QY	121 VFLPASYGVLYCKSTVAHLCSGLMGMLVQSGVGHDSCHYVMENRKRLNRLFQIIAG	180		
DB	120 ILMAISVGVLCSDPKTVAHLASAIVLGLLMMQIGFVGHDSGHYIMLTPLKLNRFMQIFTG	179		
QY	181 NVLAGSVAMWKLDHNTTHHFACNSANLDPRLOHPLIALSPKFNLSLTYYHNCKMTYDR	240		
DB	180 NCTTGISIGWKKMKNHNAHNAVNSLDVDPDLQHPFLAVSSDIFSLTSKRYGGRKMTFD	239		

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QY 241 AAFVFWHTFYPALLSVLYLFIISFKVFSNNKRVKRSOELIGYAAFLTWSILL 300
DB 240 IARLISFOHMTFYPWAIKARINIFAQSF-ILLISKRPVDRALLEGWFMWYLL 298
QY 301 SRPNMDEWYFTSCLAVAGFQWQPSLNHFASNVYTGLPBGNDWFHQOTKTLNTAS 360
DB 299 ACUPNMBERAMVYMSFAVSGYQHIOFLNHFSAHTVGGPPPCNDWEKOTKGFIDISC 358
QY 361 AMMDWFHGLHFOJENHLFPRMPKCHFRKISPIYNKLCOKNLSYETATWMEANKMYST 420
DB 359 TMDWFEHGLHFOJENHLFPRMPKCHFRKISPIYNKLCOKNLSYETATWMEANKMYST 418
QY 421 LRAVAMEAKDVTKVPKXNMVMEANTFG 448
DB 419 LRNALQARDLTNPRLVWEAVNTHG 446

RESULT 6
ID 004353 PRELIMINARY; PRT: 448 AA.
AC 004353;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Delta 6 desaturase.
OS Borage officinalis (Bourrache) (Borage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Boraginaceae; Borage.
OX NCBI_TaxID=13363;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97268723; PubMed=9108131.
RA Sayanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,
RA Christie W.W., Shewry P.R., Napier J.A.;
RT Expression of a borage desaturase cDNA containing an N-terminal
RT cytochrome b5 domain results in the accumulation of high levels of
RT delta-desaturated fatty acids in transgenic tobacco.
RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL: U79010; AAC49700.1; -
DR InterPro: IPR001199; Cyt_B5.
DR InterPro: IPR005804; FA_desat_fam.
DR Pfam: PF00487; FA_desaturase_1.
DR Pfam: PF00173; heme_1; 1.
DR ProDom: PD000612; Cyt_B5; 1.
DR ProDom: PD001081; FA_desat_fam; 1.
DR PROSITE: PSS0255; CYTOCHROME_B5_2; 1.
KM Heme.
SQ SEQUENCE 448 AA; 51635 MW; B62EEB701680909F CRC64;

Query Match 59.1%; Score 1460.5; DB 10; Length 448;
Best Local Similarity 55.2%; Pred. No. 8.8e-122;
Matches 245; Conservative 90; Mismatches 108; Indels 1; Gaps 1;

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DB 246 FVSGHMTFYPICARLNNYQSL-IMLTKNVSYRAHELIGCVFSIMYDLVSLP 304
QY 305 NMPERVYFTSCLAVAGFQWQPSLNHFASNVYTGLPBGNDWFHQOTKTLNTASAMD 364
DB 305 NMBERIWEFVYASISVGMQVQPSLNHFSVYVGRKGNWBEKOTDGLDISCPWMD 364
QY 365 WFGHGLHFOJENHLFPRMPKCHFRKISPIYNKLCOKNLSYETATWMEANKMYSTLRAV 424
DB 365 WFGHGLHFOJENHLFPRMPKCHFRKISPIYNKLCOKNLSYETATWMEANKMYSTLRAV 424
QY 425 AMEAKDVTKVPKXNMVMEANTFG 448
DB 425 ALQARDITKPLPKLVWEALHTHG 448

RESULT 7
ID 08L717 PRELIMINARY; PRT: 448 AA.
AC 08L717;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Delta-6-desaturase.
OS Argania spinosa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Sapotaceae; Argania.
OX NCBI_TaxID=85884;
RN [1]
RP SEQUENCE FROM N.A.
RA El Filali A., Anderson M., Abbas K.;
RT Characterization and cloning of delta-6-desaturase in Argania spinosa
RT fruit.
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL: AY13138; AAM94345.1; -
DR InterPro: IPR001199; Cyt_B5.
DR InterPro: IPR005804; FA_desat_fam.
DR Pfam: PF00487; FA_desaturase_1.
DR Pfam: PF00173; heme_1; 1.
DR ProDom: PD000612; Cyt_B5; 1.
DR ProDom: PD001081; FA_desat_fam; 1.
DR PROSITE: PSS0255; CYTOCHROME_B5_2; 1.
KM Heme.
SQ SEQUENCE 448 AA; 51304 MW; 0B46F81B7DEB29BF CRC64;

Query Match 56.3%; Score 1405.5; DB 10; Length 448;
Best Local Similarity 54.1%; Pred. No. 7.1e-117;
Matches 240; Conservative 86; Mismatches 117; Indels 1; Gaps 1;

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Db	305	NMGEIMEVJASLSV	TGMQOV	FSLNHPSS	YVVGKPN	NMMFENQ	TGDTCL	LISCP	MMWD	365																											
Qy	365	MFHGJLH	QI	EHLE	FFP	KP	KCF	FRK	IS	PI	VNKL	CO	RNI	SY	TATW	EANK	VY	STL	RAV	424																	
Db	365	MFHGJLH	QI	EHLE	FFP	KP	KCF	FRK	IS	PI	VNKL	CO	RNI	SY	TATW	EANK	VY	STL	RAV	424																	
Qy	425	AMEADV	TR	KPV	KXN	VW	MEAM	TNG	448																												
Db	425	AMEADV	TR	KPV	KXN	VW	MEAM	TNG	448																												
Qy	425	ALQARD	IT	KPL	PKN	LW	EM	AL	HTHG	448																											
Db	425	ALQARD	IT	KPL	PKN	LW	EM	AL	HTHG	448																											
RESULT 8																																					
Q9ZRP8	Q9ZRP8	PRELIMINARY: PRT: 449 AA.																																			
AC	Q9ZRP8																																				
DT	01-MAY-1999	(TREMBLrel. 10, Created)																																			
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)																																			
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)																																			
DE	Delta-8 sphingolipid desaturase.																																				
GN	SLD1.																																				
OC	Brassica napus (Rape).																																				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;																																				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;																																				
OC	eucosids II; Brassicales; Brassicaceae; Brassica.																																				
OX	NCBI_TaxID=3708;																																				
RN	[1]																																				
RP	SEQUENCE FROM N.A.																																				
RC	STRAIN=cv. Drakkar; TISSUE=Ripening embryos;																																				
RC	MEDLINE=99003197; PubMed=9786850;																																				
RA	Sperling P., Zaehring U., Heinz B.;																																				

Oy		365	WFGHGLHPQJHEHLPMPKCFHKFPIVAKLCOKNLSIETATMEANIKVVSTLEAV	424
Dd		366	WFEGGLOPQJHEHLPRPLRCHLRGVSPVVOELCKGNLPRSLSWNEANVTLTARKA	425
Oy		425	AMEAKDVTKPVKNMVEAMNTFG	448
Dd		426	AVQARVDVTNPVLNLTWEALNTHG	449
 RESULT 9				
ID	Q43469	PREDIMINARY;	PRT;	458 AA.
AC	Q43469			
DT	01-NOV-1996 (TREMblrel. 01, Created)			
DT	01-NOV-1996 (TREMblrel. 01, Last sequence update)			
DT	01-OCT-2002 (TREMblrel. 22, last annotation update)			
DE	Delta-8 sphingolipid desaturase.			
GN	SLD1.			
OC	Helianthus annuus (Common sunflower).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Asteridae; campanulids; Asterales; Asteraceae; Asteroidae;			
OC	Heliantheae; Helianthus.			
OX	NCBI_TaxId=4232;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Inbred line HA89;			
RC	TISSUE=Cotyledons of developing sunflower fruits;			
RX	MEDLINE=96028121; PubMed=7588718;			
RA	Spearling P., Schmitt H., Heinz B.;			
RT	"A cyclochrome b5-containing fusion protein similar to plant acyl lipid			
RT	desaturases.";			
RL	Eur. J. Biochem. 232:798-805(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Inbred line HA89;			
RC	TISSUE=Cotyledons of developing sunflower fruits;			
RX	MEDLINE=2116801; PubMed=11171153;			
RA	Spearling P., Blume A., Zaehring U., Heinz E.;			
RT	"Further characterization of delta 8-sphingolipid desaturases from			
RT	higher plants.";			
RL	Biochim. Soc. Trans. 28:638-641(2000).			
CC	-1 - SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.			
DR	EMBL: X87143; CAA60621.1; -.			
DR	HSSP: P00173; IFO3.			
DR	IneerPro: IPRO01199; CyC_B5.			
DR	IneerPro: IPR005804; FA_desat.fam.			
DR	Pfam: PF00487; FA_desaturase; 1.			
DR	Pfam: PF00173; heme 1; 1.			
DR	Prodrom: PD000612; CyC_B5; 1.			
DR	Prodrom: PD001081; FA_desat.fam; 1.			
DR	PROSITE: PS50255; CYTOCHROME_B5_2; 1.			
Kw	Heme.			
SO	SEQUENCE	458 AA;	52231 MW;	D182287AB0E9245 CRC64;
 Query March 56.3%; Score 1391.5; DB 10; Length 458; Best Local Similarity 52.7%; Pred. No. 1.3e-115; Matches 234; Conservative 90; Mismatches 119; Indels 1; Gaps 1;				
Oy		5	KKHISQADLAHKPOGDLMWSIKGYVDISKWKTEHFGBELPLSPAGQDVTDFAIAYHP	64
Dd		16	KKYITSEKLKKHNPNNDLWISILGKVYNTWEAKEHGGDAPRLNLAGQDVTDFAIAHP	75
Oy		65	GTAHQYLDRFFTYGVDDYSVESKSQRRLVSEFSKGLFKTTGKGYYGSIFFVSULFA	124
Dd		76	GTAWKHLDKLFPTGHLDYQVSDISRDKLASFAACGMFEKKGHGVIYSLCFVSLLS	135
Oy		125	LASYGVLYCGSTAAHLCSGLMGMLMQSGVNGHDSCHYGVMPPRKUNRLRQLIAGNVYA	184
Dd		136	ACYGVGVLYSSFPVHMLHSAILGLAMQOIVAYLGHDAGHYQMMAARGNNKPAIGITICIT	195
Oy		185	GVSAVAWMKDHTHTHFACNSANILDPDIIAISPKFPNSLTSYHNCKMTYDRAAF	244

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Db 196 GISTAMKMTNNAHIAICNSLDYDPLQHLPMILAVS SKLFNSITSVFYGRQLTFDPLARF 255
Qy 245 FVSTQHTFTYFALLSVLRYLFILSKYVFNKKRVRSOEIIGYAFITWYSLLSRLP 304
Db 256 FVSTQHTFTYFALLSVLRYLFILSKYVFNKKRVRSOEIIGYAFITWYSLLSRLP 314
Qy 305 NMPERVVYFTFSCLAIVAGFOHMFSLNHPASVNTYGLPSGNDWPHQOTKGTINTITASA 364
Db 315 NMPERVVYFTFSCLAIVAGFOHMFSLNHPASVNTYGLPSGNDWPHQOTKGTINTITASA 374
Qy 365 WFFGGLFOLEHHLFPRMPKCHFRKISPIYVKLCOKNLSYETATWMEANKMYSTLR 424
Db 375 WFFGGLFOLEHHLFPRMPKCHFRKISPIYVKLCOKNLSYETATWMEANKMYSTLR 434
Qy 425 AMEAKDVTXKPVKPMVMEANMTFG 448
Db 435 ALQARDLTNPAPQNLWAEAFVTHG 458

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RESULT 10

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O8LB96 PRELIMINARY; PRT; 449 AA.
ID O8LB96
AC O8LB96;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE Delta-8 sphingolipid desaturase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volicovsky N., Town C.D., Troupkan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RL annotation."
RL Genome Biol. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troupkan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AY087345; AAM64895.1; -
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA desat fam.
DR Pfam; PF00487; FA desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA desat fam; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 449 AA; 51744 MW; A1EB5578BC803E18 CRC64;
Query Match 55.6%; Score 1372.5; DB 10; Length 449;
Best Local Similarity 51.7%; Pred. No. 6,2e-114;
Matches 231; Conservative 95; Mismatches 120; Indels 1; Gaps 1;
Qy 2 EEPKXHSQADLAKGKQPDLMISIKKVVYDISKTEHSGEGLPLSPAGQDVTDAFIA 61
Db 4 ETEKXVITNEDLTKGHNKSGDLMIAIQGKVVNVSDWIKTHPGSDTVILNLVGQDVTDAFIA 63
Qy 62 YHFGTAQYLDRTFTGYVODYSVSEMSKQVRRVLVSEFSKMGFLPRTGKGVYCSIFVSV 121
Db 64 FHEPTAHHDHDLTGTHIRDFQVSESRDVRMAAEFRKLGLENKGHTVLYTLATVAA 123
Qy 122 LFLASVGVLYCKSTWHLCSGLLMGLMLOSQGVNGVDSCHYQVMPKRLNRLFOIAGN 181
Db 124 MFLRLVGLVACTSVFAHQIQAALLGLIMIGSAVIQDHSYVIMSNKSYVRPAQLLSGN 183

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Qy 182 VIAGSVAAWKLDHNTTHFACNSANLDPDIQHLPIAISPKEFNSLTSYHNCMTYDRA 241
Db 184 CLTGISIAWKMTNNAHIAICNSLDYDPLQHLPMILAVS SKLFNSITSVFYGRQLTFDPLARF 243
Qy 242 ARFVSFQHTFTYFALLSVLRYLFILSKYVFNKKRVRSOEIIGYAFITWYSLLSRLP 301
Db 244 ARFVSFQHTFTYFALLSVLRYLFILSKYVFNKKRVRSOEIIGYAFITWYSLLSRLP 302
Qy 302 RLNMPERVVYFTFSCLAIVAGFOHMFSLNHPASVNTYGLPSGNDWPHQOTKGTINTITASA 361
Db 303 RLNMPERVVYFTFSCLAIVAGFOHMFSLNHPASVNTYGLPSGNDWPHQOTKGTINTITASA 362
Qy 362 WMDWFGGLFOLEHHLFPRMPKCHFRKISPIYVKLCOKNLSYETATWMEANKMYSTLR 421
Db 363 YMDWFGGLFOLEHHLFPRMPKCHFRKISPIYVKLCOKNLSYETATWMEANKMYSTLR 422
Qy 422 RAVAMEAKDVTXKPVKPMVMEANMTFG 448
Db 423 KTAAYQARDVANPVKLVWAEALNTHG 449

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RESULT 11

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Q92RP7 PRELIMINARY; PRT; 449 AA.
ID Q92RP7
AC Q92RP7;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE Delta-8 sphingolipid desaturase (AT3G61580/P2A19_180).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CV Columbia; TISSUE=flower, MAINLY GREEN PARTS, and Root;
RC MEDLINE=99003197; PubMed=9766850;
RX Speirling P., Zaehring U., Heinz B.;
RT cytochrome b5 fusion protein."
RL J. Biol. Chem. 273:28590-28596(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA De Haan M., Maarse A.C., Grivell L.A., Mewes H.W., Lemcke K.,
RA Meyer K.F.X., Queller F., Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carlini P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida U., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Mu T.,
RA Carlini P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
RA Deng J.M., Hayashizaki Y., Heuan V.W., Lee J.M., Ishida U., Kamiya A.,
RA Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Shinozaki K., Tang C.C., Toriumi M., Wallender E.K., Wong C.,
RA Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,

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RA Theologis A., Davis R.W.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AJ224161; CAAL158.1; -
 DR EMBL: AL132962; CAB71088.1; -
 DR EMBL: AF428420; AAL16189.1; -
 DR EMBL: BT000442; AAN17419.1; -
 DR HSSP: P00171; 115U.
 DR InterPro: IPR001199; Cyt B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD00612; Cyt_B5; 1.
 DR ProDom: PD01081; FA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 449 AA; 51675 MW; 1450489FIDJ35964 CRC64;
 Query Match 55.6%; Score 1372.5; DB 10; Length 449;
 Best Local Similarity 51.7%; Pred. No. 6.2e-114;
 Matches 231; Conservative 95; Mismatches 120; Indels 1; Gaps 1;
 QY 2 EEPKKIISQADLAKHOPGLMISIKGVYDISKTKHPGSLPLISFAGQDVTDAFLA 61
 DB 4 ETEKKYITMEDLKKHKSGLMIAIOGVYVSDWIKTHGSDPTVILNLGVQDVTDAFLA 63
 QY 62 YHFGTAMOVLDKRPFGYVVDYVSSEMSKDYRRLVSEPSKGLFKTPGKGVYCSIFPVSV 121
 DB 64 FHEGTAMHDLFTGTHINDPQVSEVSRDYRMALEFRLGLFENKGVTLTYTLAFVAA 123
 QY 122 LPAISYGVLYCKSTAAHLCGLMGLMLOSQVGHDSCHYQVMPNKLRLPQIAG 181
 DB 124 MFLGVLYGVLAGSVFAHQIAAALLGLMIAQSAVIGHDSGHYVIMNKSINRAQLSGN 183
 QY 182 VIAGSVAAWKLNDHNTTHFACNSANLDPDIOHLPIAISPFENSLTSYHNCKMTYDRA 241
 DB 184 CLTGISIAWKMTHNAHIAACNSLDYDPLQHPVPAVSTKFPSSILTSRPYDKLTEDPV 243
 QY 242 ARPFVFOHMTFEPALSLVLYFLISPKVPSNNKRYKRSQELIGYAAFLTWYSLLS 301
 DB 244 ARLVYQHFTTYVPCFGRINLFIQTFLLFS-KKEVPRALNFAIGLVFWTWPFLLVS 302
 QY 302 RLPPWPERVWYFTSCLAVAGFOHQSINHFASNVYTGLPSCNDWFHOQTGTLNITAS 361
 DB 303 CLPWNERRFFVYVTSFTVTLQHOITLNFADVYVGPPTGSDMEKQAGITIDISCS 362
 QY 362 WMDWFGGLHFOLEHNLPRMPKCHFRKISPIYNKLCKQNLSEYATATMEANKVYSTL 421
 DB 363 YMDWFGGLHFOLEHNLPRMPKCHFRKISPIYNKLCKQNLSEYATATMEANKVYSTL 422
 QY 422 RAVAMEAKDVTKRPVKMMWEANTFG 448
 DB 423 KTAAYQARDVANPVKLVWEALNTHG 449
 RESULT 12
 Q9FR82 PRELIMINARY; PRT; 446 AA.
 AC Q9FR82;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, last annotation update)
 DE Delta 8-sphingolipid desaturase.
 GN SUD1.
 OS Borago officinalis (Borragaceae) (Borage).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Boraginaceae; Borago.
 OC NCBI_TaxID=13363;
 OX [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=1092516; PubMed=11162428;
 RA Libisch B., Michaelson L.V., Lewis M.J., Shewry P.R., Napier J.A.;

RT "Chimeras of Delta6-fatty acid and Delta8-sphingolipid desaturases";
 RL Biochem. Biophys. Res. Commun. 279:779-785(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21260464; PubMed=11369168;
 RA Sperling P., Libisch B., Zaehring U., Napier J.A., Heinz E.;
 RT "Functional identification of a delta 8-sphingolipid desaturase from
 RT Borago officinalis";
 RL Arch. Biochem. Biophys. 388:293-298(2001).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AF133728; AAG43277.1; -
 DR HSSP: P00171; 115U.
 DR InterPro: IPR001199; Cyt B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD00612; Cyt_B5; 1.
 DR ProDom: PD01081; FA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 446 AA; 50926 MW; EBD579F035A3AF0C CRC64;
 Query Match 53.6%; Score 1325; DB 10; Length 446;
 Best Local Similarity 50.7%; Pred. No. 1.1e-109;
 Matches 227; Conservative 95; Mismatches 124; Indels 2; Gaps 2;
 QY 1 MEPPKHISQADLAKHOPGLMISIKGVYDISKTKHPGSLPLISFAGQDVTDAFLA 60
 DB 1 MEGTKKYSVGLGEGKNGDGVWISIOGVYVVTWIKHGPQGDVFINMLAQDADATDAFL 60
 QY 61 AHPGTAOVLDKRPFGYVVDYVSSEMSKDYRRLVSEPSKGLFKTPGKGVYCSIFPVSV 120
 DB 61 AHPGTAOVLDKRPFGYVVDYVSSEMSKDYRRLVSEPSKGLFKTPGKGVYCSIFPVSV 120
 QY 121 VFLASVGVLYCKSTAAHLCGLMGLMLOSQVGHDSCHYQVMPNKLRLPQIAG 180
 DB 121 LLLCGVGVLYCKSTAAHLCGLMGLMLOSQVGHDSCHYQVMPNKLRLPQIAG 180
 QY 181 NVIAGSVAAWKLNDHNTTHFACNSANLDPDIOHLPIAISPFENSLTSYHNCKMTYDRA 240
 DB 181 NCLTGISIAWKMTHNAHIAACNSLDYDPLQHPVPAVSSFPFSLTSRPFYGRBLTFDQ 240
 QY 241 AARFVFOHMTFEPALSLVLYFLISPKVPSNNKRYKRSQELIGYAAFLTWYSLLS 300
 DB 241 LSRFLVYQHFTTYVPCFGRINLFIQTFLLFS-VPRALNIGLVFWTWPFLLVS 299
 QY 301 SRLPPWPERVWYFTSCLAVAGFOHQSINHFASNVYTGLPSCNDWFHOQTGTLNITAS 360
 DB 300 SCLPWNERRFFVYVTSFTVTLQHOITLNFADVYVGPPTGSDMEKQAGITIDISCS 359
 QY 361 AAMDWFGGLHFOLEHNLPRMPKCHFRKISPIYNKLCKQNLSEYATATMEANKVYSTL 420
 DB 360 SMDWFGGLHFOLEHNLPRMPKCHFRKISPIYNKLCKQNLSEYATATMEANKVYSTL 419
 QY 421 RAVAMEAKDVTKRPVKMMWEANTFG 448
 DB 420 LRTALQARDLT-VVPQNLWEALNTHG 446
 RESULT 13
 Q9ZTU8 PRELIMINARY; PRT; 469 AA.
 AC Q9ZTU8;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
 DE S276.
 GN Triticum aestivum (Wheat).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticaceae; Triticum.
 OC NCBI_TaxID=4565;

[1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=CV. ERT3;
 RC Delhaize E., Hebb D.M., Gardner R.C., Richards K.D.;
 RT "Aluminum tolerance in yeast conferred by over-expression of wheat
 RT genes";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AF031194; AAD10250.1; -.
 DR HSSP: P00171; 11SU
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR InterPro: IPR001092; HLH_basic.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR PRINTS: PR00363; CYTOCHROMEBS.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 DR PROSITE: PS00038; HLH_1; 1.
 KW Heme.
 SQ SEQUENCE 469 AA; 52617 MW; 16F223CC1F79740D CRC64;
 Query Match 52.4%; Score 1293.5; DB 10; Length 469;
 Best Local Similarity 52.0%; Pred. No. 7.3e-107;
 Matches 230; Conservative 75; Mismatches 134; Indels 3; Gaps 3;
 QY 8 ISQADLAKHQPGLMISIKGYVDISKWKERHFGELPLISFAGQVTDPAFIYHGTAW 67
 DB 30 ISTTELOAHAAADLMWISIGDYYDVVPLRHHGEGVPLITLTAODATTAFFMAVHPSPV 89
 QY 68 WOYLDREFTGYVYDVSVSEMSKDYRLVSEFSGKGLFKTPGKGVCSIFPVSVLPALSV 127
 DB 90 RPLLRFFVG-RLTDYVPPASADPRKLLAQSLSGAFPERVGHTRPKLLVAMSVLPFIAL 148
 QY 128 YGVLYCKSTMAHLCSGLLMGLMLOSGVGHDSCHYVMPNPKLNRLFOIAGVINGV 187
 DB 149 YCVLACSTGAHMPAGGLIGFIVTIGSGMIGHDSGHQITRHPALNRLLOYVSGNCLGLG 208
 QY 188 VAWMKLDHNTHTHPCNSANADPDQHPITAIISPFPNSLTSTYHNCMTYDRAARFVS 247
 DB 209 IAWMKFNHTHTSCNSLDHPDQHPPLFAVSTKLNNMLSVCEYRTLAFDAISKEFVS 268
 QY 248 FOHWTFFPALLSVRLYLFIISFKVVFSGNNKRVYKSOEILGYAFLTWYSLLSRLNWP 307
 DB 269 YOHNTFFPWGFAFINLLVOSI-VFLITQKKVROKMEIAGVAFFWYPLVSLCPNMM 327
 QY 308 ERVWYFTSCLAVAGFOHMQFSLNHFASNVYTGLPBGNDWPHOQTKTLNTITASAMDMFH 367
 DB 328 ERVAFVLASFVITGIVQFCLNHFSSAVYVGPKNQDWFERQTAGTLDIKCSPPMDMFH 387
 QY 368 GGLHFOIEHLFPMPKCHPRKISPIYVKLCQKNLSYETATMEANKMYSTIRAVAME 427
 DB 388 GGLQFOVEHHLFPLPRCHYRMVAPIVRDLCKKHGLSYGAATFEAVMVMKTLRAALQ 447
 QY 428 AKDYTK-PVPRKNMWEAMNTFG 448
 DB 448 AREATTGAAPKRLVWEALNTHG 469

RP SEQUENCE FROM N.A.
 RC STRAIN=wc3; TISSUB=Protonemata;
 RX MEDLINE=20307617; PubMed=10848999;
 RA Sperling P., Lee M., Gierke T., Zaehring U., Stryme S., Heinz E.;
 RT "A bifunctional delta 6-fatty acyl acetylase/desaturase from the
 RT moss Ceratodon purpureus. A new member of the cytochrome b5
 RT superfamily";
 RL Eur. J. Biochem. 267:3801-3811(2000).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: A1250734; CAB9492.1; -.
 DR HSSP: P04166; 1BSM.
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 2.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 483 AA; 54857 MW; C451D042169AB1C2 CRC64;
 Query Match 26.9%; Score 663.5; DB 10; Length 483;
 Best Local Similarity 35.7%; Pred. No. 1.1e-50;
 Matches 154; Conservative 71; Mismatches 177; Indels 29; Gaps 12;
 QY 9 SQADLAKHQPGLMISIKGYVDISKWKERHFGELPLISFAGQVTDPAFIYHGTAW 68
 DB 64 SLADVASHDRPGDCMIVKEKYVDISRPAHDHGGTV-ISTYGRGCTDVFAFHPPAAW 122
 QY 69 QYLDREFTGYVYDVSVSEMSKDYRLVSEFSGKGLFKTPGKGVCSIFPVSVLPALSV 128
 DB 123 KQNDYYIGDLAREEPLDELKDYDRMAEFVEGKFSKAWFLQTLINALFAASTA 182
 QY 129 GVIYCKSTMAHLCSGLLMGLMLOSGVGHDSCHYVMPNPKLNRLFOIAGVINGV 188
 DB 183 TICYDYSYVAIVLSASLMGLFVQCCGLMADFHQGVFFENRTANSFGLVFGCVLGFVS 242
 QY 189 AMWKLDHNTHTHPCNSAN-----LDPDQHPITAIISPFPNSLTSTYHNCMTYDRAAR 243
 DB 243 SMRTKHNHTHTHPNCEDEGYTLPDEDITPLIANSKELATVES-----KRLR 253
 QY 244 FVSPQHWTFYPALLSVRL-YLF--ILSFKVVFSGNNKRVYKSOEILGYAFLTWYSLLS 299
 DB 294 -VQYGHYMLPLFLMARSWTFSGSLTFENPDLSSTTKGIEKGVAFHYAFV-SNAAFH 351
 QY 300 LSLPLMPPEKVMYFTSCLAVAG-FQHMQFSLNHFASNVYTGLPBGNDWPHOQTKTLNT 358
 DB 352 I-LPGVAKPLAMVATELVAGLLGFVFTLSNGKEVYN--ESKDPVRAQVITTRN-T 405
 QY 359 ASAMW-DMFGHGLHFOIEHLFPMPKCHPRKISPIYVKLCQKNLSYETATMEANKMY 417
 DB 406 KRWMPNDWFTGSLDTQIEHLFPMPKCHPRKISPIYVKLCQKNLSYETATMEANKMY 465
 QY 418 YSTLRVAMEA 428
 DB 466 VKALKELADEA 476

RESULT 14
 Q9LENO PRELIMINARY; PRT; 483 AA.
 AC Q9LENO;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta 6-fatty acetylase.
 OS Ceratodon purpureus (Moss).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
 OX NCBI_TaxId=3225;
 RN [1]

RESULT 15
 Q9LEM9 PRELIMINARY; PRT; 520 AA.
 AC Q9LEM9;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta 6-fatty acid desaturase.
 OS Ceratodon purpureus (Moss).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
 OX NCBI_TaxId=3225;
 RP SEQUENCE FROM N.A.
 RC STRAIN=wc3; TISSUB=Protonemata;

RX MEDLINE=20307617; PubMed=10848999;
 RA Sperling P., Lee M., Giske T., Zaehrer U., Stymne S., Heinz E.;
 RT "A bifunctional delta 6-fatty acyl acetylase/desaturase from the
 RT moss *Ceratodon purpureus*. A new member of the cytochrome b5
 RT superfamily.";
 RL Eur. J. Biochem. 267:3801-3811(2000).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AJ250735; CAB94993.1; -.
 DR HSSP; P00171; IEHB.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme 1; 1.
 DR ProDom; PD000612; Cyt B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 2.
 DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 520 AA; 59160 MW; 5A9332BEC153439 CRC64;

Query Match 25.3%; Score 626; DB 10; Length 520;
 Best local Similarity 35.2%; Pred. No 2.7e-47;
 Matches 156; Conservative 65; Mismatches 176; Indels 46; Gaps 12;

QY 3 EPRKHI--SQADIAKIKOPGDLWISIKGYDYSKWTKEHGGELPLSPAGDVTDAFI 60
 DB 93 QPKKPTVYSLKDVASHDMQDCWIIIEKYVDVSTFAEQHGGTV-INTYFGSDATDVS 151
 QY 61 AHPGTANQYLDREFFGYGYQDYSEMSKDYRLVSEFSKMGLEKTPGKGVCSIFVFS 120
 DB 152 TFFASTSMKILQNFYIGNLVREPTLELKEYRELALFLREQLFKS-SKSYVLPFTLIN 210
 QY 121 V-LFALSYGVLYCKSTWMAHLSGLMGMLQSGWVGHDSCHYOVMPPNRKLNRLFOIA 179
 DB 211 VSVIATSIATISLYKSYRAVLLSASLMGLFIQCCGMWLDHQLHGVFETRMINDVGYV 270
 QY 180 GNVIAGVSAVMWKL DNTHTHHFACNSAN-----LDPDIOHLPIAISPKEFNSLYTS----- 229
 DB 271 GNVVLGFSVSWWTKTNLHLHAAPNECDQKYPIDEDIDTLPIAWSKDLATVESKTMRL 330
 QY 230 ---YHN---NCKMTYDRAARFFVFSQHWTFYPALLSVRLYLFTLSFKVVFSSNNKRYKRS 283
 DB 331 VLQYQHLFFVLVLTTPARAS-----WLFWSAAFTLRPELTL-----GEKLLERG 373
 QY 284 QELIGYAAFLTWY-SLLLSRLPWPBRVWYFTSCLAAGFQHWQPSLNHPASNVYTGSPS 342
 DB 374 TVALMT-----INPNSVAFYLLPGMKPVWNVVSELSGFLGYVFWLSHGMEVYN--T 426
 QY 343 GNDWFHQTKGTINLTASAMWDMFHGSLHPOIEHHLFPRMPKCHFRKISPIVNLCKQHN 402
 DB 427 SKDPVNAQIASTRDIKAGVNDWFTGILNRQIEHHLFPTMPRNHNKISPHVETLCKKIG 486
 QY 403 LSYETATMWEANKMVTSTLRAVA 425
 DB 487 LYEEDVSMASGTYYVLKTLKDVA 509

Search completed: January 1, 2004, 06:33:52
 Job time : 43.4085 secs

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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 15.5646 Seconds
(without alignments)
1217.848 Million cell updates/sec

Title: US-09-857-524B-2

Perfect score: 2470
Sequence: 1 MEEPKHISQADLAKHKQPG.....KDVTKVPKRWMEANMTEG 448

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patents AA:*
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3: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
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5: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1459.5	59.1	448	1 US-08-366-779-5	Sequence 5, Appl1
2	1459.5	59.1	448	1 US-08-789-936-5	Sequence 5, Appl1
3	1459.5	59.1	448	1 US-08-934-254-5	Sequence 5, Appl1
4	1451.5	58.8	446	2 US-08-834-033A-15	Sequence 5, Appl1
5	1451.5	58.8	446	3 US-08-834-033A-15	Sequence 15, Appl1
6	1314.5	53.2	452	4 US-08-934-234-27	Sequence 27, Appl1
7	733.5	29.7	252	2 US-08-834-655-7	Sequence 7, Appl1
8	733.5	29.7	252	3 US-08-834-033A-8	Sequence 8, Appl1
9	733.5	29.7	252	3 US-09-363-574-7	Sequence 7, Appl1
10	733.5	29.7	252	3 US-09-363-574-7	Sequence 7, Appl1
11	549	22.2	457	2 US-08-834-655-2	Sequence 2, Appl1
12	549	22.2	457	3 US-08-834-033A-2	Sequence 2, Appl1
13	549	22.2	457	3 US-09-363-574-2	Sequence 2, Appl1
14	549	22.2	457	4 US-09-363-526-2	Sequence 2, Appl1
15	549	22.2	457	4 US-09-330-235-18	Sequence 18, Appl1
16	549	22.2	458	4 US-09-439-261-10	Sequence 10, Appl1
17	549	22.2	458	4 US-09-439-261-10	Sequence 10, Appl1
18	549	22.2	458	4 US-09-439-261-10	Sequence 10, Appl1
19	549	22.2	458	4 US-09-439-261-10	Sequence 10, Appl1
20	546	22.1	457	2 US-08-833-610-4	Sequence 11, Appl1
21	546	22.1	457	2 US-08-833-610-4	Sequence 11, Appl1
22	451.5	18.3	444	4 US-08-834-033A-14	Sequence 14, Appl1
23	442.5	17.9	444	4 US-09-439-261-11	Sequence 11, Appl1
24	442.5	17.9	444	4 US-09-439-261-12	Sequence 12, Appl1
25	442.5	17.9	445	4 US-09-439-261-13	Sequence 13, Appl1
26	442.5	17.9	445	4 US-09-439-261-13	Sequence 13, Appl1
27	440	17.8	444	4 US-09-439-261-13	Sequence 13, Appl1

28	440	17.8	444	4 US-09-227-613-42	Sequence 42, Appl1
29	436	17.7	355	2 US-08-834-655-5	Sequence 5, Appl1
30	436	17.7	355	3 US-08-834-033A-6	Sequence 6, Appl1
31	436	17.7	355	3 US-09-363-574-5	Sequence 5, Appl1
32	436	17.7	355	4 US-09-363-526-5	Sequence 5, Appl1
33	431.5	17.5	445	4 US-09-048-888-1	Sequence 1, Appl1
34	429	17.4	432	4 US-09-439-261-9	Sequence 9, Appl1
35	429	17.4	432	4 US-09-227-613-9	Sequence 9, Appl1
36	429	17.4	465	4 US-09-439-261-40	Sequence 40, Appl1
37	429	17.4	465	4 US-09-227-613-38	Sequence 38, Appl1
38	419	17.0	323	4 US-09-439-261-17	Sequence 17, Appl1
39	419	17.0	323	4 US-09-227-613-17	Sequence 17, Appl1
40	355.5	14.4	125	2 US-08-834-655-8	Sequence 8, Appl1
41	355.5	14.4	125	3 US-08-834-033A-9	Sequence 9, Appl1
42	355.5	14.4	125	3 US-09-363-574-8	Sequence 8, Appl1
43	355.5	14.4	125	4 US-09-363-526-8	Sequence 8, Appl1
44	320	13.0	446	2 US-08-833-610-2	Sequence 2, Appl1
45	320	13.0	446	3 US-08-834-033A-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-08-366-779-5
Sequence 5, Application US/08366779
Patent No. 5614393
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Reddy, Avutu S.
APPLICANT: Nuccio, Michael
APPLICANT: Freysinet, Georges L.
APPLICANT: Nunberg, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
NUMBER OF SEQUENCES: 25
TITLE OF INVENTION: DELTA 6-DESATURASE
CORRESPONDENCE ADDRESS:
ADDRESSER: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,779
FILING DATE: 30-DEC-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET INFORMATION:
TELEPHONE: (516) 742-4366
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-366-779-5

Query Match 59.1%; Score 1459.5; DB 1; Length 448;
Best Local Similarity 55.2%; Pred. No. 3.6e-150;
Matches 245; Conservative 90; Mismatches 108; Indels 1; Gaps 1;
QY 5 KKHISQADLAKHKQGDWLISIKGVYDISKWTKEHGEELPLLSFAGQDVTDATVYHP 64

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; US-08-789-936-5

Query Match      59.1%; Score 1459.5; DB 1; Length 448;
Best Local Similarity 55.2%; Pred. No. 3.6e-150;
Matches 245; Conservative 90; Mismatches 108; Indels 1; Gaps 1;

Db      6 KKYTSDCLKNDKHPDGLMISIQKAYDVSDWKDHPGSGFPLKSLAGQVTDAPFAVAFHP 65
Qy      65 GRAMQYLDREFFTGYIYQDYSVSEMSKDYRLVSEFSKMGJFKTPGKGVYCSIFPVSLFA 124
Db      66 ASTWKMLDKFETGYIYLDKDYSEVSESKDYRLVSEFSKMGJFKTPGKGVYCSIFPVSLFA 125
Qy      125 LSYVGYLVCKSTVAHLCGSLMGMLMLOSQGVGHDSCHYOVMPNRKLNRLFOIAGNVIA 184
Db      126 MSYVGYLVFCBGVYLHPLSGCLMGFLMIQSGMIGHDGHVWVSDSLNKMGJFPAANCIS 185
Qy      185 GVSVAWMLDKDHTHFAACNSANLDPDIQHLPLIAISPKFENSJTSYYHNCKMTYDRAAP 244
Db      186 GISIGWKNHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAH 245
Qy      245 FVSFQHTYTPYIPALLSVRLYLFILSFYKVVSNKRYKRSOELLGYAFLTWISLLSRP 304
Db      246 FVSQHTYTPYIPICARLNMYVQSL-IMLTGKNVSVRAQELGCLVFSIMYPLVSCLP 304
Qy      305 NMPERVMTFSCLAVAGFOHMOFSLNHPASNVTYGLPSGNDMFHOOTKGTINTASAMMD 364
Db      305 NMGERIMFVIASISVGMQOVQPSLNHFSSSVYVGPKNMFEKOTDGLDISCPAMD 364
Qy      365 WFGGLHFOIEHLFPRMPCFKRKSIPYVNLCKQKHLSEYETATWMEANKMYSTLRAY 424
Db      365 WFGGSGQFOIEHLFPRMPCRNLRKISPYIELCKGKHLPNYVNASPSKANEMTLRLTRNT 424
Qy      425 AMEAKDVTYKVPKNMYMEANMTFG 448
Db      425 ALQARDITKPLPNLWELALHTHG 448

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RESULT 2
US-08-789-936-5
Sequence 5, Application US/08789936

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; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Reddy, Avutu S.
; APPLICANT: Nuccio, Michael
; APPLICANT: Freysinet, Georges L.
; APPLICANT: Numborg, Andrew N.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,936
; FILING DATE: 28-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/366,779
; FILING DATE: 30-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 8383ZYXW
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 5:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; US-08-789-936-5

Query Match      59.1%; Score 1459.5; DB 1; Length 448;
Best Local Similarity 55.2%; Pred. No. 3.6e-150;
Matches 245; Conservative 90; Mismatches 108; Indels 1; Gaps 1;

Db      5 KKHISQADLAKHNPGLMISIQKAYDVSDWKDHPGSGFPLKSLAGQVTDAPFAVAFHP 64
Qy      6 KKYTSDCLKNDKHPDGLMISIQKAYDVSDWKDHPGSGFPLKSLAGQVTDAPFAVAFHP 65
Db      66 ASTWKMLDKFETGYIYLDKDYSEVSESKDYRLVSEFSKMGJFKTPGKGVYCSIFPVSLFA 125
Qy      65 GRAMQYLDREFFTGYIYQDYSVSEMSKDYRLVSEFSKMGJFKTPGKGVYCSIFPVSLFA 124
Db      66 ASTWKMLDKFETGYIYLDKDYSEVSESKDYRLVSEFSKMGJFKTPGKGVYCSIFPVSLFA 125
Qy      125 LSYVGYLVCKSTVAHLCGSLMGMLMLOSQGVGHDSCHYOVMPNRKLNRLFOIAGNVIA 184
Db      126 MSYVGYLVFCBGVYLHPLSGCLMGFLMIQSGMIGHDGHVWVSDSLNKMGJFPAANCIS 185
Qy      185 GVSVAWMLDKDHTHFAACNSANLDPDIQHLPLIAISPKFENSJTSYYHNCKMTYDRAAP 244
Db      186 GISIGWKNHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAH 245
Qy      245 FVSFQHTYTPYIPALLSVRLYLFILSFYKVVSNKRYKRSOELLGYAFLTWISLLSRP 304
Db      246 FVSQHTYTPYIPICARLNMYVQSL-IMLTGKNVSVRAQELGCLVFSIMYPLVSCLP 304
Qy      305 NMPERVMTFSCLAVAGFOHMOFSLNHPASNVTYGLPSGNDMFHOOTKGTINTASAMMD 364
Db      305 NMGERIMFVIASISVGMQOVQPSLNHFSSSVYVGPKNMFEKOTDGLDISCPAMD 364
Qy      365 WFGGLHFOIEHLFPRMPCFKRKSIPYVNLCKQKHLSEYETATWMEANKMYSTLRAY 424
Db      365 WFGGSGQFOIEHLFPRMPCRNLRKISPYIELCKGKHLPNYVNASPSKANEMTLRLTRNT 424
Qy      425 AMEAKDVTYKVPKNMYMEANMTFG 448
Db      425 ALQARDITKPLPNLWELALHTHG 448

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RESULT 3

US-08-934-254-5
Sequence 5, Application US/08934254

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; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,254
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 8383ZYXWVU

```

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 448 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-934-254-5

Query Match 59.1%; Score 1459.5; DB 4; Length 448;
 Best Local Similarity 55.2%; Pred. No. 3.6e-150;
 Matches 245; Conservative 90; Mismatches 108; Indels 1; Gaps 1;

QY 5 KKHISQADLAKKQKQDLMISIKGKYDISKWTKEHGGELPLSPAGQVTDAPFAVHP 64
 DB 6 KKYITSDELKNDKDKGDLWISIQGKAYVSDWKDHPGSPFLKSLAQGEVTDAPFAVHP 65
 QY 65 GTAMQYLDRFPTGYVYVODYSVSEMSKDYRLVSEFSKMGLEFPTPKGVYCSIFPVSVLPA 124
 DB 66 ASTWKNLDRFPTGYVYVODYSVSEMSKDYRLVSEFSKMGLEFPTPKGVYCSIFPVSVLPA 125
 QY 125 LSVYGLVYCKSTWALHCSGLMGLMLOSGLVGHDSCHYQVMPNRLNRLFOIAGNVIA 184
 DB 126 MSYGVVLCEGVLVHLFSGCLMGFLMIOGWLGHDAHYMVVSDRLNKFMGIFPANCIS 185
 QY 185 GVSVAWMLDHTHTHFPACNSANLDPDIQHLPIAISPKFNSLTSYHNCKMTYDRAAF 244
 DB 186 GISIGMWKNNHNAHIIACNSLEYDPLQYIPLVVSSKFFGSLTSHFYEKRLTFPSLSRF 245
 QY 245 FVSFQHTFYPRLSVRLVFLFSFKVVSNNKRYKSOEILGYAAFLTWYSLLSRP 304
 DB 246 FVSYQHTFYPRLMCAARLMYVQSL-IMLTGRNVSYRAQELLCGLVSIWPLVSCLP 304
 QY 305 NMPERVMYFTSCLAVAGFQHMQFSLNHPASNYTGLPSGNDWFHOOTKGTINLTASAWMD 364
 DB 305 NMGERIMFVIALSLVTGMQVQFSLNHPSSVYVGKPKGNMFEKQTDGTLDISCPWMD 364
 QY 365 WFGGLHFOIEHHLFPPRPKCHFRKISPIVNLCKQNLSTETATMEANKKVVSTLRV 424
 DB 365 WFGGSGFOIEHHLFPPKPRCNLRKISPIVIELCKGNLPYVYVSSKANEMTLTRLRNT 424
 QY 425 AMEADVTKPVKNNWMEAMTFG 448
 DB 425 ALQARDITKPLKPLWMEALHTHG 448

RESULT 4

US-08-833-610-5
 Sequence 5, Application US/08833610
 Patent No. 5972664
 GENERAL INFORMATION:
 APPLICANT: KUTUZZON, DEBORAH
 APPLICANT: MURKERJI, PRADIP
 APPLICANT: HUANG, YONG-SHENG
 APPLICANT: THURMOND, JENNIFER
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
 STREET: 260 SHERIDAN AVE, P.O. BOX 60039
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/833,610
 FILING DATE: 11-APR-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: RAE-VENTER, BARBARA
 REGISTRATION NUMBER: 32,750
 REFERENCE/DOCKET NUMBER: CGNE.123.00US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 328-4400
 TELEFAX: (650) 328-4477
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 446 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-833-610-5

Query Match 58.8%; Score 1451.5; DB 2; Length 446;
 Best Local Similarity 55.2%; Pred. No. 2.6e-149;
 Matches 244; Conservative 90; Mismatches 107; Indels 1; Gaps 1;

QY 5 KKHISQADLAKKQKQDLMISIKGKYDISKWTKEHGGELPLSPAGQVTDAPFAVHP 64
 DB 6 KKYITSDELKNDKDKGDLWISIQGKAYVSDWKDHPGSPFLKSLAQGEVTDAPFAVHP 65
 QY 65 GTAMQYLDRFPTGYVYVODYSVSEMSKDYRLVSEFSKMGLEFPTPKGVYCSIFPVSVLPA 124
 DB 66 ASTWKNLDRFPTGYVYVODYSVSEMSKDYRLVSEFSKMGLEFPTPKGVYCSIFPVSVLPA 125
 QY 125 LSVYGLVYCKSTWALHCSGLMGLMLOSGLVGHDSCHYQVMPNRLNRLFOIAGNVIA 184
 DB 126 MSYGVVLCEGVLVHLFSGCLMGFLMIOGWLGHDAHYMVVSDRLNKFMGIFPANCIS 185
 QY 185 GVSVAWMLDHTHTHFPACNSANLDPDIQHLPIAISPKFNSLTSYHNCKMTYDRAAF 244
 DB 186 GISIGMWKNNHNAHIIACNSLEYDPLQYIPLVVSSKFFGSLTSHFYEKRLTFPSLSRF 245
 QY 245 FVSFQHTFYPRLSVRLVFLFSFKVVSNNKRYKSOEILGYAAFLTWYSLLSRP 304
 DB 246 FVSYQHTFYPRLMCAARLMYVQSL-IMLTGRNVSYRAQELLCGLVSIWPLVSCLP 304
 QY 305 NMPERVMYFTSCLAVAGFQHMQFSLNHPASNYTGLPSGNDWFHOOTKGTINLTASAWMD 364
 DB 305 NMGERIMFVIALSLVTGMQVQFSLNHPSSVYVGKPKGNMFEKQTDGTLDISCPWMD 364
 QY 365 WFGGLHFOIEHHLFPPRPKCHFRKISPIVNLCKQNLSTETATMEANKKVVSTLRV 424
 DB 365 WFGGSGFOIEHHLFPPKPRCNLRKISPIVIELCKGNLPYVYVSSKANEMTLTRLRNT 424
 QY 425 AMEADVTKPVKNNWMEAMTFG 446
 DB 425 ALQARDITKPLKPLWMEALHT 446

RESULT 5

US-08-834-033A-15
 Sequence 15, Application US/08834033A
 Patent No. 6075183
 GENERAL INFORMATION:
 APPLICANT: KUTUZZON, DEBORAH
 APPLICANT: MURKERJI, PRADIP
 APPLICANT: HUANG, YONG-SHENG
 APPLICANT: THURMOND, JENNIFER
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:

```

ADDRESS: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300.USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-15

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Query Match 58.8%; Score 1451.5; DB 3; Length 446;
Best Local Similarity 55.2%; Pred. No. 2.6e-149;
Matches 244; Conservative 90; Mismatches 107; Indels 1; Gaps 1;

QY 5 KKHISOADLAKHKOPDLWISIKGKYVDISKMTKEHGGELPLSPAGQDVDTAFIAYHP 64
DB 6 KKITIDELKHKDPDLWISIGKAYDVSWYKDHGSGFPLKSLAGQVTTAFVAFHP 65
QY 65 GRAMQYLDPRFTGYVQDYVSSEMSKDYRRLVSEFSKMGJFKTPGKGVYCSIFVSVLPA 124
DB 66 ASTWKMLDKFETGYLKDYSSEVSKYRKLVEFSKMGJYDKKHGMFATLCFIAMLEFA 125
QY 125 LSYGYLVYCKSTVAHICSGLLMGLMLOSQGVGHDSCHYOVMPNRKLNRLFOIAGNVIA 184
DB 126 MSYGYLVFCEGVLVHLPFGCLMGFPLWISQGMIGHDGHVWVSDSRLNKMGIFANCLIS 185
QY 185 GSVAVAMKLDHNTNHPACNSANLDPDIQHLPIAISPKEFNSLTSYYHNCMTYDRAAP 244
DB 186 GISIGMMKNHNHNLACNSLEYDPLQYIFPLVSKFSGSLTSHFYEKRLTFDSLSRF 245
QY 245 FVSFGQWTFYRLLSVRLYLFIISFKVVSNNKRVYKRSOELIGYAEFLTWYGLLSRLP 304
DB 246 FVSQWTFYRLLSVRLYLFIISFKVVSNNKRVYKRSOELIGYAEFLTWYGLLSRLP 304
QY 305 NMPEIRMYFTSCLAIVAGFOHMOFSLNHPASNVTGCLPSGNDWFHOOTKGTINTTASAMD 364
DB 305 NMGERIMFYIASLIVGMQOVQFSLNHPSSVYVGKGNWFEKQDGLDLSCEPMD 364
QY 365 WFGGHLFOIEHLFPRMPKCHFRKISPIYVKLCQKHNLSYETATWAEAKMYSTLRAY 424
DB 365 WFGGGLFOIEHLFPRMPKCHFRKISPIYVKLCQKHNLPYNYASFSKANEMTLRTLRNT 424
QY 425 AMEAKDVTRKVPKMYEAMNT 446
DB 425 ALQARDITKPLPKNLVWEALHT 446

```

RESULT 6
 US-08-934-254-27
 Sequence 27, Application US/08934254
 Patent No. 6355861

```

GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESS: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-934-254-27

```

```

Query Match 53.2%; Score 1314.5; DB 4; Length 452;
Best Local Similarity 51.8%; Pred. No. 2.2e-134;
Matches 233; Conservative 86; Mismatches 126; Indels 5; Gaps 5;

QY 3 EPKHISOADLAKHKOPDLWISIKGKYVDISKMTKEHGGELPLSPAGQDVDTAFIAY 62
DB 4 EAKYITADLDRHNKSGDLWISIGKAYDCSMAEHHGGELPLSLAGQDVDTAFIAY 63
QY 63 HPGTAMQYLDPRFTGYVQDYVSSEMSKDYRRLVSEFSKMGJFKTPGKGVYCSIFVSV 121
DB 64 HPGTAMRHLDPLEFTGYLKDYSSEVSKYRKLVEFSKMGJYDKKHGMFATLCFIAMLEFA 123
QY 122 LPSLYGYLVYCKSTVAHICSGLLMGLMLOSQGVGHDSCHYOVMPNRKLNRLFOIAGN 181
DB 124 MPAALTYGYLVASVGVHNLCSGLLGLMLIQAYVGHDSGHYOVMTGRGNRTQOLIAGN 183
QY 182 VIAGSVAMKLDHNTNHPACNSANLDPDIQHLPIAISPKEFNSLTSYYHNCMTYDRA 241
DB 184 ILTGSIAMWKNHNLACNSLDYDPLQHPVAVSTRLENSTSYFYGVLKEDV 243
QY 242 ARFVSFGQWTFYRLLSVRLYLFIISFKVVSNNKRVYKRSOELIGYAEFLTWYGLLS 301
DB 244 ARFLVSQWTFYRLLSVRLYLFIISFKVVSNNKRVYKRSOELIGYAEFLTWYGLLS 302
QY 302 RLPMPEIRMYFTSCLAIVAGFOHMOFSLNHPASNVTGCLPSGNDWFHOOTKGTINTTAS 361
DB 303 CLPMPEIRMGFPLIASVAVTAIQHVOFTLHFSQDITVSGNDWFHOOTKGTINTTAS 362
QY 362 WMDWFGGHLFOIEHLFPRMPKCHFRKISPIYVKLCQKHNLSYETATWAEAKMYSTLR 420
DB 363 WMDWFGGGLFOIEHLFPRMPKCHFRKISPIYVKLCQKHNLPYNYASFSKANEMTLRT 422
QY 421 LRAVAMEAKDV-TRKVPKMYEAMNTTG 448
DB 423 LRDAAVQARDLINSAPCPKGLGYGEAVNTG 452

```

```

RESULT 7
US-08-834-655-7
; Sequence 7, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KUTZON, DEBORAH
; APPLICANT: MURKERT, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-834-655-7

Query Match      29.7%; Score 733.5; DB 2; Length 252;
Best Local Similarity 49.4%; Pred. No. 1.7e-71;
Matches 124; Conservative 52; Mismatches 74; Indels 1; Gaps 1;

QY 127 VGVGYCKSTMAHLCSGLMGLMGLSGVGHDSCHYQVMPRKLNRLFOITAGNVIAGV 186
DB 3 LVGVACTSVFAHQIAAALLGLMLTQSAVYIGHDSGHYVIMSKSYNRFQAQLLSGNCCTGI 62
QY 187 SVAMWKLHNTNTHFACNSANLDPDIOHLPIAISPKFNSLTSYHNCMTYDRAARFV 246
DB 63 SIAMWKMTHNAHLACNSLDYDPDIOHLPFAVSTKFSLSLTSRFDRLTGPVAPFLV 122
QY 247 SFQWTFYPALLSVLYLFIISFKVVFSSNNKRYKRSQEIILGYAFLTYSSILSLRLPW 306
DB 123 SYQHTTYVAVNCFGRINLFIQTFILLFS-KREVPRALNPAFGLIVFWTWPFLVSCLPW 181
QY 307 PERVWTFYSCLAIVAGQWQFSLNHFASVNYTGLPSGNDWFHQQTGTLNTITASAMWDF 366
DB 182 PERFFVFTSFVTALQHIQFTLNHPADVYVGPPTGSDWFEKQAAGTIDISCRSYMDF 241
QY 367 HGGHLPQIEHH 377
DB 242 FGGLOFQLEHH 252

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US-08-834-033A-8
; Sequence 8, Application US/08834033A
; Patent No. 6075183
; GENERAL INFORMATION:
; APPLICANT: KUTZON, DEBORAH
; APPLICANT: MURKERT, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 PERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,033A
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-300.USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-834-033A-8

Query Match      29.7%; Score 733.5; DB 3; Length 252;
Best Local Similarity 49.4%; Pred. No. 1.7e-71;
Matches 124; Conservative 52; Mismatches 74; Indels 1; Gaps 1;

QY 127 VGVGYCKSTMAHLCSGLMGLMGLSGVGHDSCHYQVMPRKLNRLFOITAGNVIAGV 186
DB 3 LVGVACTSVFAHQIAAALLGLMLTQSAVYIGHDSGHYVIMSKSYNRFQAQLLSGNCCTGI 62
QY 187 SVAMWKLHNTNTHFACNSANLDPDIOHLPIAISPKFNSLTSYHNCMTYDRAARFV 246
DB 63 SIAMWKMTHNAHLACNSLDYDPDIOHLPFAVSTKFSLSLTSRFDRLTGPVAPFLV 122
QY 247 SFQWTFYPALLSVLYLFIISFKVVFSSNNKRYKRSQEIILGYAFLTYSSILSLRLPW 306
DB 123 SYQHTTYVAVNCFGRINLFIQTFILLFS-KREVPRALNPAFGLIVFWTWPFLVSCLPW 181
QY 307 PERVWTFYSCLAIVAGQWQFSLNHFASVNYTGLPSGNDWFHQQTGTLNTITASAMWDF 366
DB 182 PERFFVFTSFVTALQHIQFTLNHPADVYVGPPTGSDWFEKQAAGTIDISCRSYMDF 241
QY 367 HGGHLPQIEHH 377
DB 242 FGGLOFQLEHH 252

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RESULT 8

RESULT 9
US-09-363-574-7
; Sequence 7, Application US/09363574

RESULT 10
US-09-363-526-7
; Sequence 7, Application US/09363526
; Patent No. 6410288
; GENERAL INFORMATION:

RESULT 11
US-08-834-655-2
; Sequence 2, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNUITZON, DEBORAH
; APPLICANT: MUKERJI, PRADIP

APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
NUMBER OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-655-2

Query Match 22.2%; Score 549; DB 2; Length 457;
Best Local Similarity 33.3%; Pred. No. 5.1e-51;
Matches 147; Conservative 58; Mismatches 181; Indels 56; Gaps 13;
QY 26 IKGKVDISKMTKEHGGELPLISFAGODVDTAFIAHYHGTAMQYDRPFTGYVYV---D 82
DB 36 IDNKYVDAREFPDHPGGSV-ILTHVKGKGTVDFTFHEAAETLANFYVGDIDSDRD 94
QY 83 YSVSEMSKYRRLVSEFSKMGLEKTPGKGYVCSIFVSVLFALSVYV---VLVCK---S 135
DB 95 IKNDDEPAABVRKRLTFLQSLGYVDS-SKAYVA---FKVSFNLCTMGSLTVIAVAKGQTS 149
QY 136 TMAHLCGSLMGMLWQSGVGHDSCHYQVMPKRLNRLFOIIAGNVIAVGVAAWKLDH 195
DB 150 TLANTVLSAALLGLFMQCCGLADFLHGVFQDRFGMDLFGAFLGVCQGFSSSWWKDGH 209
QY 196 NTHHFAANSANLDPDIOHLPIAISPKFNSLTYYHNCMTYD-----RAARFVS 247
DB 210 NTHHAAPNVHGBDPDIDTFLP-----LTWSEHAIEMFSDVDDELTRMMSRFML 259
QY 248 FOHMTFYPALLSVRLYFLISFKVVFNSNNK-----RVYKRSQELIGYAFLTWYSLLL 300
DB 260 NQWTFEFLISFARLSWCOSILFVLPNGOAHKPGSGARVPSILVEQLSLAMHTWYLATM 319
QY 301 SRLPNRP-ERVMYFTISCLAVAG-FOHMQPSLNHPASNVYTGLP-----SGNDWFHQQT 351
DB 320 FLFIKDPVMMLVYFLVSOAVCGNLAIIVESLNH-----NGMVISKEEAVDMDPFTXOI 373
QY 352 KGTLLNTASAMMWFHGGHLEFOIEHHLFPRMKCHERKTSPIYNTKCOGHNLSYERATWM 411
DB 374 IIGRDVHFGGLFAWMTGGGLNYQLEHHLFSPMPRHNSKIQPAVELCKKYNNVYHTTGM 433
QY 412 EANKVYVSTLRAVAMEAKDVTK 433

DB 434 EGTAEVFSRLNEVSKAASRMKG 455
RESULT 12
US-08-834-033A-2
Sequence 2, Application US/08834033A
Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KUTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
NUMBER OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300. USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-2

Query Match 22.2%; Score 549; DB 3; Length 457;
Best Local Similarity 33.3%; Pred. No. 5.1e-51;
Matches 147; Conservative 58; Mismatches 181; Indels 56; Gaps 13;
QY 26 IKGKVDISKMTKEHGGELPLISFAGODVDTAFIAHYHGTAMQYDRPFTGYVYV---D 82
DB 36 IDNKYVDAREFPDHPGGSV-ILTHVKGKGTVDFTFHEAAETLANFYVGDIDSDRD 94
QY 83 YSVSEMSKYRRLVSEFSKMGLEKTPGKGYVCSIFVSVLFALSVYV---VLVCK---S 135
DB 95 IKNDDEPAABVRKRLTFLQSLGYVDS-SKAYVA---FKVSFNLCTMGSLTVIAVAKGQTS 149
QY 136 TMAHLCGSLMGMLWQSGVGHDSCHYQVMPKRLNRLFOIIAGNVIAVGVAAWKLDH 195
DB 150 TLANTVLSAALLGLFMQCCGLADFLHGVFQDRFGMDLFGAFLGVCQGFSSSWWKDGH 209
QY 196 NTHHFAANSANLDPDIOHLPIAISPKFNSLTYYHNCMTYD-----RAARFVS 247
DB 210 NTHHAAPNVHGBDPDIDTFLP-----LTWSEHAIEMFSDVDDELTRMMSRFML 259
QY 248 FOHMTFYPALLSVRLYFLISFKVVFNSNNK-----RVYKRSQELIGYAFLTWYSLLL 300
DB 260 NQWTFEFLISFARLSWCOSILFVLPNGOAHKPGSGARVPSILVEQLSLAMHTWYLATM 319

QY 301 SRLPNP-ERWYFTSCLAVAG-FQHWQSLNHFASNYTGLP-----SGNDWFHOQT 351
DB 320 FLFIKDPVNMVLYFVLSQAVCGNLIAIVFSLNH-----NGMVISKEEAVDMDFTKQ1 373
QY 352 KGTNLITASAMMDWPHGGLHFOIEHHLFPRMPKCHFRKISPIYVKLCQKKNLSYETATW 411
DB 374 ITRGDVHPLGFANWFPGGLNYQIEHHLFSPMPRHNFSKLOPAVETLCKKNVYHTTGM1 433
QY 412 EANKWYSTLRAYAMEAKDVTK 433
DB 434 EGTAEVFSRLNEVSKAASKMGK 455

RESULT 13

US-09-363-574-2
Sequence 2, Application US/09363574

GENERAL INFORMATION:

APPLICANT: KNOTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:

ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 PERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/363,574
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-574-2

Query Match 22.2%; Score 549; DB 3; Length 457;
Best Local Similarity 33.3%; Pred. No. 5,1e-51;
Matches 147; Conservative 58; Mismatches 181; Indels 56; Gaps 13;

QY 26 IAKGYVDISKWTKENHGGELPLISFAGQVTDAPFIAYHPTANQYLDREFTGYVQ--D 82
DB 36 IDNKVYDVHREPVVDHGGGV-ILTHVKGQDGVDFDFHPEAWEITLANFYVDIDSSDRD 94
QY 83 YSVSEMSKQVRRLVSEFSKMGKFKTPGKGYCSIFVSVFALSYVG--VLCK-----S 135
DB 95 IKNDPFAERKRTITFQSLGYVDS-SKAYYA---FKVSFNLCIWSLSTVIAKKGQTS 149
QY 136 TWAHCSGLTLMGLMQLQSGWVGHDSCHYQVMPNRKLNRLFOIITAGNVIAQSVAMWKLDR 195

DB 150 TLANVLASALLGLFWOCCGLAHDFLHGVFODRFWGLFGAFLGVCQGSSSWMDKH 209
QY 196 NTHFPAQNSANLDPDIOHLPIITASPKFNSLTSYHNCMTVD-----BAAPFVS 247
DB 210 NTHAAPNHNHGEPPDIDTHPL-----LWSEHALEMSVDVDEELTRWMSRFTVL 259
QY 248 FQHWTEYFALLSVRLYFLISFQVFSNNK-----RYVKSOEILGYAFLTWYSLLL 300
DB 260 NQTFWFYFLISFARLWSGLQSLIFVLPNGQAHKPSGARVPISLVEQLSLMHWTLATM 319
QY 301 SRLPNP-ERWYFTSCLAVAG-FQHWQSLNHFASNYTGLP-----SGNDWFHOQT 351
DB 320 FLFIKDPVNMVLYFVLSQAVCGNLIAIVFSLNH-----NGMVISKEEAVDMDFTKQ1 373
QY 352 KGTNLITASAMMDWPHGGLHFOIEHHLFPRMPKCHFRKISPIYVKLCQKKNLSYETATW 411
DB 374 ITRGDVHPLGFANWFPGGLNYQIEHHLFSPMPRHNFSKLOPAVETLCKKNVYHTTGM1 433
QY 412 EANKWYSTLRAYAMEAKDVTK 433
DB 434 EGTAEVFSRLNEVSKAASKMGK 455

RESULT 14

US-09-363-526-2
Sequence 2, Application US/09363526

GENERAL INFORMATION:

APPLICANT: KNOTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:

ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 PERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/363,526
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-201 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-526-2

Query Match 22.2%; Score 549; DB 4; Length 457;
Best Local Similarity 33.3%; Pred. No. 5,1e-51;
Matches 147; Conservative 58; Mismatches 181; Indels 56; Gaps 13;

[illegible]

Db 66 ASTWKNLDFEFTGYLLKDYSVSESKDYRLVFEFSKMGJYDKKGHIMFATLCFIAMFLA 125
Qy 125 LSYGYVLYCKSTWAHLCSGLMGMLWLGSGWGHDSCHYQVMPNRKLNRLFOIIAGNVIA 184
Db 126 MSYGYVLFCEGYLVHLEFSGCLMGFLWLGSGWGHDSCHYQVMPNRKLNRLFOIIAGNVIA 185
Qy 185 GVSAAWKKLDHNTTHFACNSANLDPDIOHLPILAIISPFNFNSLTSYHNCKMTYDRAARF 244
Db 186 GISIGWKKNNHNAHIAACNSLEYDPLQYIPLVSSKFFGSLTSHYERKRLFPDLSRF 245
Qy 245 FVSFOHMTFYPALLSVRLYLFIISFKVPSNNKRVKRSOEIIQYAAFLTWYSLLSRP 304
Db 246 FVSFOHMTFYPICARLNMYVOSL-IMLLTKRNVSYRAHELIGCLVFSIWPYDLVSCLP 304
Qy 305 NMPERVMTFSCLAIVAGFQHMOPSLNHPASNYVTGLPSGNDWFHQOTKTLNTITASAMD 364
Db 305 NMPERVMTFSCLAIVAGFQHMOPSLNHPASNYVTGLPSGNDWFHQOTKTLNTITASAMD 364
Qy 365 WFGGHLFOIEHLFPRMPCFKRKSIPVYNKLCOKHNLSEYATATWEANKMYSTLRAY 424
Db 365 WFGGHLFOIEHLFPRMPCFKRKSIPVYNKLCOKHNLSEYATATWEANKMYSTLRAY 424
Qy 425 AMEAKDVTKPVKPMVMEAMNTFG 448
Db 425 ALQARDITKPLPKNLWEALHTHG 448

RESULT 2
US-10-029-756-5
Sequence 5, Application US/10029756
Publication No. US20020108147A1
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/029, 756
FILING DATE: 21-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/934,254
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83832XXWVU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-029-756-5

Query Match 59.1%; Score 1459.5; DB 14; Length 448;

Best Local Similarity 55.2%; Pred. No. 4,3e-135;
Matches 245; Conservative 90; Mismatches 108; Indels 1; Gaps 1;
Qy 5 KKHISQADLAKKQPDWIMISIKGYTDSKMTKEHPGELPLPSAGQDYDAFLAHP 64
Db 6 KKYITSDBLKNDKPDWIMISIGKAYDVSQVWCKHFGSFLPKSLAGQDYDAFLAHP 65
Qy 65 GTAWQYLDLDFPGYGYQDYSVSESKDYRLVSEFSKMGJYDKKGHIMFATLCFIAMFLA 124
Db 66 ASTWKNLDFEFTGYLLKDYSVSESKDYRLVFEFSKMGJYDKKGHIMFATLCFIAMFLA 125
Qy 125 LSYGYVLYCKSTWAHLCSGLMGMLWLGSGWGHDSCHYQVMPNRKLNRLFOIIAGNVIA 184
Db 126 MSYGYVLFCEGYLVHLEFSGCLMGFLWLGSGWGHDSCHYQVMPNRKLNRLFOIIAGNVIA 185
Qy 185 GVSAAWKKLDHNTTHFACNSANLDPDIOHLPILAIISPFNFNSLTSYHNCKMTYDRAARF 244
Db 186 GISIGWKKNNHNAHIAACNSLEYDPLQYIPLVSSKFFGSLTSHYERKRLFPDLSRF 245
Qy 245 FVSFOHMTFYPALLSVRLYLFIISFKVPSNNKRVKRSOEIIQYAAFLTWYSLLSRP 304
Db 246 FVSFOHMTFYPICARLNMYVOSL-IMLLTKRNVSYRAHELIGCLVFSIWPYDLVSCLP 304
Qy 305 NMPERVMTFSCLAIVAGFQHMOPSLNHPASNYVTGLPSGNDWFHQOTKTLNTITASAMD 364
Db 305 NMPERVMTFSCLAIVAGFQHMOPSLNHPASNYVTGLPSGNDWFHQOTKTLNTITASAMD 364
Qy 365 WFGGHLFOIEHLFPRMPCFKRKSIPVYNKLCOKHNLSEYATATWEANKMYSTLRAY 424
Db 365 WFGGHLFOIEHLFPRMPCFKRKSIPVYNKLCOKHNLSEYATATWEANKMYSTLRAY 424
Qy 425 AMEAKDVTKPVKPMVMEAMNTFG 448
Db 425 ALQARDITKPLPKNLWEALHTHG 448

RESULT 3
US-10-340-779A-11
Sequence 11, Application US/10340779A
Publication No. US20030152983A1
GENERAL INFORMATION:
APPLICANT: Napier, Johnathan A.
APPLICANT: Michaelson, Louise
APPLICANT: Stobart, Keith
TITLE OF INVENTION: Desaturase
FILE REFERENCE: 005407.00004
CURRENT APPLICATION NUMBER: US/10/340,779A
CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 09/582,034
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: PCT/GB98/03895
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: UK 9814034.6
PRIOR FILING DATE: 1998-06-29
PRIOR APPLICATION NUMBER: UK 9727256.1
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FaestSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 458
TYPE: PRT
ORGANISM: Helianthus annuus
US-10-340-779A-11

Query Match 56.3%; Score 1391.5; DB 12; Length 458;
Best Local Similarity 52.7%; Pred. No. 2,2e-128;
Matches 234; Conservative 90; Mismatches 119; Indels 1; Gaps 1;
Qy 5 KKHISQADLAKKQPDWIMISIKGYTDSKMTKEHPGELPLPSAGQDYDAFLAHP 64
Db 16 KKYITSDBLKNDKPDWIMISIGKAYDVSQVWCKHFGSFLPKSLAGQDYDAFLAHP 75
Qy 65 GTAWQYLDLDFPGYGYQDYSVSESKDYRLVSEFSKMGJYDKKGHIMFATLCFIAMFLA 124

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DB 76 GTAMHLDLFTGYHLDKQVDSIDRDYKLAISEFAKAGMFKKHGVYSLCFYSLLS 135
QY 125 LSVGYLVYCKSTWMAHLCGLMGMMLQSGWGHDSCHYQVMPNKLNLFOIAGNYA 184
DB 136 ACVYGLVSGSFWIMHLSGAILGLAMMOQYAYLGHADGHYQMMATRGWNAFAGIPIGNCIT 195
QY 185 GSVAMWKLNDHTTHFACNSANLDDPDLOHLPPIAISPKFNSLTSTYHNCCKMTYRAARF 244
DB 196 GSIAMWKTTHAHNHACNSLDYDPDLOHLPMLAVSSKLFNSITTSYFYGRQUTPDLARF 255
QY 245 FVSFOHMTFYPALLSVRLYLFLISFKVVSNNKRVYKSOEILGYAFLTWYSLLSRLP 304
DB 256 FVSQHYLYLPIIMCVARVNLVLIQTILLISKRR-IPDRGLNLTGLIFMTWPLVSRLP 314
QY 305 NMPERVMYPTSCIAVAGFQHWQFSLNHPASNYTGLPSGNDWPHOOTKGTTLNITASAMD 364
DB 315 NMPERVAFLVSECVTGIOHIOFTLNHFGSDYVGPCKDNWFEKOTGTIDIDACSSMD 374
QY 365 WFGHGLHFOIEHNLFPRLMPKCHFRKISPIVNLCKOHNLSYATATWNAKNVYSLRAV 424
DB 375 WFFGGIOFQLEHNLFPRLPRCHLRISPICRELCKKNLPYVLSFYDANVTTLKTLIRA 434
QY 425 AMEAKDVTKRPVKMVMWEAMNTFG 448
DB 435 ALQARDLTNPAPONLAMEAFNTHG 458

```

RESULT 4

US-10-029-756-27
Sequence 27, Application US/10029756
Publication No. US20020108147A1

GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
DELTA 6-DESATURASE

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/029,756
FILING DATE: 21-Dec-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/934,254
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83832YXWVU

TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SAMS UR

INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-029-756-27

Query Match 53.2%; Score 1314.5; DB 14; Length 452;
Best Local Similarity 51.8%; Pred. No. 8,66-121;
Matches 233; Conservative 86; Mismatches 126; Indels 5; Gaps 5;

```

QY 3 EPKHSIQADLAKHQPDDLMISTKGYDDISKMTKEHPGGLPLISFAGDVTDAFLAY 62
DB 4 EAKYITMEDLRNHNKSDMLISIQKAYDCSRMAEHPGGEVPLISLAGDVTDAFLAY 63
QY 63 HPGTAMOXLDLPEFTG-YVVDYVSSEMSKDYRRLVSEFSKMGLEFPTPKGVYCSIFPVS 121
DB 64 HPGTAMHLDLFTGYIYKDFEVEISKDYRRLNENSRGIFPKKHHLIMTGVAV 123
QY 122 LPLSVGYLVYCKSTWMAHLCGLMGMMLQSGWGHDSCHYQVMPNKLNLFOIAGN 181
DB 124 MDAIVGYGLVASESGVAMLCGALLGLMIOQAAYVGHDSGHYQVMPNKTITOLIGN 183
QY 182 VIAGSVAMWKLNDHTTHFACNSANLDDPDLOHLPPIAISPKFNSLTSTYHNCCKMTYRA 241
DB 184 ILTGISIAMWKTTHAHNHACNSLDYDPDLOHLPFAVSTRLENSITTSYFYGRVULKFEV 243
QY 242 AREFVSFOHMTFYPALLSVRLYLFLISFKVVSNNKRVYKSOEILGYAFLTWYSLLS 301
DB 244 AREFVSYQHWIYYPVMTIGRVNLFIQTILLIT-RDVPDRALNMGIAVFTWPLVFS 302
QY 302 RLNMPERVMYPTSCIAVAGFQHWQFSLNHPASNYTGLPSGNDWPHOOTKGTTLNITAS 361
DB 303 CLPNMPERGFVLISFAVTAIOHVOFTLNHFGSDTYVGPCKDNWFEKOTGTIDITCP 362
QY 362 WWDWFGHGLHFOIEHNLFPRLMPKCHFRKISPIVNLCKOHNLSYATATWNAKNVYSL 420
DB 363 WWDWFFGGIOFQLEHNLFPRLPRCHLRISPICRELCKKNLPYVLSFYDANVTTLKTL 422
QY 421 LRAVAMEAKDV-TKRPVKMVM-EMAMNTFG 448
DB 423 LRDAAVQARDLNSACPKLGYGEAYNTHG 452

```

RESULT 5

US-09-967-477B-8
Sequence 8, Application US/09967477B
Patent No. US20020156254A1

GENERAL INFORMATION:
APPLICANT: Xiao Qiu
TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL
TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: BNZ-001
CURRENT APPLICATION NUMBER: US/09/967,477B
CURRENT FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: 60/236,303
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/297,562
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 459
TYPE: PRT
ORGANISM: Thraustochytrium sp.

Query Match 22.7%; Score 560.5; DB 10; Length 459;
Best Local Similarity 31.0%; Pred. No. 1,8e-46;
Matches 149; Conservative 70; Mismatches 182; Indels 79; Gaps 17;

```

QY 5 KHAISQADLAKHQPDDLMISTKGYDDISKMTKEHPGGLPLISFAGDVTDAFLAY 64
DB 9 KRLVSWKEIRREHATPATAMIVIHKKYDISKW-DSHPGSAV-MLTQAGEDATAPAVFHP 66
QY 65 GTAMOXLDLPEFTGYVVDYVSSEMSK-----DYRLVSEFS 100
DB 67 SSALKLLEQTVG-----DVTETSAKLEIGEPASDEERARRRINEFLASVRLAVKVK 120

```

QY 101 KAGLEKTEGKGVCSIFPVSVLFAISVYGLVC---KSTWALCSGLMGLMQLQSGWVG 157
 Db 121 GAGLY--DASALYYAMKLVST--FGIAVLASMAICFFRNSFAMYMAGVLMGLFIOQSGMLA 177
 QY 158 HDSCHYQVMPKRLNRLFOIIAGNVIAVSVAMWKLDNTHHFAANSANTL-----DPD 210
 Db 178 HDPLHNOVCENRTLGNLIGCLVGNAMQGSVQVMWKNKLNHLHVAVNLHSADEGFIQDPD 237
 QY 211 IQHPIAISPKFNSLTSYHNCKMTYDRAARFFVSQGHHTFFPALLSVLYIFILSEK 270
 Db 238 IDTWPLMWSKEMARKAPESAH-----GPFIRNOAFLYPLLLNLMLSLWLAOSFF 288
 QY 271 VVFSNNK-----RYKKSQELIYAALFTWYSLLSRLPNWP--ERYVVF-----TSC--- 316
 Db 289 YVFTFESFGIDKVEFPGPEKAGLIYHIV--QLAIPIFCNMSLFEQVAYFLMGQASGCL 347
 QY 317 LAVAGFQHWQPSLNHFASNVYTGILPSGNDWFHQOTKTLNTASAMWDFHGLHFOIEH 376
 Db 348 LALV-----FSIGHNGMSVYE--RETKPDEFWOLQVTTNRIRASVFMDFGGLNYQIDH 400
 QY 377 HLFPRMKCHPRKISPIVNLCOCKNLSYEPATWMEANKWYSLRAVAMEAKDVTCPVP 436
 Db 401 HLPFLVPRHNLPRKVNLIKSLCKEPDIPHEGTGWEQ--IYEVVDHLADISKEFTTEFP 457

RESULT 6
 US-10-278-391-4
 ; Sequence 4, Application US/10278391
 ; Publication No. US20030159164A1

GENERAL INFORMATION:

APPLICANT: KOPCHIK, JOHN J.

KEIDER, BRUCE

HUANG, YUNG-SHENG

KIRCHNER, STEPHEN J.

MUKERJI, PRADIP

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM

PRODUCTS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/278,391

FILING DATE: 23-Oct-2002

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/087,578

FILING DATE: 29-MAY-1998

ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETER G.

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: OHU-03348

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 457 amino acids

TYPE: amino acid

STRANDEDNESS: No. US20030159164A1 Relevant

TOPOLOGY: No. US20030159164A1 Relevant

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-278-391-4

Query Match

Best Local Similarity 22.2%; Score 549; DB 12; Length 457;

Matches 147; Conservative 58; Mismatches 181; Indels 56; Gaps 13;

QY 26 IKKRVYDISKWTENHGGELPLSPFGQDVTDAFIATVPGTAQYIDRFPTGYVQ---D 82

Db 36 IDKKVYDVREVFVDHFGSV-ILTHVGKQGTVDFTFHEPAWETLANFYVGDIDSDRD 94

QY 83 YSVSEMSKDYRRRLVSEFSKMGLEFKTPGKGVCSIFPVSVLFAISVYGLVC---VLCCK-----S 135

Db 95 IKKDDPAEVRKRLRTLPQSLGYDS--SKAYYA---FKYSFNLCINGSLVIAKMGQTS 149

QY 136 TWAHCSGLMGLMQLQSGWVGDSCHYOVMENKRLNRLFOIIAGNVIAVSVAMWKLDPH 195

Db 150 TLANVLSAALIGLFWQCGWLADFLHQVQDRFGDGLFGAFLGVCQGFSSMKDKH 209

QY 196 NTHHFAANSANTDPDIQHLPIAISPKFNSLTSYHNCKMTYD-----RAAFVVS 247

Db 210 NTHHAAPNVHGEDPDIDTHPL-----LTWSEHALEMSDVDEBLTRWMSRFVVL 259

QY 248 FQHWTFYPALLSVRLYLFILSEKVFSSNNK-----RYKKSQELIYAALFTWYSLLL 300

Db 260 NQTMWYFFPLISFARLSWCQSLIFVLPNQAHKPSGARPIGLVEQLSLAMHTVYLAHM 319

QY 301 SRLPNWP--ERYVFTFSCLAVAG--FQHWQPSLNHFASNVYTGILP-----SGNDWFHQOT 351

Db 320 FLFIKDPVNMVLYFLVSAVCGNLAIVFSLNH-----NGMPVISKEBADVMDFFTKOI 373

QY 352 KGLNTASAMWDFHGLHFOIEHHLFPRMKCHPRKISPIVNLCOCKNLSYEPATWME 411

Db 374 ITRGDVHPLFANWFLGGLNYQIDHHLFSPMRHNSKIQPAVETLCKKYNVRYHTTGM 433

QY 412 EANKWYSLTRAVAMEAKDVTK 433

Db 434 EGTAEVFSRLNEVSXAASKMGK 455

RESULT 7

US-10-191-513A-11

; Sequence 11, Application US/10191513A

; Publication No. US20030104596A1

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Mukerji, Pradip

APPLICANT: Leonard, Amanda E.

APPLICANT: Huang, Yung-Sheng

APPLICANT: Tapas, Das

TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF

FILE REFERENCE: 6295.US.D3

CURRENT APPLICATION NUMBER: US/10/191,513A

PRIOR FILING DATE: 2002-09-25

PRIOR APPLICATION NUMBER: US 09/227,613

PRIOR FILING DATE: 1999-01-08

PRIOR APPLICATION NUMBER: PCT/US98/07422

PRIOR FILING DATE: 1998-04-10

PRIOR APPLICATION NUMBER: US 08/833,610

NUMBER OF SEQ ID NOS: 54

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11

LENGTH: 458

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: VARIANT

LOCATION: (458)...

OTHER INFORMATION: Xaa = Unknown or other at position 458

US-10-191-513A-11

Query Match

Best Local Similarity 22.2%; Score 549; DB 15; Length 458;

Matches 147; Conservative 58; Mismatches 181; Indels 56; Gaps 13;

QY 26 IKKRVYDISKWTENHGGELPLSPFGQDVTDAFIATVPGTAQYIDRFPTGYVQ---D 82

Matches 147; Conservative 58; Mismatches 181; Indels 56; Gaps 13;

Qy 26 IKGKVVYDREKHEGELPLISFAGQVDTDAFIAYHPTAMQVYDRFETGYVVO---D 82
 Db 36 IINRKYDVAEFPVDPHGGSV-ILTHVGKGTVDFTFHEAAWETLANFYVGDIDESDD 94

Qy 83 YSVSEMSKDYRLVSEFSGMLFKTPGKGVCSIFVSVLPALSVYG---VLXCK---S 135
 Db 95 IKNDPFAAEVRKRLTFLQSLGYDS-SKAYYA---FKVSFNLCTIGSLSTVIVAKMGOTS 149

Qy 136 TWAHCSGLMGMLVQSGWVGHDSCHYOVMBRKLNLRFQIIAGNVLAGSVANMKLDH 195
 Db 150 TLAVNLASALLGLFMQCCGMLAHDFLHQVFDREMGDLFGAFLGVCVCGFSSSWMKDXH 209

Qy 196 NTHHFAACNSANDPDIQHLPIAISPFPNSLTSYHNCKMTYD-----RAARFVS 247
 Db 210 NTHHAAPVNHGSDPDIDTHPL-----LTWSEHLEMFSDVDEBELTMMWSFVVL 259

Qy 248 FOHMTFFPALLSVRILYFLISFKVFSNNK-----RYKKRSOELLGYAAFLTWYSLLL 300
 Db 260 NQWTFYFPLISFARLSWCQSLIFVLPRGQAHKPSGARVPISLVQSLAMHMTWYLATM 319

Qy 301 SRLPMP-ERVVYFISCLAVAG-FOHWPFSLNHFASNVYGLP-----SGNDMFHOOT 351
 Db 320 FLFIKDPVNMVLYFLVQAVCGNLALVPSLNH-----NGMPVSKERAVMDPFTKOI 373

Qy 352 KGTNLITASAMWDFHGLHFOIEHLLFPRMPKCHFRKISPIVNLCOCHNLSEYATM 411
 Db 374 ITGRDVHGLFANWFTGGLNYQIEHLLFSPMPRHNSKIQPAVELTCKKYNVRYHTTGM 433

Qy 412 EANKVYSTLRVAMEAKDVTK 433
 Db 434 EGTAEVFSRLNEVSKAASKMGK 455

RESULT 8
 US-10-191-513A-41
 ; Sequence 41, Application US/10191513A
 ; Publication No. US20030104596A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pradiip
 ; APPLICANT: Leonard, Amanda E.
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Tapas, Das
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
 ; FILE REFERENCE: 6295.US.D3
 ; CURRENT APPLICATION NUMBER: US/10/191,513A
 ; PRIOR FILING DATE: 2002-09-25
 ; PRIOR APPLICATION NUMBER: US 09/227,613
 ; PRIOR FILING DATE: 1999-01-08
 ; PRIOR APPLICATION NUMBER: PCT/US98/07422
 ; PRIOR FILING DATE: 1998-04-10
 ; PRIOR APPLICATION NUMBER: US 08/833,610
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 41
 ; LENGTH: 458
 ; TYPE: PRN
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (458)...(458)
 ; OTHER INFORMATION: Xaa = Unknown or other at position 458
 US-10-191-513A-41

Query Match 22.2%; Score 549; DB 15; Length 458;
 Best Local Similarity 33.3%; Pred. No. 2.4e-45;
 Matches 147; Conservative 58; Mismatches 181; Indels 56; Gaps 13;

Qy 26 IKGKVVYDREKHEGELPLISFAGQVDTDAFIAYHPTAMQVYDRFETGYVVO---D 82
 Db 36 IINRKYDVAEFPVDPHGGSV-ILTHVGKGTVDFTFHEAAWETLANFYVGDIDESDD 94

Db 36 IINRKYDVAEFPVDPHGGSV-ILTHVGKGTVDFTFHEAAWETLANFYVGDIDESDD 94
 Qy 83 YSVSEMSKDYRLVSEFSGMLFKTPGKGVCSIFVSVLPALSVYG---VLXCK---S 135
 Db 95 IKNDPFAAEVRKRLTFLQSLGYDS-SKAYYA---FKVSFNLCTIGSLSTVIVAKMGOTS 149

Qy 136 TWAHCSGLMGMLVQSGWVGHDSCHYOVMBRKLNLRFQIIAGNVLAGSVANMKLDH 195
 Db 150 TLAVNLASALLGLFMQCCGMLAHDFLHQVFDREMGDLFGAFLGVCVCGFSSSWMKDXH 209

Qy 196 NTHHFAACNSANDPDIQHLPIAISPFPNSLTSYHNCKMTYD-----RAARFVS 247
 Db 210 NTHHAAPVNHGSDPDIDTHPL-----LTWSEHLEMFSDVDEBELTMMWSFVVL 259

Qy 248 FOHMTFFPALLSVRILYFLISFKVFSNNK-----RYKKRSOELLGYAAFLTWYSLLL 300
 Db 260 NQWTFYFPLISFARLSWCQSLIFVLPRGQAHKPSGARVPISLVQSLAMHMTWYLATM 319

Qy 301 SRLPMP-ERVVYFISCLAVAG-FOHWPFSLNHFASNVYGLP-----SGNDMFHOOT 351
 Db 320 FLFIKDPVNMVLYFLVQAVCGNLALVPSLNH-----NGMPVSKERAVMDPFTKOI 373

Qy 352 KGTNLITASAMWDFHGLHFOIEHLLFPRMPKCHFRKISPIVNLCOCHNLSEYATM 411
 Db 374 ITGRDVHGLFANWFTGGLNYQIEHLLFSPMPRHNSKIQPAVELTCKKYNVRYHTTGM 433

Qy 412 EANKVYSTLRVAMEAKDVTK 433
 Db 434 EGTAEVFSRLNEVSKAASKMGK 455

RESULT 9
 US-09-769-863-14
 ; Sequence 14, Application US/09769863
 ; Publication No. US20030157144A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pradiip
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Das, Tapas
 ; APPLICANT: Thurmond, Jennifer
 ; APPLICANT: Pereira, Suzette L.
 ; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
 ; FILE REFERENCE: 6763.US.01
 ; CURRENT APPLICATION NUMBER: US/09/769,863
 ; CURRENT FILING DATE: 2001-01-25
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 453
 ; TYPE: PRN
 ; ORGANISM: Saprolegnia diclina
 US-09-769-863-14

Query Match 21.0%; Score 519; DB 12; Length 453;
 Best Local Similarity 30.2%; Pred. No. 2.1e-42;
 Matches 132; Conservative 78; Mismatches 165; Indels 62; Gaps 13;

Qy 8 ISQADLAKHKGPGDLMISIKGVYDISKWKHEGELPLISFAGQVDTDAFIAYHPTA 67
 Db 10 ISMATIREHNRQDNAMVIYHNKVVYDISAF-EDHPGQ-VVMFTQAGBDATDAFAVHPSSA 67

Qy 68 WQYLDREFTGYVQ-----DYSVSEMSK-----DYRLVSEFSGMLFKTPGKGVY- 113
 Db 68 LKLEQYVGVGDVOSTAVIDTISDEVKKSQSDFIASRYKRLVEYKRLGLYDS-SKLYLL 126

Qy 114 --CSIFPSVLPALSVYGVLVCKSTWMAHCSGLMGMLVQSGWVGHDSCHYOVMBRKL 171
 Db 127 YKCASTLIALVSAAI--CLHFDSTAMTWVAIVILGLFQCCGMLAHDFLHQVENVHLF 184

Qy 172 NRLFQIIAGNVLAGSVANMKLDHNTTHFACN-----SANLDPDIQHLPIAISPFP 224
 Db 185 GDLVGVMGNLQGSVQVMWKNKINTHTHALPRLNATPRELAFHGDIDIDTMTPLANSLKVA 244

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QY 225 NSLTSYHNCKMTYDBAARFVFSQHTFYFALLSVRLYLFLSPKVFESN--NKRUYK 281
DB 245 QHAYD-----SPVGLFPMRYQAVLYFPIILFPAISVWIOSAMAFINVBPGGFEDK 295
QY 282 RSOEILGYAFLTWYSLLSLRSLPMPERVMY-----FTSCLAVAGPQHMOPS 328
DB 296 VOYPLERAGLLLY-----GMNLGLVYAANMSLLQAALFVFSQASCGFLAMVFS 347
QY 329 LNHFAVNYTGLPSGNDWFHQOTKGTINTITASAMWDMFHGHLFQIENHLFPRMPKCHFR 388
DB 348 VGNHMEVF-DKDSKDPFWKQVLTSTNVTSLSLMDWFMGGLNYQIDHHLFPMVPRHNL 406
QY 389 KISPIVVKLCQKHNLSY 405
DB 407 ALNVLVKSJCKOYDIPY 423

RESULT 10
US-10-054-534B-14
; Sequence 14, Application US/10054534B
; Publication No. US20030167525A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer M.
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763-US-P1
; CURRENT APPLICATION NUMBER: US/10/054,534B
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 09/769,863
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FaestSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: PRF
; ORGANISM: Saprolegnia diclina
US-10-054-534B-14

Query Match 21.0%; Score 519; DB 12; Length 453;
Best Local Similarity 30.2%; Pred. No. 2,1e-42;
Matches 132; Conservative 78; Mismatches 165; Indels 62; Gaps 13;

QY 8 ISQADIAKHQOPDMLWISIKGVYDISKWTKEHPGGLPLSPAGODVTDAFTAYHPGTA 67
DB 10 ISWATIREHNRQONAMIVIHKKYVDISAF-EDHPGG-VVMFTQAGEDATDAFAVHPHSSA 67
QY 68 WQYLDKFFFTGYVQ-----DYVSEMSK-----DYRLVSEFSKMLFKTPGKGVY- 113
DB 68 LKLEQYVGDVDQSTAAVDTISIDEVKSQSDFIASRYKRLLEVRLGLYDS-SKLYYL 126
QY 114 --CSIFVSVLFAISYGVLYCKSTWHLCSGLMGLMLOSQGVGHDSCHYQVMPNRKL 171
DB 127 YKCASTLSTALVSAI--CLHFDSTAMVVAAYIIGLFYQCGMLANDLPHQVFNHLF 184
QY 172 NRLFQIIAGNVIAGVSAVMKLDHNTHPACN-----SANDDPDIQHLPIIASPKFF 224
DB 185 GDLGVVGNVNLMOGFSVQWKKKKNHTHAIPLNHAETPEIAFHDGPDIDTMTPLAMSLKMA 244
QY 225 NSLTSYHNCKMTYDBAARFVFSQHTFYFALLSVRLYLFLSPKVFESN--NKRUYK 281
DB 245 QHAYD-----SPVGLFPMRYQAVLYFPIILFPAISVWIOSAMAFINVBPGGFEDK 295
QY 282 RSOEILGYAFLTWYSLLSLRSLPMPERVMY-----FTSCLAVAGPQHMOPS 328
DB 296 VOYPLERAGLLLY-----GMNLGLVYAANMSLLQAALFVFSQASCGFLAMVFS 347
QY 329 LNHFAVNYTGLPSGNDWFHQOTKGTINTITASAMWDMFHGHLFQIENHLFPRMPKCHFR 388

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DB 348 VGNHMEVF-DKDSKDPFWKQVLTSTNVTSLSLMDWFMGGLNYQIDHHLFPMVPRHNL 406
QY 389 KISPIVVKLCQKHNLSY 405
DB 407 ALNVLVKSJCKOYDIPY 423

RESULT 11
US-10-431-952-14
; Sequence 14, Application US/10431952
; Publication No. US20030190733A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763-US-O1
; CURRENT APPLICATION NUMBER: US/10/431,952
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US/09/769,863
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FaestSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: PRF
; ORGANISM: Saprolegnia diclina
US-10-431-952-14

Query Match 21.0%; Score 519; DB 12; Length 453;
Best Local Similarity 30.2%; Pred. No. 2,1e-42;
Matches 132; Conservative 78; Mismatches 165; Indels 62; Gaps 13;

QY 8 ISQADIAKHQOPDMLWISIKGVYDISKWTKEHPGGLPLSPAGODVTDAFTAYHPGTA 67
DB 10 ISWATIREHNRQONAMIVIHKKYVDISAF-EDHPGG-VVMFTQAGEDATDAFAVHPHSSA 67
QY 68 WQYLDKFFFTGYVQ-----DYVSEMSK-----DYRLVSEFSKMLFKTPGKGVY- 113
DB 68 LKLEQYVGDVDQSTAAVDTISIDEVKSQSDFIASRYKRLLEVRLGLYDS-SKLYYL 126
QY 114 --CSIFVSVLFAISYGVLYCKSTWHLCSGLMGLMLOSQGVGHDSCHYQVMPNRKL 171
DB 127 YKCASTLSTALVSAI--CLHFDSTAMVVAAYIIGLFYQCGMLANDLPHQVFNHLF 184
QY 172 NRLFQIIAGNVIAGVSAVMKLDHNTHPACN-----SANDDPDIQHLPIIASPKFF 224
DB 185 GDLGVVGNVNLMOGFSVQWKKKKNHTHAIPLNHAETPEIAFHDGPDIDTMTPLAMSLKMA 244
QY 225 NSLTSYHNCKMTYDBAARFVFSQHTFYFALLSVRLYLFLSPKVFESN--NKRUYK 281
DB 245 QHAYD-----SPVGLFPMRYQAVLYFPIILFPAISVWIOSAMAFINVBPGGFEDK 295
QY 282 RSOEILGYAFLTWYSLLSLRSLPMPERVMY-----FTSCLAVAGPQHMOPS 328
DB 296 VOYPLERAGLLLY-----GMNLGLVYAANMSLLQAALFVFSQASCGFLAMVFS 347
QY 329 LNHFAVNYTGLPSGNDWFHQOTKGTINTITASAMWDMFHGHLFQIENHLFPRMPKCHFR 388
DB 348 VGNHMEVF-DKDSKDPFWKQVLTSTNVTSLSLMDWFMGGLNYQIDHHLFPMVPRHNL 406
QY 389 KISPIVVKLCQKHNLSY 405
DB 407 ALNVLVKSJCKOYDIPY 423

RESULT 12
US-10-369-493-4137
; Sequence 4137, Application US/10369493
; Publication No. US2003023675A1

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; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052) B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4137
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-369-493-4137

Query Match      19.3%; Score 477; DB 12; Length 366;
Best Local Similarity 31.6%; Pred. No. 2,2e-38;
Matches 113; Conservative 63; Mismatches 156; Indels 26; Gaps 9;

QY 90 KDRRLVSEFSKMGLEFKTPGKGVYCSIFVSVLPALSVGLYC-----KSTMAHLCG 143
DB 5 RYKREINERIKAEGLVD-----CN--YVAVAIEGFRITLFCGLLPLKMG- YVPSA 54

QY 144 LMGMLWLGSGVGHDSCHYQVMPNKRNLRFQIAGNVIAGVAVAMKLDHNTTHFACN 203
DB 55 FCLGSFMHQLVFPYADAGHMGITHHFHVDTVIGIILADFIGLSLGMWKNHNVHIIIN 114

QY 204 SANLDDIQLHPIAISPKRFNSLTSYHNCKTTPRAARFVSFOHMTFYPALLSVRLY 263
DB 115 SPEDHDIHLPLFPALSHREFTLRSTYYDRVMEYDIFAKFVSLQHYLYIIMFARLN 174

QY 264 LFLISEKVF-----SNKRKYKRSOEILGYAFLTW--YSLLSRLP--NMPEPVYFTS 315
DB 175 LRLSWBYLLKGAPRGHGRMMHRLHLEVOQVFWCMFGYIMYKALDGNM--NRPFPMI 233

QY 316 CLAVAGFOHWFQSLNFPASNVTYGLPSGNDWFHOQTKGLINTITASAMWDFHGLHFOIE 375
DB 234 SHAVTSPRLHVQITLSHFAMST--SDLGPHSEFPQRMRLRTTMDVDCPMLDPFHGLQFOAI 292

QY 376 HHLFPMPCHPKIKIPYVVKLCQKKNLSYETATMEANKMNVSTLRVAAMEKDYTK 433
DB 293 HHLYPRIPRHNLKTKLVQDFCNDVGIPYALYGVFEGKGVIGRLADVARQALIRK 350

RESULT 13
US-10-340-779A-20
; Sequence 20, Application US/10340779A
; Publication No. US20030152983A1
; GENERAL INFORMATION:
; APPLICANT: Napier, Jonathan A.
; APPLICANT: Michelson, Louise
; APPLICANT: Stobart, Keith
; TITLE OF INVENTION: Desaturase
; FILE REFERENCE: 005407, 00004
; CURRENT APPLICATION NUMBER: US/10/340,779A
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/582,034
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/GB98/03895
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: UK 9814034.6
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: UK 9727256.1
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 443

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; TYPE: PRT
; ORGANISM: C. elegans
US-10-340-779A-20

Query Match      18.7%; Score 461; DB 12; Length 443;
Best Local Similarity 29.5%; Pred. No. 1.1e-36;
Matches 116; Conservative 65; Mismatches 188; Indels 72; Gaps 17;

QY 17 KQPGDLMSIKRK--VYDISKTKRHPGSELPLSPAGOVDTAFAYHGTAMQY----- 70
DB 5 KNASGLRMKVDGKMWLYLSEELVKHPGGAV--IEQYNSDATHI FFAFHGSSOATKQDL 63

QY 71 -----LDREFTGYVYDVSSEMSKDRRLVSEFSK-----GLF 105
DB 64 LKKGHDEFLKQLEKRLDKVDIVNSAVDVAQEK-----MVSEFELRQKLHDDGLM 119

QY 106 KTPGKGVYCSIFVSVLPALSVYG--VLCKSTMAHLCGMLMGMLWLGSGVGHDSCHYQ 164
DB 120 KANE-----TYFLFPAISTLSIMAFAYLYQVIGWYTSACLALAMQCGMLTHFCHQO 174

QY 165 VMPNKRNLRFQIAGNVIAGVAVAMKLDHNTTHFACNSANLDPDIOHLPPIAISPKRF 224
DB 175 PKNRPLNDTISLFGNPLQGSRDWWKDKHNTTHAATNVIDHGDIDLAFLFAPF--- 231

QY 225 NSLTSYHNCKMTYDRAARFVSFOHMTFYPALLSVRLYFLISFKVFSNNKRVYKRSQ 284
DB 232 GDLCKY-----KSPFKALIKYPIYQHLVFTALPMLRFSWTOGSQVQWVKEKMEKYQ 287

QY 285 E-----ILGYAFLTWYSLLSRLPMPERVMYFTSCLAVAG--FOHWFQSLNHPAS 334
DB 288 RAUFMEQATIVGHMAMV--FYQLFL--LPTWPRVAFAFIIISGGGLLIH--VTFPHNSV 343

QY 335 NYITGLPSC---NDMFHOQTGLINTITASAMWDFHGLHFOIEHLFPRPKCFPKI 390
DB 344 DRY---PANSRIILNFPALQILITRMTSPSPIDMLGGLNYQIEHILFPTMPCNLNAC 400

QY 391 SPIVNLCKQKHLSEYETATMEANKMNVSTLRVA--MEAK 429
DB 401 VYVVKEMCKENLPLVLDYDFDGYAMNLQOLKMAEHIOAK 441

RESULT 14
US-10-262-617-3
; Sequence 3, Application US/10262617
; Publication No. US20030077747A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guejter, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS
; FILE REFERENCE: PF-0494-1 DIV
; CURRENT APPLICATION NUMBER: US/10/262,617
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: 09/048,888
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc. feature
; OTHER INFORMATION: Incyte ID No. US20030077747A1 2056310CD1
US-10-262-617-3

Query Match      18.3%; Score 451.5; DB 15; Length 444;
Best Local Similarity 27.0%; Pred. No. 9.4e-36;
Matches 121; Conservative 69; Mismatches 193; Indels 65; Gaps 12;

QY 6 KHISQADLAKHKQPGDLMSIKGYVDISKTKRHPGSELPLSPAGOVDTAFAYH-- 63

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Db      18 RYFTWDEVAQSGCEERMLVIDRKVNISETTRRHPEGSRVISHYAGQDATDEPVAFHIN 77
Qy      64 PGTAWOYLDRFFFTGY-----VQDYSVSEMSKDYRLVSEBKMGLFETPKGVCSIF 117
Db      78 KGLVKKTKMSLLIGELSPQPSPEPTKNKELTDFEFLRATVERKGLMK--ANHVFELLY 135
Qy      118 FVSVL-----PALSYGVLYCKSTWHLCSGLLMKMLVQSGWVGHDSCYQVMPNRK 170
Db      136 LHLIILLDGAAMLTWVFGT-----SFLPFLCAVLISAQAQGMLOHDGHSVSTSK 191
Qy      171 LNFLFOIAGNVAGSVAMWKLDPHTNTHFACNSANIDPDIQHLPIAISPKEFNSITSY 230
Db      192 WNLHLHFVIGIKGAPASWMMNHMFQHNKPCFRKDPDINMHPESFALGKILSVELGK 251
Qy      231 YHCKMTYDAARFFVSFOHMTFY----PALLSTRVLYFLTSPKVVSENNK----- 277
Db      252 QKKKRYPRYN-----QKRYFFLIGRPALLRPYFQWYFYF--VQKKWVDLMMIT 301
Qy      278 ---RVYKRSQELIGYAFLTWYSLLSRLPNWERVWYFTSCLAVAGFOHMOFSLNHFAS 334
Db      302 FYVRFFLTYPVPLGLAKFLLFLFIVRLBSNW-----FV-----WVQMMHIMP 345
Qy      335 NVTTGLPSGNDMFHQOTKGLNTITASAMDWFHGHLFOIEHILFPRMPKCHFRKXSPIV 394
Db      346 HI--DHDNRMDWYSTOLQATCNVHKSAFNDWFSGLHNFQIEHILFPTMPRHNYHKVAPLV 403
Qy      395 NKLCKOKHNLSEYATATWMEANKWYSTLR 422
Db      404 QSLCAKHGLEYQSKPLSLAFADIIHSLK 431

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RESULT 15

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US-10-369-493-6108
; Sequence 6108, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIORITY FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 473
; SEQ ID NO 6108
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6108

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Query Match      18.2%; Score 449; DB 12; Length 473;
Best Local Similarity 28.2%; Pred. No. 1.6e-35;
Matches 138; Conservative 65; Mismatches 187; Indels 100; Gaps 18;

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Qy      17 KQPGDLWISIKG-VYDISKTKHEHPEG-----ELPLLS----- 49
Db      5 KNSAGLRMKVDGKMLYSEELVKKHPCGAVIEQYSIPLNKIETRGIIITRGSNNLMDI 64
Qy      50 ---FAGQDVTDAFLAHPTGAMQY-----LDRFFGTGYVQDY 83
Db      65 LVEFYRNSDATHIFHAFHEGSSQAYKQDLCLKHGEHDEPLEKOLEKRLDKVDINVSAYDV 124
Qy      84 SVSEMSKDYRLVSEBKM-----GLFETPKGVCSIFVSVLFAISVG--VLCKS 135
Db      125 SVAQEEK--WVSEFEKLRQKLDHGDGLMKANE---TYFLPKAISTLSIMAFAYLY 175
Qy      136 TWAHLCSGLLMKMLVQSGWVGHDSCYQVMPNRKLNRLFOIAGNVAGSVAMWKLDPH 195

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Db      176 LGWYITSACLLALAWOQFGMLTHEFCHQOPTKNRPLNDTISLFGNLFQFSRDMWKDK 235
Qy      196 NTHHFAONSANIDPDIQHLPIAISPKEFNSLTSYYHNCMTYDRAARFFVSFOHMTFY 255
Db      236 NTHHAATNVIDHDGDDIDLAPLFAFIP--GDLCY---KASFEKAILKIVPQHLFT 288
Qy      256 ALLSVRLYFLISFKVVFSSNNKRVKRSQ-----ILGYAFLTWYSLLSRLPNMP 307
Db      289 MLPMLRFSMTGQSVQVVFKNQMEYKVYQRNAPWEGATVGHAWV-FYQLFL--LPTWP 345
Qy      308 ERYMTTSCLAVAG--FOHMOFSLNFPASNVTTGLPSG---NDWFHQOTKGLNTITASA 361
Db      346 LRAVAYFLISQMGGLLIAH-VTFNHNSTVDKY---PANSRIINNFALQILTTNNTPSP 401
Qy      362 WMDWFHGLHFOIEHILFPRMPKCHFRKXSPIYVKLCKOKHNLSEYATATWMEANKWYSTL 421
Db      402 FIDWLMGLNYQIEHILFPTMPRCNLNACMKYKXWCKENNLPLYLVDDYFDGYAMNLQOL 461
Qy      422 RAVA--MEAK 429
Db      462 KNNAAEHIOAK 471

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Search completed: January 1, 2004, 06:58:34
Job time: 86.3457 secs

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QY 1642 CATGCTTCAATAGTCTGTGTAC-----GGAGTGTCTGTCTCCCTATCAAGGT 1694
DB 1700 CAGCTTCACTTGTACTTGTACACCATTTAGATTGTGGGTTCTCTTATCATGGT 1759
QY 1695 AACTATATGA 1704
DB 1760 AACTACATCA 1769

RESULT 2
AP005554 96312 bp DNA linear HTG 24-JUL-2002
LOCUS Oryza sativa (japonica cultivar-group) chromosome 9 clone
DEFINITION OJ118 A10, *** SEQUENCING IN PROGRESS ***.
ACCESSION AP005554.1 GI:21952922
VERSION HTG; HTGS PHASE2.
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
Eriaraloideae; Oryzaceae; Oryza.
REFERENCE 1
AUTHORS Sasaki,T., Matsumoto,T., Hattori,M., Sasaki,Y. and Katayose,Y.
TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, BAC
clone:OJ118 A10
JOURNAL Published only in Database (2002)
AUTHORS 2 (bases 1 to 96312)
TITLE Sasaki,T., Matsumoto,T., Hattori,M., Sasaki,Y. and Katayose,Y.
JOURNAL Submitted (23-JUL-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program, Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasak@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
The nucleotide sequence of this BAC clone was generated by
combining Monsanto and RGP-Japan sequencing data.
NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
source
1..96312
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="9"
/clone="OJ118 A10"
BASE COUNT 26463 a 21050 c 21350 g 27309 t 100 others
ORIGIN
Query Match 56.7%; Score 1000.6; DB 2; Length 96312;
Best Local Similarity 77.2%; Pred. No. 1,7e-134;
Matches 1307; Conservative 0; Mismatches 349; Indels 37; Gaps 6;

QY 8 CTCCTCTCTCTCCCAATCTCCCGCTCCCTCAACCAATCAGCACCAGCCAGGCG 67
DB 88051 CTACTCTCTCTCTCTCAAGTTCCCAATCTCCGATCCCGCGCGCGCGCGCG 88110
QY 68 CATCCAGCCAGCGCGCGCGCGCGCGCTCTGTGATGCAATGCCGCGCGCGCGCGAC 127
DB 88111 CGACATGCTCTCGGCGATCCGACGCGCAATGCCGCGCTCCCAAGAGGCGCAG 88170
QY 128 GCGCGCGCGCGCGCGCGCGCGCGCGCGATGATCTCTCAAGAGCGCTCGCGCTCAGCTTC 187

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DB 88171 AGCGCGCGCGCGCGCGCGCTCCGCAATGATCTCTCGAAGAGCTCCGCGCGACGCGTCG 88230
QY 188 GCGGAGACCTCTGATCTCCATCTCCCGCGAGCGTGAAGCTCAAGCCCTGCGCTCCG 247
DB 88231 AGGAGACCTCTGATCTCCATCTCCCGCGAGCGTGAAGCTCAAGCGGTGGTCC 88290
QY 248 CACACCGCGCGCGCGCGCGCGCTCCGCTTCTCACCTGGCGGAGAGCCACCGAGCC 307
DB 88291 CACACCGCGCGCGCGCGCGCGCTCCGCTTCTCACCTGGCGGAGAGAGCCACCGAGCG 88350
QY 308 TTGCGCGCTTACCAACCGCGCTCTGCGCGCGCGCTCTCCGCGCTTCTTGTGCGCG 367
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DEFINITION	Primmula farinosa sphingolipid delta-8 desaturase mRNA, complete		

ACCESSION	AY234124	
VERSION	AY234124.1	GI:30350274
KEYWORDS		
SOURCE	Primula farinosa	
ORGANISM	Primula farinosa	

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; Ericales; Primulaceae; Primula.

REFERENCE
AUTHORS

1 (bases 1 to 1681)
Sayanova, O. V., Beaudoin, F., Michaelson, L. V., Shewry, P. R. and

TITLE Identification of Primula fatty acid substrate preferences(1)
JOURNAL FEBS Lett. 542 (1-3), 100-104 (2003)

MEDLINE 22615586
PUBMED 12729906

REFERENCE
AUTHORS
2 (bases 1 to 1681)
Sayanova, O. V., Beaudoin, F., Michaelson, L. V., Shewry, P. R. and
Ward, J. L.

TITLE Napier, J. A.
JOURNAL Direct Submission
Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton
Research Station, Long Ashton, Bristol BS41 9AF, UK
FEATURES Location/Qualifiers

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RESULT 4
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 LOCUS AY234126
 DEFINITION Primula viali sphingolipid delta-8 desaturase mRNA, complete cds.
 ACCESSION AY234126.1 GI:30350278
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
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 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Primulaceae; Primula.
 REFERENCE 1 (bases 1 to 1385)
 AUTHORS Savanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and Napier,J.A.
 TITLE Identification of Primula fatty acid Delta(6)-desaturases with n-3 substrate preferences(1)
 JOURNAL FEBS Lett. 542 (1-3), 100-104 (2003)
 MEDLINE 22615586
 PUBMED 12729906
 REFERENCE 2 (bases 1 to 1385)
 AUTHORS Savanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and Napier,J.A.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton Research Station, Long Ashton, Bristol BS41 9AF, UK
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 Query Match 30.4%; Score 535.6; DB 8; Length 1385;
 Best Local Similarity 63.8%; Pred. No. 1.8e-67;
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ACCESSION AR200409
VERSION AR200409.1 GI:20250483
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1. (bases 1 to 1702)
AUTHORS Thomas,T.L.
TITLE Production of gamma linolenic acid by a DELTA-6-desaturase
JOURNAL Patent: US 6355861-A 26 12-MAR-2002;
FEATURES
source 1.1702
location/Qualifiers
BASE COUNT 358 a 471 c 446 g 427 t
ORIGIN

Query Match 27.8%; Score 491.2; DB 6; Length 1702;
Best Local Similarity 62.0%; Pred. No. 4,1e-61;
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DEFINITION AY234125
ACCESSION AY234125
VERSION AY234125.1 GI:30350276
KEYWORDS
SOURCE Primula farinosa
ORGANISM Primula farinosa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Primulaceae; Primula.
1 (bases 1 to 1410)
Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and
Napier,J.A.
Identification of Primula fatty acid Delta(6)-desaturases with n-3
substrate preferences(1)
FEBS Lett. 542 (1-3), 100-104 (2003)
22615586
12729906
2 (bases 1 to 1410)
Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and
Napier,J.A.
Direct Submmission
Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton
Research Station, Long Ashton, Bristol BS41 9AF, UK
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DEFINITION complete sequence.
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VERSION HTG.
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SOURCE Arabidopsis thaliana
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1 (bases 1 to 110149)
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Shen, M., Romin, C.M., Frazer, C.M., Somerville, C.R. and Venter, J.C.
unpublished
2 (bases 1 to 110149)
Lin, X.
JOURNAL Direct Submission
AUTHORS Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
JOURNAL Medical Center Dr., Rockville, MD 20850, USA
REFERENCE 3 (bases 1 to 110149)
Town, C.D. and Kaul, S.
JOURNAL Direct Submission
AUTHORS Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
JOURNAL Medical Center Dr., Rockville, MD 20850, USA, cdrom@igr.org
COMMENT On Apr 18, 2002 this sequence version replaced gi:6598465.
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Query Match 25.7%; Score 453.8; DB 8; Length 110149;
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LOCUS Arabidopsis thaliana delta-8 sphingolipid desaturase (At3g61580)

DEFINITION mRNA, complete cds.

ACCESSION BT003379

VERSION BT003379.1 GI:28059271

KEYWORDS FLI CDNA.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE Eukaryotes, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 1491)

AUTHORS Southwick, P., Nguyen, M., Tripp, M., Palm, C.J., Jones, T., Wu, T., Carninci, P., Chen, H., Cheuk, R., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hayashizaki, Y., Huan, V.W., Lee, J.M., Ishida, J., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Onodera, C.S., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Shim, P., Tang, C.C., Toroumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinzaki, K., Becker, J., Theologis, A. and Davis, R.W.

TITLE Direct Submission

JOURNAL Submitted (29-JAN-2003) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

COMMENT e-mail for correspondence: arabsequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinzaki, K.

The Salk, Stanford, PGSC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen, M., Tripp, M., Southwick, P., Palm, C.J., Jones, T., Wu, T., Chen, H., Cheuk, R., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Huan, V.W., Lee, J.M., Kim, C.J., Quach, H.L., Onodera, C.S., Shim, P., Tang, C.C., Toroumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Becker, J., Theologis, A. and Davis, R.W.

Nguyen, M., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinzaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIs.

FEATURES

source

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BASE COUNT 365 a 370 c 299 g 457 t

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Query Match 25.2%; Score 445; DB 8; Length 1491;

Best Local Similarity 59.3%; Pred. No. 1.8e-54;

Matches 795; Conservative 0; Mismatches 540; Indels 6; Gaps 2;

Qy 189 CCGACGACCTCTGGATCTCATCTCCGGGAGCTGTACGACGCTGCTCCCC 248

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Db 122 CTGATCCCGAGGCGAGACGGTATTCATCTTGTGTCAAGCGTCACCGATGCTT 181

Qy 309 TCGCCGCTACACACCC---GCCCTCGCGCGCGGCTCTCCGCGCTTCTTGTTGGCC 365

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Qy 366 GCCTCTCTGATGAGCGGCTCTCCCGCGTCCGCGACATACCGCGGCTCTTGGCGAGC 425

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Qy 426 TATCTCCGGGGGCTCTTGAAGCGGTGGGGCCCAACCCCAAGTCCAGCTGTCTGA 485

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Query Match	25.2%	Score 445	DB 6	Length 1678
Best Local Similarity	59.3%	Pred. No. 1.76-54		
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	VERSION	AX007241.1	GI:9995107		
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	SOURCE				
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REFERENCE		1			
AUTHORS		Zaehring, U., Heinz, E., Schmidt, H. and Sperling, P.			
TITLE		Sphingolipid-desaturase			
JOURNAL		Patent: WO 0000593-A 3 06-JAN-2000;			
		ZAEHRINGER ULRICH (DE); HEINZ ERNST (DE); SCHMIDT HERMANN (DE);			
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DEFINITION	AF428420				
ACCESSION	AF428420.1	GI:16226516			
VERSION					
KEYWORDS	FLI CDNA.				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
REFERENCE	Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.				
AUTHORS	Arabidopsis CDNA clones				
TITLE	Unpublished				
JOURNAL	2 (bases 1 to 1704)				
REFERENCE	Chen, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.				
AUTHORS	Direct Submission				
TITLE	Submitted (05-OCT-2001)				
JOURNAL	Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA				
COMMENT	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPL cDNAs (RAPL CDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.				
	The Salk, Stanford, PGSC (SSP) Consortium members carried out the sequencing and annotation of the RAPL cDNAs: Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Shim, P., Banh, J., Bowser, L., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G.,				

Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J. R. (SSP/Salk) contributed equally to this work as PIs.

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Query Match 25.2%; Score 445; DB 8; Length 1704;
 Best Local Similarity 59.3%; Pred. No. 1.7e-54;
 Matches 795; Conservative 0; Mismatches 540; Indels 6; Gaps 2

Db 189 CCGACGACCTTGATCTCAATCTCCGGACGCTGACAGCTACCGCCCTGGCTCCCC 248
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 REFERENCE 1 Sperling, P., Zahringer, U. and Heinz, E.

TITLE A sphingolipid desaturase from higher plants. Identification of a
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 JOURNAL J. Biol. Chem. 273 (44), 28590-28596 (1998)
 MEDLINE 99003197
 PUBMED 9786850
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 TITLE Sperling, P., Zahringer, U. and Heinz, E.
 IDENTIFICATION OF CDNAS CODING FOR A SPHINGOLIPID DESATURASE FROM
 HIGHER PLANTS
 JOURNAL Unpublished
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 AUTHORS Sperling, P.
 TITLE Direct Submission
 JOURNAL Submitted (13-FEB-1998) Sperling P., Physiologie, Institut fuer
 Allgemeine Botanik der Universitaet Hamburg, Ohnhorststrasse 18,
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BASE COUNT

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Query Match 25.2%; Score 445; DB 8; Length 1705;
 Best Local Similarity 59.3%; Pred. No. 1.7e-54;
 Matches 795; Conservative 0; Mismatches 540; Indels 6; Gaps 2;

Qy 189 CCGAGAGCTCTGATTCATCTCCGGAGAGTGTAGAGCTCAGCGCTGCTCCCC 248
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KEYWORDS Arabidopsis thaliana (thale cress)
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 ORGANISM Arabidopsis thaliana

REFERENCE 1
 De Haan, M., Maere, A.C., Grivell, L.A., Mewes, H.W., Lemcke, K.,
 Mayer, K.F.X., Quelet, F. and Salanoubat, M.
 Unpublished

JOURNAL 2 (bases 1 to 95993)
 REFERENCE EU Arabidopsis sequencing project.
 AUTHORS Direct Submission

TITLE Submitted (31-JAN-2000) MIPS, at the Max-Planck-Institut fuer
 Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
 lemcke@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project
 Coordinator: Marcel Salanoubat and Francis Quelet, Grouperment
 d'Interet Public, Centre National de Sequencage - GENOSCOPE, 2 rue
 Gaston Cremieux, BP191, 91006 Evry Cedex, France;
 http://www.genoscope.cns.fr

COMMENT Information on performance of analysis and a more detailed
 annotation of this entry and other sequences of chromosomes 3, 4
 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.

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            Haas, B.J., Volkovskiy, N., Town, C.D., Troukhan, M., Alexandrov, N.,
            Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
            Full-length messenger RNA sequences greatly improve genome
            annotation
            JOURNAL Genome Biol. 3 (6), RESEARCH0029 (2002)
            MEDLINE 22088475
            PUBMED 12093376
            2 (bases 1 to 1652)
            Broyer, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
            Feldmann, K.
            Full-length cDNA from Arabidopsis thaliana
            JOURNAL Unpublished
            REFERENCE 3 (bases 1 to 1652)
            Broyer, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
            Feldmann, K.
            Direct Submission
            Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
            Malibu, CA 90265, USA
            COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made
            available to TIGR and Genbank. The following quality assessment of
            this set was done by comparison with known proteins: two percent
            of the clones are estimated to be 5'-truncated; less than one percent
            are 3'-truncated; approximately two percent represent alternative
            splice variants, including unspliced introns and spliced exons; one
            percent may contain premature stop codons; five percent may have
            frame shifts in a coding region. A sequence is considered to be
            5'-truncated if it lacks the translation initiation start (ATG). A

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sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or later ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genes carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

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source

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ORIGIN

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Query Match

Best Local Similarity 59.1%; Score 441.8; DB 8; Length 1652;
Matches 793; Conservative 0; Mismatches 542; Indels 6; Gaps 2;

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RESULT 15

AX505863

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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Harper, J.F., Kreps, J., Wang, X., and Zhu, T.
Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
Patent: WO 0216655-A 558 28-FEB-2002;
The Scripps Research Institute (US); Syngenta Participations AG
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Location/Qualifiers

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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SUMMARIES

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6	452	25.6	1465	21	AAC42244
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9	441.8	25.0	1650	21	AAK33846
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11	437	24.8	1594	21	AAZ44832
12	370.2	21.0	1606	21	AAZ44851
13	365.4	20.7	1684	19	AAV34398
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15	365.4	20.7	1685	17	AAT30395
16	365.4	20.7	1685	24	ABK49502
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19	314.8	17.8	823	21	AAD01354
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22	219.4	12.4	535	22	AAF25733
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ALIGNMENTS

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AC	AAZ01350;	
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KW	Corn; sphingolipid desaturase; membrane-bound desaturase;	
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B. napus sld1 DNA.
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DNA encoding Borage
Borage delta-6-des
Florigin bitterbush
Wheat sphingolipid
Soybean sphingolip
Corn ear-derived p
C. purpureus delta
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Aspergillus oryzae
S. chrysomallus ac

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 DR P-PSDB; AA71552.
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 PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries
 XX
 PS Claim 2; Page 41-42; 57pp; English.
 XX
 CC The present sequence is a cDNA encoding sphingolipid desaturase
 CC from clone cdeic.p001.08.115 isolated from corn developing
 CC embryo cDNA library, cdeic. The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is also useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
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 Db 361 TGAGCGGCTCTGAGTACGCGGCTCCCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
 QY 421 GCAGCTATCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 480
 Db 421 GCAGCTATCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 480
 QY 481 CCTGATGCGGCTCTCTTCTTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 540
 Db 481 CCTGATGCGGCTCTCTTCTTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 540
 QY 541 GGGGCACTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
 Db 541 GGGGCACTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
 QY 601 CCAAGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 660
 Db 601 CCAAGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 660
 QY 661 GCTCTCGGGAATGCTCTACCGGCGCTCAGCATGCGCTGTGAGAGTGAACCAAC 720
 Db 661 GCTCTCGGGAATGCTCTACCGGCGCTCAGCATGCGCTGTGAGAGTGAACCAAC 720

QY 721 GCACCAATCGCTGAGAGAGCTGAGCATGACCCGGAAGCTTCAGACATGCGGCTTT 780
 Db 721 GCACCAATCGCTGAGAGAGCTGAGCATGACCCGGAAGCTTCAGACATGCGGCTTT 780
 QY 781 TGCCGCTCCCGGAGAGCTGTTGGCAATATGCTCTTCTTACCAACGAGCCTGGC 840
 Db 781 TGCCGCTCCCGGAGAGCTGTTGGCAATATGCTCTTCTTACCAACGAGCCTGGC 840
 QY 841 GTTCGATGCGGCGTGAATTTCTCATCTGAGTACGAGAGCTGAGCCTTACCGGTAAT 900
 Db 841 GTTCGATGCGGCGTGAATTTCTCATCTGAGTACGAGAGCTGAGCCTTACCGGTAAT 900
 QY 901 GTTCATGCGGAGATTAATCTTCTCGGAGTCCGCTGTTGTTCTCAAGAGAGAG 960
 Db 901 GTTCATGCGGAGATTAATCTTCTCGGAGTCCGCTGTTGTTCTCAAGAGAGAG 960
 QY 961 GGTGCGGAGCGGTTGTTGAGATCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 1020
 Db 961 GGTGCGGAGCGGTTGTTGAGATCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 1020
 QY 1021 GCTGATGCTTCCTCGGAGATTTGTTGAGAGAGGCGGCGGCTTTCAGCTTAC 1080
 Db 1021 GCTGATGCTTCCTCGGAGATTTGTTGAGAGAGGCGGCGGCTTTCAGCTTAC 1080
 QY 1081 CATCTGCGGAGATTCAGACAGTCCCAATTCGCTGAACCACTTCTCGTCCGAGCTGATGT 1140
 Db 1081 CATCTGCGGAGATTCAGACAGTCCCAATTCGCTGAACCACTTCTCGTCCGAGCTGATGT 1140
 QY 1141 CGGCGCAACCAAGGAGATGATGTTGAGAAAGAGAGAGAGAGAGAGAGAGAGAG 1200
 Db 1141 CGGCGCAACCAAGGAGATGATGTTGAGAAAGAGAGAGAGAGAGAGAGAGAGAG 1200
 QY 1201 GTGCTCTCTGATGATGATGTTGTTGAGAGAGGCGGCGGCTTTCAGATGAGACATCT 1260
 Db 1201 GTGCTCTCTGATGATGATGTTGTTGAGAGAGGCGGCGGCTTTCAGATGAGACATCT 1260
 QY 1261 GTTCCCGGCTTACCTCGGAGCACTTTCGCAAGGTTGAGAGAGAGAGAGAGAG 1320
 Db 1261 GTTCCCGGCTTACCTCGGAGCACTTTCGCAAGGTTGAGAGAGAGAGAGAGAG 1320
 QY 1321 CAAGAGCATGAGGCTCACTTATTCGAGCCACATTTGAGGAGTGAAGATACGGGCTAAT 1380
 Db 1321 CAAGAGCATGAGGCTCACTTATTCGAGCCACATTTGAGGAGTGAAGATACGGGCTAAT 1380
 QY 1381 GAAGACATCAGAGGCTGCTGATGAGAGGCGGAGAGAGAGAGAGAGAGAGAGAG 1440
 Db 1381 GAAGACATCAGAGGCTGCTGATGAGAGGCGGAGAGAGAGAGAGAGAGAGAGAG 1440
 QY 1441 GAATTTGATGAGAGAGCTGTGACACCCATGAGATTAATGAGATGAAGATACGGGCTAAT 1500
 Db 1441 GAATTTGATGAGAGAGCTGTGACACCCATGAGATTAATGAGATGAAGATACGGGCTAAT 1500
 QY 1501 GGGCACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 Db 1501 GGGCACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 QY 1561 AGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 Db 1561 AGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 QY 1621 TGTCTATCAGTTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 Db 1621 TGTCTATCAGTTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 QY 1681 CTTCCTATCAGGTAATATATATATATATATATATATATATATATATATATAT 1740
 Db 1681 CTTCCTATCAGGTAATATATATATATATATATATATATATATATATATATAT 1740
 QY 1741 AAGATTAAAAAAGATTAAAAA 1764
 Db 1741 AAGATTAAAAAAGATTAAAAA 1764

RESULT 2
 AAD01353
 ID AAD01353 standard; cDNA; 1972 BP.
 XX
 AC AAD01353;
 XX
 DT 12-OCT-2000 (first entry)
 XX
 DE Wheat sphingolipid desaturase cDNA #1.
 XX
 DE Wheat sphingolipid desaturase; membrane-bound desaturase;
 XX
 KW Transgenic plant; fatty acid; ss.
 XX
 OS Triticum aestivum.
 XX
 FH Key Location/Qualifiers
 FT CDS /tag= a
 FT /product= "sphingolipid desaturase"
 XX
 PN MO200032790-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 02-DEC-1999; 99WO-US28589.
 XX
 PR 03-DEC-1998; 98US-0110784.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;
 XX
 DR MPI: 2000-412336/35.
 DR P-PSDB; AA71555.
 XX
 PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries
 XX
 PS Disclosure; Page 48-49; 57pp; English.
 XX
 CC The present sequence is a cDNA encoding sphingolipid desaturase
 CC from clone wrel.pK004.c7:fls isolated from wheat etiolated
 CC seedling root cDNA library, wrel.
 CC The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is also useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
 XX
 SQ Sequence 1972 BP; 382 A; 616 C; 490 G; 484 T; 0 other;

Query Match 61.9%; Score 1091.4; DB 21; Length 1972;
 Best Local Similarity 79.0%; Pred. No. 3.8e-211;
 Matches 1355; Conservative 0; Mismatches 341; Indels 19; Gaps 4;

QY 27 CCTCCCCGCTCCCTTACCAATCAGCACACCCAGGCGCATCCGAGCCAGCGCGG 86
 DB 89 CCCCTCTCGCGCTCCAGCTAAATCCAGCGCATCGATGGCCCGCACGGGCTCGCGAGG 148
 QY 87 CAATGCGCGCTCTGTGATGCAATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGG 146
 DB 149 CAAAGCGCGCGCGAGCGCGAGCGCATGCGCGCGCGCGCGCGCGCGCGCGCGG 202
 QY 147 TCGGCGATGATCTCTCTCAAGAGAGCTCCGCGCTTCCGCGCGAGCATCTTGATCT 206
 DB 203 TCGGCGATGATCTCTCAAGAGAGCTCGAGCGCGCGCGCGCGCGCGCGCGCGG 262
 QY 207 CCATCTCCGCGCGAGCTGTACAGAGTCAAGCGCTTCCCGCGCGAGCGCGCGCGG 266
 DB 263 CCATCTCCGCGCGAGCTGTACAGAGTCAAGCGCTTCCCGCGCGAGCGCGCGCGG 322

QY 267 TCCCGCTTCTCAACCTTGGCGGGGAGAGCCACCGGCGCTTGGCGCGCTTACACCGCG 326
 DB 323 TCCCGCTTCTCAACCTTGGCGGGGAGAGCCACCGGCGCTTGGCGCGCTTACACCGCG 382
 QY 327 CCTCGGCGCGCGCGCTTCTTCCGCGCGCTTCTTGGTGGCGCGCTTCTGACTAGCGGCT 386
 DB 383 CCTCGGCGCGCGCGCTTCTTCCGCGCGCTTCTTGGTGGCGCGCTTCTGACTAGCGGCT 442
 QY 387 CCGCGCGCTTCCGCGCGCTTCTTCCGCGCGCTTCTTGGTGGCGCGCTTCTGACTAGCGGCT 446
 DB 443 CCGCGCGCTTCCGCGCGCTTCTTCCGCGCGCTTCTTGGTGGCGCGCTTCTGACTAGCGGCT 502
 QY 447 AAGCGCTCGGCGG 506
 DB 503 AAGCGCTCGGCGG 562
 QY 507 CCGTGTACTGCTTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 566
 DB 563 CCGTGTACTGCTTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 622
 QY 567 TTGGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 626
 DB 623 TTGGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 682
 QY 627 CCGGCGG 686
 DB 683 CCGGCGG 742
 QY 687 TAGGATGCGCTTGTGGAGAGTGTACACACACACACACACACACACACACACACACG 746
 DB 743 TAGGATGCGCTTGTGGAGAGTGTACACACACACACACACACACACACACACACG 802
 QY 747 ACCATGACCGG 806
 DB 803 ACCATGACCGG 862
 QY 807 ACAATGCTCTACTTCTTCAACACGAGACCTGCGCTTCCGCGCGCGCGCGCGG 866
 DB 863 ACAATGCTCTACTTCTTCAACACGAGACCTGCGCTTCCGCGCGCGCGCGG 922
 QY 867 TAGGATGCGG 926
 DB 923 TAGGATGCGG 982
 QY 927 CCGAGTCCCGCTTCTTCTTCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 986
 DB 983 TCGAGTCAATCGTGTCTGATGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1042
 QY 987 CCGGCGG 1046
 DB 1043 CCGGAGTTCAGCGCTTCTTCTTCAACGAGAGAGAGAGAGAGAGAGAGAGAGAG 1102
 QY 1047 GGAAGAGGCTGCGTGTGTGCTTTCAGCTTCAACATCTGCGGATTCAGAGCTCAAT 1106
 DB 1103 GGAAGAGGCTGCGTGTGTGCTTTCAGAGCTTGTGATTCAGGAGATTCAGAGCTCAAT 1162
 QY 1107 TCTGCTGAACCATCTTCTGTCGAGGTATGTGCGGCGCGCGCGCGCGCGCGG 1166
 DB 1163 TCTGCTGAACCATCTTCTGTCGAGGTATGTGCGGCGCGCGCGCGCGG 1222
 QY 1167 TTGAG 1226
 DB 1223 TTGAG 1282
 QY 1227 ACGGTGCGCTGAGTTCAGATGAGACACATCTTTCGCGCGCTTACCTCGGTCGAC 1286
 DB 1283 ATGTGTGTCTGAGTTCAGATGAGACACATCTTTCGCGCGCTTACCTCGGTCGAC 1342
 QY 1287 TTGCGAGAGTTCAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 1346
 DB 1343 ATGAGATGTCTGCGCGAGATGTGCGTGTGACCTTTGAGAGAGAGAGAGAGAGAG 1402
 QY 1347 CAGCCACATTTCTGGGAGTGAATGTGTATGAGAGAGAGAGAGAGAGAGAGAGAG 1406

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Db      1403  CCGCCACATTCCTGGAGGCAAAATGATATGACATGAAAGAGCTGAGGCTGACGATTCG 1462
Qy      1407  AGGCCGAGACCGCTACAAAGTGTGTGTCTCCGAAAGATTTGGATGGAGGCTGTGAACA 1466
Db      1463  AGGCCGAGGAGGACCACTGAGAGCTGTCCCAAGATCTGTGGGAGCTTTGAACA 1522
Qy      1467  CCCATGATTAATGGAGATGAAAGATGACGGGCTTAATGGCACTTCGTGTGCTGCTGCTG 1526
Db      1523  CTCATGATGACCTGGAGTACGAGCTGAGATGAGACATTTGAAGCTGAGACCTTGGC 1582
Qy      1527  CCCATGATGATGCTGTGATGCTTCAGTTCATTTAAGATATGATTCATTCACCTGCTT 1586
Db      1583  TGCATGACATTAATCTGATTCCTTCGATTCGAGATGATGATTCCTTTAGCTGTTC 1642
Qy      1587  GAGTCAGTGTGAATTTGTGTGTGACAAAGTGTCTGTATCCAGT---TGAAGAGTTC 1642
Db      1643  GAATCTGTGTGATTTTGTGTGTGACAGTGTCTGTGTGCAATTCGTGGGTTTC 1702
Qy      1643  ATGCTTCATTAATGCTGTGTGTTCAC-----GGAGATGCTGTGTTCCTCATCAGGTA 1695
Db      1703  ATGCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1762
Qy      1696  ACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1730
Db      1763  ACTACATCA--ATAGTACTGATTTATCATCATATAA 1795

```

RESULT 3
ABK49503
ID ABK49503 standard; DNA; 1702 BP.

AC ABK49503;

DT 15-JUL-2002 (first entry)

DE DNA encoding Evening primrose delta6-desaturase.

XX delta6-desaturase; sunflower; soybean; maize; tobacco;
KM peanut; carrot; oil seed rape; gamma linolenic acid; GLA;
XX chilling tolerance; gene; ds; evening primrose.

OS Oenothera biennis.

XX Key Location/Qualifiers

FT CDS 48..1406

FT /tag= a

FT /product= "delta6-desaturase"

PN US6355861-BI.

PD 12-MAR-2002.

PF 19-SEP-1997; 97US-0934254.

PR 13-OCT-1992; 92US-0959952.

PR 10-OCT-1991; 91US-0774475.

PR 08-JAN-1992; 92US-0817919.

PR 14-SEP-1994; 94US-0307382.

PR 28-JAN-1997; 97US-0789936.

PA (RHON) RHONE-POULENC AGROCHIMIE.

PI Thomas TL;

XX WPI; 2002-380944/41.

XX P-PSDB; AAU79851.

XX Novel nucleic acid encoding evening primrose delta6-desaturase which

PT converts linolenic acid to gamma linolenic acid useful for producing

XX gamma linolenic acid in transgenic plant or bacteria

PS Claim 2; Column 41-46; 53pp; English.

XX The invention describes an isolated nucleic acid encoding an evening
CC primrose delta6-desaturase. The nucleic acid and a vector expressing the
CC nucleic acid are useful for producing a plant such as sunflower, soybean,
CC maize, tobacco, peanut, carrot or oil seed rape plant, with increased
CC gamma linolenic acid (GLA) content, and also for inducing or increasing
CC production of GLA in a bacteria or plant deficient, lacking in or
CC production of low levels of GLA. The nucleic acid is also useful for inducing
CC chilling tolerance in plants. This sequence encodes the evening primrose
CC delta6 desaturase involved in the production of gamma linolenic acid.

XX Sequence 1702 BP; 358 A; 471 C; 446 G; 427 T; 0 other;

Query Match 27.8%; Score 491.2; DB 24; Length 1702;

Best Local Similarity 62.0%; Pred. No. 6,9e-90;

Matches 832; Conservative 0; Mismatches 498; Indels 12; Gaps 3;

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Qy      155  ATCTCTCCAGAGAGCTCCGCGCTCAAGCTTCGCGGAGAGACTTGATCTTCATCTCC 214
Db      72  ATCAGCGCGGAGAGAGCTCCGCGCGCACAAAGTCCGGGATCTTGATCTTCATCTCAG 131
Qy      215  GGGGAGGTGATGAGAGTCAAGCTTCGCTCCGACACCCGGGCGGCGGCTTCGCTT 274
Db      132  GGGGAGGTGATGAGAGTCAAGCTTCGCTCCGAGGCGGCGGAGAGCTTCGCTT 191
Qy      275  CTCACCTGCGCGGCGGAGAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 334
Db      192  CTCAGTCTGCGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 251
Qy      335  CGCGCGCTCTCTCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 388
Db      252  TGGCGGAGATCTGAGATCGGCTCTTACCGGCTACTACTACTACTACTACTACTACT 311
Qy      389  CCGCGCTCGCGAGCTACCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 448
Db      312  GAGATCTCCAGAGAGCTACCGAGAGCTTTGAGAGAGATGCGGAGTCTCGGAGTCT 371
Qy      449  CGCGTCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 508
Db      372  AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431
Qy      509  CTGTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 568
Db      432  GTCTACGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 491
Qy      569  GGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 628
Db      492  GGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 551
Qy      629  GGCATCGCGGTCTCTGACCGCGGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 688
Db      552  CCAACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 611
Qy      689  AGCATGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 748
Db      612  AGCATGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 671
Qy      749  CATGACCGGAGAGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 808
Db      672  TAGACCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 731
Qy      809  ATATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 868
Db      732  ATCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 791
Qy      869  AGCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 928
Db      792  AGCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 851
Qy      929  CAGTCCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 988
Db      852  CAGACCTTTTATGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 911

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QY 989 GGGGTGCGCAATCTGGGCTTGTAACCCGTTGCTGTGCTTCCCTGCCGAATGGTGA 1048
DB 912 GATATCGCGATTCTTGACAGTGTTCCTCGCTCTTGTAATCTGTCCCGAATGGCC 971
QY 1049 GAGAGGTGCGCTTTGTGCTTTTACGTTTCAATCTGCGGGATTGACAGCTTCAATTC 1108
DB 972 GAACGGTGTGGGTTCTCTCATCAGCTTGTGCGGTCAAGCGCATTCAGCAGTCCAGTTC 1031
QY 1109 TGCCTGAACCACTTCTCTGCGAGCTGTAATGTGCGGCGCAACCAAGGGCAATGATGTTT 1168
DB 1032 AGCTCAACCACTTCTCTGCGGCGACATATGCTGGCCCCCGCAAGGCGCAACTGTTT 1091
QY 1169 GAGAACGACAGCGGACGACGCTGACATCTGTGCTCTCTTGAATGATGTTTCCAC 1228
DB 1092 GAGAACGACAGCAAGAGAGCATGATTCAGCTGCCACCGTGAATGACGTGTTCTTT 1151
QY 1229 GGTGGCTGCACTTCCAGATTGACACCATCTTGTTCCTCCGCTTACCTGGTCCACCTT 1288
DB 1152 GGTGGCTGCACTTCCAGATTGACACCATCTTGTTCCTGAAGCTGCGGCGGACGCTT 1211
QY 1289 CGAAGTTGCAACCGGCGCGCTGCGACCTTTCAGAAAGATGGGCTCACTTATTCGCA 1348
DB 1212 AGAAGATTGCGCTCTTGGCTCGGACCTTGTGAAGAGACGCGATGCCGTAATGAGAC 1271
QY 1349 GCCACATCTCTG--GATGCAATGTGCTTACATGAGACACTCAGGCTGCTGATTTG 1405
DB 1272 TTGGGTTTGGGAGACGCTAATGTCAAGACATTCGACGCTGAGGATGCGGCGGTT 1331
QY 1406 CAGGCCAGACCGCTACAAAGTGTGCTCTCGAAGAAATTTGGTAT--GGAGGCTGTG 1462
DB 1332 CAGGCCGCTGACCTTATTCGCGCCGCTGCTTAAGAACTTGGTATGGGAGGCTTAT 1391
QY 1463 AACACCATGATTAATGGAT 1484
DB 1392 AACACCATGATTAATGGAT 1413

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RESULT 4

ABX15367

ID ABX15367 standard; cDNA; 1702 BP.

XX ABX15367;

DT 16-APR-2003 (first entry)

XX Evening primrose delta-6-desaturase #1 cDNA.

KW Delta-6-desaturase; gene; ss; delta-12-desaturase; sunflower; soybean;
 KW maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
 KW octadecatrienoic acid; alpha-linolenic acid; delta-15-desaturase;
 KW evening primrose.

XX Oenothera biennis.

FH Key Location/Qualifiers

FT CDS 48..1406

FT /tag= a /product= "Evening primrose delta-6-desaturase #1"

FT US2002108147-A1.

XX 08-AUG-2002.

PD 21-DEC-2001; 2001US-0029756.

XX 13-OCT-1992; 92US-0959952.

PR 19-SEP-1997; 97US-0934254.

PR 10-OCT-1991; 91US-0774475.

PR 08-JAN-1993; 92US-0817819.

PR 14-SEP-1994; 94US-0307382.

PR 28-JAN-1997; 97US-0789936.

XX (THOM/) THOMAS T L.

XX Thomas TL;
 XX WPI, 2003-066659/06.
 DR P-PSDB; ABG73416.
 XX Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
 PT for producing plant with increased gamma linolenic acid content, and
 PT for inducing octadecatrienoic acid production in plant
 PS Claim 2, Fig 10; 55pp; English.

XX The invention relates to a nucleic acid encoding an evening primrose
 CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
 CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
 CC for producing a plant (such as sunflower, soybean, maize, tobacco,
 CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
 CC acid (GLA) content by transforming a plant cell with the nucleic acid or
 CC vector and regenerating a plant with increased GLA content from the plant
 CC cell, for inducing or increasing production of GLA in an organism lacking
 CC in or producing low levels of GLA and for inducing production of
 CC octadecatrienoic acid in at least one of a plant deficient or lacking
 CC in or producing low levels of octadecatrienoic acid, a bacterium which
 CC produces alpha-linolenic acid or a bacterium which exhibits a
 CC delta-15-desaturase activity on a GLA substrate. This sequence represents
 CC cDNA encoding an evening primrose delta-6-desaturase polypeptide.

Sequence 1702 BP; 358 A; 471 C; 446 G; 427 T; 0 other;

Query Match 27.8%; Score 491.2; DB 25; Length 1702;

Best Local Similarity 62.0%; Pred. No. 6.9e-90; Matches 832; Conservative 0; Mismatches 498; Indels 12; Gaps 3;

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QY 155 ATCTCTCCAGAGTCTCCGCTCAAGCTTCCGCGACGACTGTGATTCATCTCC 214
DB 72 ATACGCGCGAGAGACTCCGCGCCACCAAGTCCGCGATCTGATCTTCATCCAG 131
QY 215 GGGAGCTGTAGAGTCAAGGCTGCGCTCCGCGCCACCAAGCGGCGGAGACCTCCGCGTT 274
DB 132 GGGAGCTGTAGAGTCAAGGCTGCGCTCCGCGCCACCAAGCGGCGGAGACCTCCGCGTT 191
QY 275 CTCACCTTGGCGGCGAGACGCCACCGAGCTTCCGCGCTTACCAAGCGGCGGCGG 314
DB 192 CTCAGTCTGGCGGCGAGACGCCACCGAGCTTATTCAGCAAGCGGCGGCGG 251
QY 335 CGCCGCTCTCTCGCGCTTCTTCTGTTG-----CGGCTCTGACTACGCGCTCTC 388
DB 252 TGGCGGCACTGATCGCTCTTCAAGCGGCTTCTGACTTCAAGGACTTCAAGTGTG 311
QY 389 CCGCGTCCGCGAGTCAAGCGGCGGCTTCTGAGCTTCTCGGCGGCGGCGGCGG 448
DB 312 GAGATCTTCAAGAGTCAAGCGGCTTCTGAGAGATTCGCGGCTTCTGAG 371
QY 449 CCGGTGCGGCGGCGGCGGCGGCTGCTGATGAGCGGCTCTTCTTCAAGCGGCG 508
DB 372 AAGAGGCGGCGGCGGCGGCGGCTTCTGATGAGCGGCTTCTTCAAGCGGCGG 431
QY 509 CTGTAATCTGCTCTGCAATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 568
DB 432 GTCTAGCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 491
QY 569 GGGTCTGCTGTGATCTCAAGTCTGAGTGGGCGGCGGCGGCGGCGGCGGCGG 628
DB 492 GGGTCTGCTGTGATCTCAAGTCTGAGTGGGCGGCGGCGGCGGCGGCGGCGG 551
QY 629 GGCATCGGCTCTGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 688
DB 552 CCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 611
QY 689 AGCATCGGCTGTGAGTGTATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 748
DB 612 AGCATCGGCTGTGAGTGTATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 671

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QY 749 CATGACCCGACCTCCAGACATGCGCTCTTTCGCTCTCCCAAGCTGTTCGCAAC 808
 DB 672 TAGACCCCGACCTCCAGACATGCGCTCTTTCGCTCTCCCAAGCTGTTCGCAAC 731
 QY 809 ATATGCTCTACTTCTTCAACAGGACCTTGGCTGTGATCCGCTTGAATTTCTTATC 868
 DB 732 ATCACTCTGCTCTTCAATGAGCCAGTCTTGAATTCACCAATGTGACCGTCTTCAATC 791
 QY 869 AGCTACAGACATGACCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 928
 DB 792 AGCTACAGACATGACCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 851
 QY 929 CAGTCCGCTCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 988
 DB 852 CAGACCTTTTATTTGCTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 911
 QY 989 GGGGTGCGACATTTCTGCTTGAATGTGACGCTTGAATTTCTTATC 1048
 DB 912 GGTATCGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 971
 QY 1049 GAGAGGCTGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 1108
 DB 972 GAGAGGCTGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 1031
 QY 1109 TGCTGACACCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 1168
 DB 1032 AGCTTCAACCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 1091
 QY 1169 GAGAGGCTGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 1228
 DB 1092 GAGAGGCTGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 1151
 QY 1229 GAGAGGCTGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 1288
 DB 1152 GAGAGGCTGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 1211
 QY 1289 CGCAGGCTGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 1348
 DB 1212 AGGAGGCTGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 1271
 QY 1349 GCGACGCTGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 1405
 DB 1272 TTGCGGCTGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 1331
 QY 1406 CAGGCGCTGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 1462
 DB 1332 CAGGCGCTGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 1391
 QY 1463 AACACCGCTGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 1484
 DB 1392 AACACCGCTGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 1413

RESULT 5
 AAD01352
 ID AAD01352 standard; cDNA; 1934 BP.
 XX AAD01352;
 AC
 XX
 XX 12-OCT-2000 (first entry)
 DT
 XX
 XX Soybean sphingolipid desaturase cDNA #2.
 DE
 XX
 XX Soybean sphingolipid desaturase; membrane-bound desaturase;
 KW transgenic plant; fatty acid; ss.
 XX
 XX Glycine max.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 305..1657
 FT /tag= a
 FT /product= "Sphingolipid desaturase"
 XX

PN W0200032790-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 02-DEC-1999; 99MO-US28589.
 XX
 PR 03-DEC-1998; 98US-0110784.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 XX
 PI Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;
 XX
 DR WPI; 2000-412336/35.
 DR P-PSDB; AAY71554.
 XX
 PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries
 XX
 PS Claim 2; Page 46; 57pp; English.
 XX
 CC The present sequence is a cDNA encoding sphingolipid desaturase
 CC from clone sbl.pk0017.b4.15 isolated from soybean seedling cDNA
 CC library, sbl. The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is also useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
 XX
 SQ Sequence 1934 BP; 505 A; 367 C; 448 G; 614 T; 0 other;

Query Match 27.2%; Score 479.8; DB 21; Length 1934;
 Best Local Similarity 60.9%; Pred. No. 1.4e-87;
 Matches 816; Conservative 0; Mismatches 517; Indels 6; Gaps 2;

QY 155 ATCTCTCCAGAGCTCCGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 214
 DB 335 ATACTCTCCAGAGCTCCGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 394
 QY 215 GCGAGCTGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 274
 DB 395 GGTAGGCTGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 454
 QY 275 CTACCTCTGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 334
 DB 455 TCACCTCTGCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 514
 QY 335 CGCGCTCTCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 391
 DB 515 TGCTCTCTTCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 574
 QY 392 GCGTCTCTTCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 451
 DB 575 GTGTCTCTTCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 634
 QY 452 GTGTCTCTTCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 511
 DB 635 AAGGCTCTTCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 694
 QY 512 TACCTCTCTTCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 571
 DB 695 TATGCTCTTCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 754
 QY 572 TTGCTCTTCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 631
 DB 755 TTGCTCTTCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 814
 QY 632 CATCTCTCTTCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 691
 DB 815 ACCAATGCTTCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 874
 QY 692 ATGCTCTGCTTCTTCTTCAACGCTTGAATGTGACGCTTGAATTTCTTATC 751

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Db      875 ATGCTGTGGAGAGGAGCTACAAATGCTCAACCAATGCGGCAACAGCCTTGACCAT 934
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Db      995 ACCTCTCATTTCTATGAGGAGAGAGTTGAGTTGATTTCTATGCTAGTTCTTGATCTGC 1054
Qy      872 TACCACTGAGACCTTCTACCCGATATGTCATGCGCAGATTAATCTTCTCGGCGAG 931
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Qy      932 TCCGCTCTGCTTCTTCTACGAGAGAGAGGCTGCCAGGCTTGTGATGCTCGGCGG 991
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Qy      992 GTCCGCAATTCCTGAGCTGTGTACCCGCTTCTGCTGCTGCTTCCCTGCGAATGCTGGAG 1051
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Qy      1412 AAGACCGCTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1471
Db      1595 AAGGACTTAACA--ACCTGCGCTTAAGAAATTTGTTGAGGAGGAGGAGGAGGAGGAGG 1651
Qy      1472 GGATTAATGAGATGAAGAT 1490
Db      1652 GGCTGAGCATTTGGAGTT 1670

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XX AAC42244;
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XX 17-OCT-2000 (first entry)
XX
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XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
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XX
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Query Match 25.6%; Score 452; DB 21; Length 1465;
 Best Local Similarity 60.4%; Pred. No. 5, 6e-82;
 Matches 781; Conservative 0; Mismatches 505; Indels 6; Gaps 2;

QY 189 CCGACGACCTTGTGATCTCTGATCTCCGCGAGCGTGTACGACGTCAGCCCTGCTCCCC 248
 DB 177 CTGGAGATTATGATTGATTGATTCAAGTTAAAGTTTACAGCTTTCGATTGGTTAAAT 236
 QY 249 ACCACCGGCGGCGGAGCTCCGCTTCTACCCCTGCGGGGAGAGCGCCAGCGCCT 308
 DB 237 CTGATCCGAGCGGAGAGAGCGATTTCTCATCTCGCCGCGCAAGCTTACCGAGCGCT 296
 QY 309 TCGCCGCTTACCAACCGGCGCTCGCGCGCGCGCTCTCTCGCGCGCTTCTTGTGGC--C 365
 DB 297 TCATCGCTTACATCCCGAAGCGCATGGACACACTTAAGAAAGTTTCAATGCTATC 356
 QY 366 GCGTCTGTGATGAGCGGCTCTCCCGCGCTCCGCGAGCTACGCGCGCGCTCTCGCCAGC 425
 DB 357 ACCTGAGAGACCAACGAGTGTACAGAGTGTACAGTACTACGTCTTAAAGCGCGAGT 416
 QY 426 TATCTCCGCGGCGCTTCTGAAAGCGGTGCGGCCACCCCAAGGTCCAGTGTCTGA 485
 DB 417 TCTCAAGCGGCGCTTCTGACAAAAAAGTACGTACTCTTTACACATCACTGCGG 476
 QY 486 TGGCGCTCTCTTCTTACGCGCGGCTGTACCTGCTCTGATCCGCGAGCGCTGGGCGC 545
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 QY 546 ACCTCTCTCGGCGGCTCTGATGCTGTCTGTGATTCAGTCCGAGTGGAGCGAG 605
 DB 537 ACCTCATCTCGCGGCTTACTGCTCTCTCTGATTCAAAGCGCTTACGTCGCGCAG 596
 QY 606 ACTCGGCGCACCAACCGCATTCACCGGCGATCCGCTCTCTGACCGCGCTGTGAGGTCTCT 665

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Db      597  ATTCGGGTCACAGGTCACGTCACCAACCGGTAAACCAATATCCAGCTTCTCT 656
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Db      657  CCGGTAACTGTCTCACCGGATCTCAATCGGTGGTGAATGAGCAGCAACGCTCAC 716
Qy      726  ACATGCGCTGCAACAGGCTGAGCAGTACCGGACCTCCAGCAGATGCGCTCTTGCCG 785
Db      717  ACATGCGTGTAAACAGCTTACAGCATGCGGATCTACAAACATCCGATCTTGCCG 776
Qy      786  TCTCCCGCAAGCTGTGGCAATATGTCTTACTTTCACACGAGCCCTGGCTTCG 845
Db      777  TCTCTCAAAATCTTCAATTCATGACGTCACGTTTCTATGACAGAAATTAACATTCG 836
Qy      846  ATGCGCGCTCGAAATCTTATGACGTCACGAGCAGTACGAGCTTACCCGCTAATGTGA 905
Db      837  ATCTCTAGTCGATCTTAAATGACGTCACCAACAGTGAATTTACCCAGTATGTGCG 896
Qy      906  TCGCCAGATTAATCTTCTCGCGCAGTCGCGCTGTCTCTACGAGAAAGAGGTGC 965
Db      897  TCGGAAGATCAACCTTCTATCCAAACATTCCTATTGCTATCTGAAACGCACTCC 956
Qy      966  CCGAGCGGTGCTTGAGATGCGGGGTCGCCAATCTGAGGCTGTGTAACCGTGTGG 1025
Db      957  CAGATCGGGCTTGAAATCGCGGATTTAGTTTCTGACATGTTCTCTCTTAG 1016
Qy      1026  TGGCTTCCCTGCGGAATGTGGAGAGGCTGCGCTTGTGCTTTCAGCTTACCATCT 1085
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XX      XX  Arabidopsis thaliana.
XX      OS  EP1033405-A2.
XX      PN  06-SEP-2000.
XX      PD  25-FEB-2000; 2000EP-0301439.
XX      PF  99US-0121825.
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RESULT 7
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XX 18-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 68612.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.

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 DB 268 CTGGAGATCTATGATCGCGATTCAAGGCTTACACGTCCTCGATTGATTA 327
 QY 249 ACCACCCGGGCGGCGACCTCCCGCTTCTGACCCCTGGCGGGGAGAGCGCCACCGACCT 308
 DB 328 CTATCCCGGAGGCGACAGGATATCTCAATCTCGTGGTCAAGACGTCACGATGCTT 387
 QY 309 TCGCCCGCTACACACCC---GCCCTGGCGCGCCCGCTTCTCCCGCCCTTCTTGCGCC 365
 DB 388 TCATCGCATTTCAATCCCGGAAACCGCTTGGACCATCTGACCAATCTTTCACCGGTTACC 447
 QY 366 GCCTCTCTGACTAGCGCGCTCTCCCGCGTCCGCGGACTACGCGCCGCTCTCCGCGAGC 425
 DB 448 ACATCAGAGATTTTCAAGTCTCCGAGTCTCAGCGCATTAACGTCGATGAGCGCGAGT 507
 QY 426 TATCTCCGGGGGCTCTTGAACGGGTGGGCCCCACCCCAAGTTCAGCTGCTCTGA 485
 DB 508 TTGTAACCTGGCTCTTTCGAAAAACAAGTCAAGTCACTCTCTACACTGAGCTTGC 567
 QY 486 TGGCGCTCTCTTCTACGCGCGCTGACTGCTCTCTCGATGCGGACGCGCTGAGCGC 545
 DB 568 TCGCCGCGCATGTTCCCTCGGAGTCTCTACGAGTCTTGGCTTGTACTCTCGTTCGCTC 627
 QY 546 ACCTCTCGCGGGGGGTCTCATTTGCTTGTGATTCAGTCCGCGCTGGATGGGCGACG 605


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Db      628 ACCAAATCCGCGCGCGCTTCGTCTCTCTGATCCAGACGGCTTACATAGTCACG 687
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Qy      666 CCGGGAATGCTCTCACCGGCTCAGCATCGCTGTGTGAAGTGTAAACCAACACGACGACC 725
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Qy      726 ACATGCGCTGTGCAACAGCTGTGACCATGACCCGACCTCCAGACATGCGCTCTTTGCCG 785
Db      808 ATCTAGCTGTGAACAGCTGTGATTAAGATCAATGATCAACAACATCCCTGTCTTGCCG 867
Qy      786 TCTCCCCCAAGCTGTGTGCAATATGATCTCTTCTTCAACGAGACCTTGCGCTTG 845
Db      868 TCTCCACCAATCTCTCTCTCATGACCTGAGATCTTACGATCGGAACTCACGCTTG 927
Qy      846 ATGCGGCTGTGAATCTTCTCATGAGTACGAGACTGAGACCTTCTACCGGTAATGTGA 905
Db      928 ATCTAGCTGTGAACAGCTGTGATTAAGATCAATGATCAACAACATCCCTGTCTTGCCG 967
Qy      906 TCGCAGATTAATCTCTGTGCGCAGTCCGCTGTCTGTCTTCAACGAGAGAGGCTGC 965
Db      988 TTGGAAGATCAATCTCTCTCATGACCTGAGATCTTCTCTCTTCTCTCAACGTAAGTAC 1047
Qy      966 CGGAGGCTGTGATGATGCGGCGGCTGCCACATTTGGGCTGTGATCCGCTGTG 1025
Db      1048 CAGATGTGTCTTAACTTCTCGCGGAACTTCTGTAATCTTCTGTAATCTTCTCTCTCT 1107
Qy      1026 TGGCTTCCCTGCGGAAATGCTGTGAGAGGCTGCGGCTTGTGCTTTCAGCTTACCATCT 1085
Db      1108 TCTCATGTCTTACCAACTGCGCTGAGAGATCTTCTCTGCTTCAACAGCTTACCGTCA 1167
Qy      1086 GCGGGAATGACAGCTTCAATTTGCTGTAACCACTTCTGCTGCGAGTGTATGTGCGGC 1145
Db      1168 CGGCGCTTAAACATTTCAATTTCAACGCTTAACTTCTGCTGTAATGCTTACGTTGCT 1227
Qy      1146 CACCCAAGGCAATGATGCTGTGTAAGAGACAGCGGAGCGCTGTGATCTCTGCT 1205
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Qy      1206 CTCTTGTGATGATGCTGTGTAAGAGAGCGCTGTGATGTAAGAGCGCTGTGCT 1265
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Qy      1266 CCGGCTTACCTCGGTGCAACCTTTCGCAAGGTTGCAACGCGCTGCGGACCTTTGCAAG 1325
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RESULT 8
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AC AAZ44833:

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XX      27-APR-2000 (first entry)
DT      A. thaliana sld1 DNA.
XX      Sphingolipid desaturase, sld1; sphingobase; ceramide; capnoid;
DE      transgenic plant; crop plant; delta-8-unsaturated long-chain base;
XX      tolerance; resistance; soil salinity; ion stress; toxicity; drought;
XX      cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
XX      pharmaceutical; food; chemical raw material; ds.
XX      Arabidopsis thaliana.
OS      Key Location/Qualifiers
FH      CDS 172..1521
FT      /tag=a
FT      /product="sphingolipid desaturase"
XX      .DE19828850-A1.
XX      30-DEC-1999.
XX      27-JUN-1998; 98DE-1028850.
XX      27-JUN-1998; 98DE-1028850.
XX      (GVSE-) GVS GBS ERWERB & VERM LANDWIRTSCHAFTLICH.
XX      Heinz E, Zaehring U, Schmidt H, Sperling P;
XX      P-PSDB; AA51334.
XX      WPI; 2000-127549/12.
XX      P-PSDB; AA51334.
XX      New sphingolipid desaturase that selectively introduces double bond
XX      into sphingolipids and capnoids -
XX      Claim 11; Fig 3; 62pp; German.
XX      This invention describes a novel sphingolipid desaturase that selectively
XX      introduces a double bond into the sphingobase of the ceramide residue of
XX      sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
XX      desaturase, or a vector containing the DNA sequence, can be used to
XX      produce transgenic plants, especially crop plants, with an increased or
XX      decreased delta-8-unsaturated long-chain base content or an altered
XX      delta-8-unsaturated long-chain base cis/trans ratio, especially to
XX      compensate for a delta-8-unsaturated long-chain base deficiency, to
XX      exclude production of delta-8-unsaturated bases, to increase tolerance
XX      or resistance to soil salinity, ion stress or toxicity, drought, wet
XX      conditions, cold or frost and/or phytopathogenic microorganisms, or to
XX      alter size growth and flowering time. Cells, transgenic organisms or
XX      plants containing the DNA sequence can be used to produce sphingolipids
XX      and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
XX      can be used in cosmetics, pharmaceuticals and foods and as chemical raw
XX      materials. This sequence encodes the Arabidopsis thaliana sphingolipid
XX      desaturase sld1 protein described in the method of the invention.
XX      Sequence 1678 BP; 416 A; 408 C; 339 G; 515 T; 0 other;
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Query Match 25.2%; Score 445; DB 21; Length 1678;
Best Local Similarity 59.3%; Pred. No. 1.5e-80;
Matches 795; Conservative 0; Mismatches 540; Indels 6; Gaps 2;

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Qy      249 ACCACCCGCGCGGACCTCCGCTTTCACCTGCGCGGAGAGAGCGGACCGAGCGCT 308
Db      293 CTCATCCCGAGGCGACAGCGTGTATCTCACTGTGTGTAAAGCGTACCGAGTCTT 352
Qy      309 TCGCGGCTTACCAACC--GCCCTGCGCGCGCTCTCGCGGCTTCTTGTGTGCGC 365
Db      353 TCATGCAATTTATCCCGGAACCGCTTGGCACATCTGACCATCTCTTACCGGTTACC 412

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OY	426	TATCTCCGCGGGCTCTTCGACGCGTGGCCCCACCCCAAGGTCAAGTCTGTCTGA	485
Db	473	TTTCGTAACTGGGTCTCTTCGAAAAAAGGTCAGTTACTCTTACACTGTAGCCTTCG	532
OY	486	TGGCGGCTCTCTTTCAGCGCGGCTGTACTGTCTCTCGAATAGGCGCGCTCGGGCG	545
Db	533	TGCGCCCATGTTCTCGGAATGTTCTACGGGTGTTTGAGCTTGTAACCTCCGCTTCGCTC	592
OY	546	ACCTCTTCGCGGGGGGTCTCATTTGGCTTCGTGTGATCCAGTCCGGCTGATGGGCCACG	605
Db	593	ACCAATATGCGCGCGCGCTTCGCTGTCTCTGTGATCCAGCGGCTTAAATAGGTCAAG	652
OY	606	ACTGGGGCCACCGCATTCACCGGCAATCGGCTCTGACCGCGTCTGTGAGGTGCTCT	665
Db	653	ATTCTGGTCATTTACGTTATGTCGAACAACTTTATTAACAGATTCGCTCAGCTTCCT	712
OY	666	CCGGAAATGGCTCAACCGGCTCAGCATTCGCTGTGTGAAGTGTACACAACGACAC	725
Db	713	CCGGTAATGTTCTACCGGAATCTCAATCGGTGTGAATGACTACAAATGCTCATTC	772
OY	726	ACATTCGCTGAACGCTGGAACATGACCCGGACCTCAGACATGCGCTCTTTGCGG	785
Db	773	ATCTAGCTGTGAACGCTTCGATTCAGATTCAGATCTCAACACATCCCTGCTTCGCGC	832
OY	786	TCTCCCCCAAGCTGTTGGGCAACATATGTCCTACTTCTACCAAGGAACTCGGGCTCG	845
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OY	846	ATGCGCCCTCGAATTTCTTCATCAGCTACAGACTGGAACCTTCAACCGGTAAATGTCA	905
Db	893	ATCCAGTGGCGAGATTTTAGTCAGCTATCAACCTTTACTATTAATCAAGTTATGTGCT	952
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Db	953	TTGGAAAGATCAATCTCTTCATTCAAAGTTCTCTTCTCTTCCAAACGTGAAGTAC	1012
OY	966	CGCAGCGGTCCTAGATTCGCGGGGGTGCACATTCGGGCTTGTGATCCGGTGTGG	1026
Db	1013	CAGATCGTGCTTTAACTTCGCGGAAATCTTAGTCTTCTGACCTTGTTCCACACTTTAG	1072
OY	1026	TGGCTTCCCTCGGAATGTGGGAGAGGGTGCCTTTGTGCTTTTCAAGTTCAACATCT	1085
Db	1073	TCTCATGTCTACCAAACTGGCGCTGAGAAATTTCTTGCTTTCACAAAGCTTCAACGCTCA	1132
OY	1086	GCGGGAATCAGACGTCGAATTCGTCCGGAACACTTCCTGTGCGACGTATATGTCGGG	1145
Db	1133	CGGCGCTTCAACATTCATTTACGCTTAACTTTGCTGTATGTCTACGTGTGCT	1192
OY	1146	CACCCAAAGGCAATGACTGTGTTGAAGACAGACGGCAGGCACTGTCACATCTGTGCT	1205
Db	1193	CACCCAGCGGTAGCGACTGTGTTCGAAGAAAGCAAGCGCGGGAACATTCGATCTTGTGA	1252
OY	1206	CTCTTGGATGATTTGTTTCCAGCGGTGCTGTCAAGTTCCAGATTGAGCAACATCTGTTTC	1265
Db	1253	GATCATCATGATGATTTGTTTGTGTGATTAACAATTTCAAGCTTAGGATCATTTGTTTCC	1312
OY	1266	CCCGCTACCTCGGGCCACTTGGCAAGGTGACCGGCGGTGCGGCACTTTGACAGA	1322
Db	1313	CTCGCTTACCTGTGGCAATCTCCGGAAGTTTCTCCGGTGTTCAAAGACTTTTCAMGA	1377
OY	1326	AGCATGAGCTCATTTATTCAGACCAATTCGTGGGTGCAAAATGTGCTTATCATGGAAGA	1385
Db	1373	AGCATTAATCTTCCGATAGAGATATGTGCTGTTTGAAGCAAAATGTGTAACATTAACA	1433
OY	1386	CACCTAGGGCTGTCTGATTCGACGGCAGAGACCGCTAACAGTGTGTGTCTCCGAAGAATT	1444
Db	1433	CTTGTGAACACGACCTTATCAAGGTGTAGAGAGTGTGTATTCGGGTGTT---AAGAACT	1485

Oy		1446	TGGATGTGAGAGCGCTGTAAACCCCATGTGATAAATGGATGAAGAATACGGCTAATGCCAA	1505
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KM	Hybridisation assay; genetic mapping; gene expression control;			
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KX	metabolic pathway; promoter; termination sequence; SE.			
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PD	06-SEP-2000.			
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PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.

PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148855.
PR 13-AUG-1999; 99US-0148884.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149829.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 25.0%; Score 441.8; DB 21; Length 1650;

Best Local Similarity 59.1%; Pred. No. 6, 6e-80;

Matches 793; Conservative 0; Mismatches 542; Indels 6; Gaps 2;

Qy 189 CCGAGACCTCTGATCTTCATCTCCGGGACGTGTACGACGTACGCGCTGCTCCCC 248
Db 266 CTGGAGATCTATGATCGGATTCACAGGCAAGTCTACAAAGCTTCGATTGGATTAAA 325

QY 249 ACCACCGGCGGCGACCTCCCGTCTCAACCTGGCGGGGAGAGACCCAGCCGCT 308
 Db 326 CTGATCCCGGAGGCGACAGCGTATCTCATCTCGTGGTCAAGACTACCGATGCTT 385
 QY 309 TCGCCCGCTTACCAACC--GCCCTGGCGCGCCGCTCTCCGCGGCTTCTGTTGGCC 365
 Db 386 TCATCGCATTTCAATCCCGGAACCGCTTGGACCATCTGCACATCTCTTACCGGTTACC 445
 QY 366 GCCTCTCTGACTACCGCTCTCCCGCGCTCCGCGACTACCGCGGCTCTCGCGAGC 425
 Db 446 ACATTCAGAGATTTCCAAAGTCTCCGAATCTACCGGATACCGTGTATGAGTCCGAGT 505
 QY 426 TATCTCCGCGGCGCTCTTGAAGCGCTCGGCCACCCCAAGATGACATCTGCTTGA 485
 Db 506 TTGCTAAATCTCGGCTCTTGGAAAACAAGGTACAGTTACTCTCTACACTTACCTTCCG 565
 QY 486 TGACCGCTCTCTTCTACGCGCGCTGTACTCTGCTCGATGCGGACGCGCTGGGCGC 545
 Db 566 TCGCCGCGCATGTTCTCTAGAGTTCTTACGAGTGTGTTGGCTTGTACTCTCGTCTTGGCTC 625
 QY 546 ACCTCTCGCGGGGGGCTCTATGGCTTGTGCTTGTGATTCAGTCCGCTGATGGGCGACG 605
 Db 626 ACCAAATCGCGCGCGCTTCTCGGCTCTCTGATTCAGAGCGCTTACATAGGCTACG 685
 QY 606 ACTCGGCGCACACCGCATCAGCGCCATCCGCTCTCGACCGCGTGTGAGGCTGCT 665
 Db 686 ATTCTGTCTATTAGCTTATATGATGCGAACTTTATTAACAGATTCCTCAGCTTCTTCT 745
 QY 666 CCGGGAATCTCTACCGCGCTTACAGATGCTGTGGAAGTGTACACAGACGCGACC 725
 Db 746 CCGGTAATCTCTACCGGAATCTCAATCGGTGTGAATGGAATCAACAATGCTCATC 805
 QY 726 ACATGCTGTCAACAGCTGTGACCATGACCCGAGCTTCCAGACATGCGCTCTTGGCCG 785
 Db 806 ATCTAGCTGTCAACAGCTGTGATTAAGATCAAGATCAACAACATCTCTGCTCCGCG 865
 QY 786 TCTCCCGCAAGCTGTGTGGCAACATATGCTCTACTTCTACCAACGAGACCTGGCGCTTG 845
 Db 866 TCTTCACCAAAATCTTCTCTCTCATTAAGCTGAGATTTCTACGATCGAAATCAAGCTTGG 925
 QY 846 ATGCGCGCTTGAATTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 905
 Db 926 ATCAAGTCGGAATTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 985
 QY 906 TCGCCAGATTAATCTTCTCGCGAGTCCGCGCTGCTTCTCAAGGAGAGAGAGGTC 965
 Db 986 TTGGAAGATCAATCTCTTCAATCAACGTTTCTTCTCTTCTCTCAACGTAAGTAC 1045
 QY 966 CGGAGCGGTTGTTGAGATGCGGCGGGTCCGACATCTGGGCTTGGTACCCGTTGGTGG 1025
 Db 1046 CAATGCTGCTTAAACTTGGCGGGAATCTTAAGTCTTCTGAGCTTGGTTCCTACTTGA 1105
 QY 1026 TGGCTTCCCTGCGGAATTTGTGGAGAGAGGTGCGGTTTGTCTTTCAGCTTCAACATCT 1085
 Db 1106 TCTCATGCTTACCAAACTGCGGAGAGATTTCTTCTTCTTCAAGGCTTCAACGCTCA 1165
 QY 1086 GCGGAGTTGAGAGTCAATTTGCTGTAACCACTTCTGTCGAGAGTGTATGTGCGGC 1145
 Db 1166 CGGCGCTTCAACATCTTCAATCAACGCTTAAACATTTGCTGTGATGCTTACGTTGCTC 1225
 QY 1146 CACCAAGGCGCAATGACTGTTGAGAGAGAGAGCGGAGGACGCTGAGATCTGTGCT 1205
 Db 1226 CACCAAGGCGCAATGACTGTTGAGAGAGAGAGCGGAGGACGCTGAGATCTGTGCT 1285
 QY 1206 CTCTTGATGATTTGTTTCAAGTGTGCTGAGTTCAGATTTCAACATCTGTTTTC 1265
 Db 1286 GATCATATGATGATTTGTTTCTTGTGATTTAAGTTTCAAGTTTCAACATTTGTTTTC 1345
 QY 1266 CCGGCTACTCGGTGCGCTTTCGACAGTTGACGCGCGCTCGGACCTTGGCAAGA 1325
 Db 1346 CTGCTTACTCGGTGCGCTTTCGACAGTTTCTCGGAGTGTTCAGAGACTTGGCAAGA 1405

QY 1326 AGCATGGGCTCACTTATTTCTGACGCCACATTTCTGGGTCGAATGTCTTACATGAGAGA 1385
 Db 1406 AGCATATATCTTCCGTATAGAGATATGCTGTGTTGAAGCAAAATGTGTGACCATTAACA 1465
 QY 1386 CACTCAGGCTGTGCTGATTTGACGAGCAGACCGCTTCAAGTGTGTCTCCGAAGATT 1445
 Db 1466 CTTTGGAAGACAGAGCTTATCAAGCTAGAGACCTGTATCCGATGCTT--AAAGACT 1522
 QY 1446 TGGTATGGAGGCTGTGAACACCATGATTAATGGATGAGATTCGAGGCTAATGCAAA 1505
 Db 1523 TGGTTGGAGAGCTTTGAATTAATCAATGCTAATGATTTTATCAAAAATAATGCTT 1582
 QY 1506 CTCTGTGATTTCACTGCTGAGT 1526
 Db 1583 TTGTTGGGTTAATTTGATG 1603

RESULT 10
 AB212753
 ID AB212753 standard; DNA; 1350 BP.
 XX
 AC AB212753;
 XX
 DT 21-JAN-2003 (first entry)
 XX
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 558.
 XX
 KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 PN MO200216655-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 24-AUG-2001; 2001MO-US26685.
 XX
 PR 24-AUG-2000; 2000US-227866P.
 PR 26-JAN-2001; 2001US-264647P.
 PR 22-JUN-2001; 2001US-300111P.
 XX
 PA (SCRI) SCRIPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Harper JF, Kreps J, Wang X, Zhu T;
 XX
 DR WPI; 2002-304127/34.
 XX
 PT Identifying a stress condition to which a plant cell has been exposed
 PT and producing plants with increased tolerance to these abiotic stresses
 XX
 PS Claim 6; SEQ ID NO 558; 577pp + Sequence Listing; English.
 XX
 CC The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising:
 CC (a) contacting nucleic acid representative of expressed polynucleotides
 CC in the plant cell with an array or probes representative of the plant
 CC cell genome; and
 CC (b) detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
 CC in methods of the invention.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied to Derwent by
 CC the European Patent Office.
 XX
 SQ Sequence 1350 BP; 325 A; 359 C; 274 G; 392 T; 0 other;
 Query Match 24.9%; Score 439.2; DB 24; Length 1350;
 Best Local Similarity 59.8%; Pred. No. 2.1e-79;

CC plants containing the DNA sequence can be used to produce sphingolipids
CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
CC materials. This sequence encodes the *Brassica napus* sphingolipid
CC desaturase sld1 protein described in the method of the invention.

XX Sequence 1594 BP; 382 A; 369 C; 375 G; 468 T; 0 other;

Query Match 24.8%; Score 437; DB 21; Length 1594;

Best Local Similarity 59.7%; Pred. No. 6.1e-79; Mismatches 515; Indels 6; Gaps 2;

Matches 772; Conservative 0; Mismatches 515; Indels 6; Gaps 2;

189 CCGACGACCTCTGATCTCCAGCAGTGAAGACGTCACGCTGCTCCGCC 248
112 CCGAGATTATGATTTCAATCCAAAGCTACGAGCTCTCCCATGGTCAAT 171
249 ACCACCGGGGCGGACCTCCGCTTCTACCTCGGGGGGAGAGCCACGAGCT 308
172 CCGATCCCGGAGGCGAAGCAGCATCTTAACCTCGCGGTCAAGAGCTACGAGCT 231
309 TCGCGGCTTACCAACC--GCCCTGGGGGGCGCGCTCCCGCGCTTCTTGCGCC 365
232 TCAATGCTTACCAATCCCGAAGCGCATGCGCACTCGAAAACCTTCACAGCGCTAAC 291
366 GCGCTCTGACTACGCGCTCCCGCGCTCCCGCGCATACCGCGCTCTCGCGAGC 425
292 AGCTGAAGAGCAGCAGCTGCTCCGAGCTGCGGTGATCACTCGTTTACCGCGGAGT 351
426 TATCTCCGCGGCGCTTCTGAAAGCGTGGCCCGCCACCCCAAGTTCAGCTGCTGA 485
352 TTTCAAACCGGAGCTTCTGATTAATAAAGTCAAGTCTTACACGCTCAGCTGCG 411
486 TGGCGGCTCTCTTCTACGCGCGCTGATCTGCTCCCGGATCGCGAGCGCTGGCGC 545
412 TCGCTCCCATGCTCGCGCGGCTTGTATACGCTGTTGTGATGACAGATATGCGCC 471
546 ACCTCTCGCGGAGGCTCTATGCTTCTGATCTGATCCAGTCCGCTGATGGGCGACG 605
472 ACTTATATTCGCGGCTTCTGCTGCTGCTGATACGAGCGCTTACGTGGGACATG 531
606 ACTGGGAGCAGCAGCGCATCAGCGGCTGCTGAGCGCGCTGCTGAGCTGCT 665
532 ACTCTGCTATTAACAAGTACGTCACGAAGCGGTGATTAATACGCTGCTGCTGT 591
666 CCGGGAAGTGGCTTCCAGCGCTGATGCTGCTGATGCTGATACCAACAGCAGAC 725
592 CTGCTACATGATCAGCGGAGATATCGATCGGTGGGAAATGAGCAGATACGCTACC 651
726 ACATCGCTGCAACAGCTGATGATGATGATGATGATGATGATGATGATGATG 785
652 ATATCTCTTGTATATGCTTGTATGATGATGATGATGATGATGATGATGATG 711
786 TCTCCCAAGCTGTTTGGGACATATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 845
712 TCTCAACAAGTCTTAACTGATGATGATGATGATGATGATGATGATGATGATG 771
846 ATGCGCGCTGCAATCTTCTGATGATGATGATGATGATGATGATGATGATGATG 905
772 ATCTACTAGTCTGATCTTGTATGATGATGATGATGATGATGATGATGATGATG 831
906 TCGCGAGATTAATCTTCTGCGCAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 965
832 TGGGAGAGATCAATCTTCTTATCCAAAGTATCTTCTGATCTTCTGAGAGCTTACGTT 891
966 CCGAGCGGTTGCTTGAATGCGGAGGCTGCGCATCTGAGGCTTGTACCGCTGCTG 1025
892 CTGATGAGGCTTGAACATGCTGGGATCTTGTCTTCTGAGAGTGGTTTCTCTTTAG 951
1026 TGGCTTCTCTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1085
952 TATCTCTCTTACCAACTGGCAGAGAGATCACTTTTGTCTTTTAAAGATGGCGCTCA 1011
1086 GCGGATTCAGCAGTCAATTCGCTGTAACCACTTCTGCTGAGCTGATGCGGCG 1145

DB 1012 CCGGATTCAGCAGTTCAGTCTGTTTAAACCATTTTGGCGAGATGTTTACACGCTC 1071
QY 1146 CACCAAGGAGCATGACTGTTTGAAGACAGACCGCAGGACGCTGATCTGCT 1205
DB 1072 CCGCTAATGGAGAGATGTTTGAAGAGCAACGCTGATGATGATGATGATGATG 1131
QY 1206 CTCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1265
DB 1132 GGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1191
QY 1266 CCGGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1325
DB 1192 CTAGGCTACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1251
QY 1326 AGCATGAGCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1385
DB 1252 AGCATGATCTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1311
QY 1386 CACTCAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1445
DB 1312 CTCTGAGAGAGAGGCGGCTTCAAGCTAG--AGATGACTAATCTGCTTGGAGATT 1368
QY 1446 TGGTATGAGAGGCTGTAACACCATGATTA 1478
DB 1369 TGGTATGAGAGGCTGTAATCTGATGATGATGATGATGATGATGATGATGATG 1401

RESULT 12
AAZ44851
ID AAZ44851 standard; DNA; 1606 BP.
XX
AC AAZ44851;
XX
DT 27-APR-2000 (first entry)
XX
DE Sphingolipid desaturase DNA.
XX
KW Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
KW pharmaceutical; food; chemical raw material; ds.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 88..1464
FT /tag= a
FT /product= "sphingolipid desaturase"
XX
FN DE19828850-A1.
XX
XX 30-DEC-1999.
XX
PF 27-JUN-1998; 98DE-1028850.
XX
PR 27-JUN-1998; 98DE-1028850.
XX
PA (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
XX
PI Heinz E, Zaehring U, Schmidt H, Sperling P;
XX
XX WPI; 2000-127549/12.
XX
XX P-PSDB; AAY51348.
XX
XX New sphingolipid desaturase that selectively introduces double bond
XX into sphingolipids and capnoids -
XX disclosure; Fig 15; 62pp; German.
XX
XX This invention describes a novel sphingolipid desaturase that selectively
XX introduces a double bond into the sphingobase of the ceramide residue of

CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to
 CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered
 CC delta-8-unsaturated long-chain base c18/tra ratio, especially to
 CC compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 CC materials. This sequence encodes a sphingolipid desaturase protein
 CC described in the method of the invention.

XX Sequence 1606 BP; 412 A; 338 C; 370 G; 486 T; 0 other;

Query Match 21.0%; Score 370.2; DB 21; Length 1606;

Best Local Similarity 56.0%; Pred. No. 1.9e-65;

Matches 743; Conservative 0; Mismatches 578; Indels 6; Gaps 2;

155 ATCTCTCCAGAGAGCTCCGCGCTCAAGCTTCGCGAGAGCTTGATTCATTCCTCC 214
 142 ATAAACATCAAAAGAGTTAAAGACATTAACACCTTAATGACCTTGGATCTCAATTTTG 201
 215 GGGAGCTGATGAGCTGACGCTGCTCCGCTCCGACACCCGGGGCGGACCTCCGCTT 274
 202 GGGAAAGTTTACACCTTACAGATGGGCTAAAGACATTCGGGTGGCATGCCCCGTG 261
 275 CTCACCTCGGCGGAGAGAGCGCCAGACGCTTCGCGCTTACACCGCGCTTCGGCG 334
 262 ATTAACTGCGGGCGGAGATGTAAGTGAAGCATTTATGCAATTCACCGTACTGG 321
 335 CGCCGCTCTCT--CGCGCTTCTTCTGTTGGCGGCTCTGACTAGCGCGCTTCCCC 391
 322 TGGAGCATCTGAGACAACTATTCACCGGATCATCTTAAAGATTACAGAGTTTGCAC 381
 392 GGGTCCGCGAGCTACCGCGGCTCTCGGAGCATCTCCGCGGCGCTTTCGAGCGC 451
 382 ATTTCTAGAGACTACCGGAACTCGCTTGAAGATTGCAAAAGCGGTATGTTTGAAG 441
 452 GTGCGCCCAACCCCAAGGCTCCAGCTGCTGCTGATGGCGCTCTTCTACGCGCGCTG 511
 442 AAAGGTCAAGGTGTAATTTACTCATCTTGTTCGTCTGCTACTGCTTCCGCTGTG 501
 512 TACCTGCTCGCATGCGCCAGCGCTGCGGCGACCTCTCGCGGGGCTCTCATTTGC 571
 502 TATGGGTGTATATTCGGAAGCTTCTGATTCATATGCTTTTGGGGCGATATTGGGA 561
 572 TTGCTGTGATCCAGTCCGCTGATGAGGCGACGATCGGGCGACACCGCATCACCGC 631
 562 TTAGCATGATGAAATTTCTTATTTGGGTCAATGAGCGGGTCAATTAACAAATGATGG 621
 632 CATCGGCTCGTGAACCGCGCTGCGAGTCTCTCGGGAACGCTCTCCGCGCGCTCAG 691
 622 ACCCGGGGTGAACAAGTTTCCGGAATTTATGGAATTTGATAACCGGAATTAAC 681
 692 ATGCGCTGTGTAAGTGAACCAACACAGCAACCATGCGCTGCAACAGCTTGACAT 751
 682 ATGCGGTGTGGAATGAGCGATTAACGACATCATGCTGTGTAACAGTCTGATTAT 741
 752 GACCGGAGCTCGAGCATGCGCTCTTGGCGCTTCCCGCAAGTGTTCGCAACATA 811
 742 GATCTGATCTTCAGCATTTACGATTTAGCGGTCTTCTCCAAAGCTTTTAACTCAATA 801
 812 TGGTCTACTCTTACCAACGAGACCTGGGTTGATGCGCGCTCGAAATTTCTCATCAGC 871
 802 ACTTCTGTTTCTATGAGAGACGATTGACCTTTGACCCGTTTCTTCGAGC 861
 872 TACGAGACTGACCTTCTACCGGTAAATGATGCGAGATAAATCTTCTCGCGAG 931
 862 TACGAGACTTACTTATATTAACCGGATCATGATGATGCGCGGTCAACCTCTATTAACA 921

QY 932 TCCGCTGTTGTTCTCAGGAGAGAGGNGCCGAGCGGTGCTTGAGATCCGCGG 991
 DB 922 ACATCTCTGTTCTATTTCAAAAGAAAGATTCGCGAGAGTTTAACTACTCGGA 981
 QY 992 GTCCGACATTTGCGGCTTGTGTAACCGGTGCTGTGAGCTTCCCTCGGAATGTGGAG 1051
 DB 982 ACCCTATCTTCTGACGAGGTTTCGTTACTGTTTCTCGCTTACCGAATGCGCCGGA 1041
 QY 1052 AGGTCGGGTTTGTGCTTTTACGTTACATCTCGGAGTTTACAGCTGCAATTTCTCC 1111
 DB 1042 CGCGGGGGTGTGTGTGTTAGCTTCTGTGTAACGGGTATACACATATTCAGTTTACA 1101
 QY 1112 CTGAGCACTTCTGTCGAGCGTATGTCGGGCGCACCCGGAAGGGAATGATGTTGAG 1171
 DB 1102 CTGAACCATTTTCTGCGGAGTGTATTAAGTGGCCCGCCCAAAAGAGACATTTGTCGAG 1161
 QY 1172 AAGCAGCGGAGGAGCGCTGACATCTGTCCTCTCTGATGATGATTTGCCAGGT 1231
 DB 1162 AAACAAAGCGGTGGAGCATGATATCGGTTCTTCTTGATGATGATTTGTTTCGGA 1221
 QY 1232 GGCCTGCACTTCCAGATTGAGACCATCTGTTTCCCGCTTACCTCGGTGCCACTTCCG 1291
 DB 1222 GGTTTACAGTTTCACTTGAAGCATTTGTTTCTTAGGTTGCCAGGTTCTACTTGAAG 1281
 QY 1292 AAGTTGACCGGCGGCTCGGACCTTTGCAAGAGCATGGGCTCACTTATCTGACGCC 1351
 DB 1282 TCGATTTCTCTATATGTAGAGAACTTGCAGAAATATTAATTAATTAATGATTTG 1341
 QY 1352 ACATCTGCGGAGTCAAAATGTGCTTACATGAGAAAGACACTCAGGCTGTGATTTGAGCGC 1411
 DB 1342 TCGTTTATGATGCAATGTAGTACGACCTTGAAGAGCTTGAAGACGCGGCTTACAGGGA 1401
 QY 1412 AGGACCGTCAAGTGTGTGTGCTCGAAGAAATTTGTATGAGGAGCTGTGAACCCAT 1471
 DB 1402 CGTGACCTTACGA--ACCGGCCCCCAGAAATTTAGCTTGGGAAGCTTTCAACACCAT 1458
 QY 1472 GGATTA 1478
 DB 1459 GGTGAA 1465

RESULT 13

AAV34398
 ID AAV34398 standard; DNA; 1684 BP.

AAV34398;

02-MAR-1999 (first entry)

Borage delta-6 desaturase gene.

Upstream region; regulatory region; sunflower, albumin; seed; expression;

lipid metabolism; delta-6 desaturase; transgenic plant; ds.

Borage officialis.

Location/Qualifiers

key 43..1389

product="delta-6 desaturase"

primer_bind complement (616..632)

primer_bind 1165..1181

primer_bind 1165..1181

MO9845460-A1.

15-OCT-1998.

09-APR-1998; 98MO-US07178.

09-APR-1997; 97US-0831570.

XX (RHON) RHONE-POULENC AGROCHIMIE.
 XX Beremand PD, Nunberg AN, Thomas TL;
 XX WPI; 1998-583201/49.
 XX P-PSDB; AAM67471.
 XX
 PT New sunflower albumin 5' regulatory region - useful for directing
 altered lipid metabolism in plant seeds
 PS Example 2; Fig 1; 38p; English.
 XX This sequence is the gene encoding the borage (Borago officinalis)
 CC delta-6 desaturase enzyme. The lipid metabolism gene is an example
 CC of a heterologous gene which can be expressed at high levels in a
 CC seed-specific manner in transgenic plants, when placed under control
 CC of the sunflower albumin gene 5' regulatory region (AAV34397).
 XX
 SQ Sequence 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 other;
 Query Match 20.7%; Score 365.4; DB 19; Length 1684;
 Best Local Similarity 55.8%; Pred. No. 1.8e-64;
 Matches 740; Conservative 0; Mismatches 581; Indels 6; Gaps 2;

QY 155 ATCTCTCCAGAGAGCTCCGCGCTCAGCTCCGCGGAGACCTCTGATCTCATCTCC 214
 DB 67 ATTACCTCAGATGATCTCAGAAACACAGATTAACCCGAGATCTATGATCTGATTCAA 126
 QY 215 GGGCAGGTGATGACAGCTCAGCGCTCCGCTCCGCGGAGACCTCCGCTT 274
 DB 127 GGGAAAGCTATGATGTTTGGATTTGGATTTGAAAGACATCAGATGAGCTTCCCTTG 186
 QY 275 CTACCTCTGGCGGGGAGAGAGCGCAGCGCTTCCGCTTACCAACCGGCTTGGGG 334
 DB 187 AAGAGCTTGTCTGATCAAGAGGATCAATGATGATTTGCTCAATCTGCTCTTACA 246
 QY 335 CGCGCGCTCTCCGCGCTCTTCTGTTG---CGGCTCTCTGATGAGCGCTCTCCG 391
 DB 247 TGAAGAGATTTGATTAAGATTTTCTACGAGATTTATTTAAAGATTAATCTGTTTCTGAG 306
 QY 392 GCGTCCGCGAGTACCGCGCTCTCTGCGAGCTATCTCTCGGCGCTCTTGAAGCG 451
 DB 307 GTTCTTAAGATTAATGAGAGCTTGTGATTTGATTTCTAAATGGGTTTGTATGACAA 366
 QY 452 GTGCGCCCAACCCCAAGTCCAGCTCTGATGCGCTCTCTTCTTACCGCGCTG 511
 DB 367 AAGAGCTATTTATTTGATTTGCACTTTGTCTTATAGCAATGCTGTTGCTATGATGTT 426
 QY 512 TACCTGCTCTCGATGCGCGAGCGCTGAGCGAGCTCTCTCGGCGGCGCTCATTTGC 571
 DB 427 TATGGGCTTTTGTGTGTGAGGCTTTTGTGTATATTTGTTCTGTGGGTTTGTGATGGG 486
 QY 572 TTGCTGATTCAGTCCGCTGATGAGCGCAGCATCTGGGCGCAACACCGCATCACCGG 631
 DB 487 TTCTTTGATTCAGAGTGTGATGATGACATGATGCTGGGATTAATATGATGATGCT 546
 QY 632 CATCCGCTCTCAACCGCTGTGAGAGTCTCTCGGGAATGCTCTACCGGCTCAGC 691
 DB 547 GATTCAAGGCTTATTAATGATTTATGAGATTTTGTGCAAAATTTGCTTTCAGAAATTAAGT 606
 QY 692 ATGCGCTGATGAGATGATCAACAGCAACAGCAACATGCGCTGCAACAGCTGAGCAT 751
 DB 607 ATTGTTGATGAGAAATGAGAACTAATGCAATGCAATGCTCTGTAATAGCTTTGATAT 666
 QY 752 GACCCGAGCTCCAGCATGATGCGCTTCTGCGCTCTCCCAAGCTGTTGGCAACATA 811
 DB 667 GACCTGATTTACATATATATACATCTTGTGTGTCTTCAAGTTTGTGATCCTC 726
 QY 812 TGGTCTACTTTTACCAACGAGCGAGCTGCGCTGAGTCCGCTGAAATTTCTATCAGC 871
 DB 727 ACCTTCATTTATGAGAAAGGTTGACTTTGACTTTATACAGATTTCTTGAATG 786

QY 872 TACAGACAGTGCACCTTCTACCGGATATGATGATCGGAGATTAATCTTCTCGGAG 931
 DB 787 TATGACATTTGACATTTTACCTTATATGTGTGCTGATAGGCTCAATATGATATGACAA 846
 QY 932 TCCGCGCTGTTGTTCTACGAGAAAGAGGTGCGGAGCGGTTGTTGATGCGGG 991
 DB 847 TCTCTATATATGTTGTGACCAAGAAATGTGCTTATCGAGCTCAGGAACTTTGGGA 906
 QY 992 GTGCGCAATTCGCGCTGTTGATCCGCTGCTGAGTGGCTTCCCTGCGAATTTGAGGAG 1051
 DB 907 TGCCTAGTGTCTCGATTTGGTACCGGCTTGTGTTCTTGTGCTTAATTTGGGTTGA 966
 QY 1052 AGGTCGCTTGTGCTTCTTACGCTTCAACATCTGCGGATTCAGACCGTCCAAATCTGC 1111
 DB 967 AGAATATATGTTTATTTATGCAAGTTTATAGTACGATGAGATGAGAAAGTTCAAGTTCTGC 1026
 QY 1112 CTGACCACTTCTGTGCGACGTTATGTTGCGGCAACCAAGGCAATGACTGTTTGA 1171
 DB 1027 TTGACCACTTCTTCAAGTGTATGTTGGAAGCTTAAGGCAATATGTTGTTGAG 1086
 QY 1172 AAGCAGAGGAGGAGCAGCTGACATCTGCTCTCTGATGATGATGTTGCCAGGT 1231
 DB 1087 AAGCAAGAGATGAGGACACTTGAATTTCTTCTCTTGAATGATGTTGATGAT 1146
 QY 1232 GGCCTGAGTTCAGATTTGAGCAGCATCTGTTTCCGCGCTTACCTGCTGCGACCTTCCG 1291
 DB 1147 GATTTGATTTCCAAATTTAGATCATTTGTTTCCAAATGCTATGATGCAACTTAAG 1206
 QY 1292 AAGTTGACACCGCGCTCGGACCTTTGCAAGAGCATGAGCTCATATTTCTGAGCG 1351
 DB 1207 AAATCTCCGCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1266
 QY 1352 ACAATCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1411
 DB 1267 TCTTTCTCAAGGCAATTAATGATGATGATGATGATGATGATGATGATGATGAT 1326
 QY 1412 AGGACCGTACAAAGTGTGCTCCGAAATTTGATGAGAGGCTGTGAACACCAT 1471
 DB 1327 AGG---GATTTAACAAGCGGCTCCGAAATTTGATGAGAGCTTTCACTCAT 1383
 QY 1472 GGATTA 1478
 DB 1384 GGTTAA 1390

RESULT 14
 AAX24917
 ID AAX24917 standard; cDNA; 1684 BP.
 XX
 AC AAX24917;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Borage delta-6 desaturase cDNA.
 XX
 KW Delta-6 desaturase; borage; oleosin; At521; promoter;
 KW transgenic plant; seed, lipid; fatty acid; oilseed; vegetable oil;
 KW gamma-linolenic acid; octadecatrienoic acid; ds.
 XX
 OS Borago officinalis.
 XX
 FH Key Location/Qualifiers
 FT CDS 43..1389
 FT /tag= a
 XX
 PN W0845461-A1.
 XX
 PD 15-OCT-1998.
 XX
 PF 09-APR-1998; 98MO-US07179.
 XX
 PR 09-APR-1997; 97US-0831575.
 XX

PA (RHON) RHONE-POULENC AGROCHIMIE

PI Li Z, Thomas TL;
vv

DR WPI; 1999-180333/15
DR P-PSDB; AA098130

DR P-PSDB; AA98130.

PT Nucleic acid containing oleosin 5'-regulatory region - useful for
PT modulating fatty acid synthesis and lipid metabolism in plants,
PT particularly to increase content of gamma-linolenic acid
XX

PS Example 2; Page 59-61; 101pp; English.
XX

The present sequence encodes borage delta-6 desaturase (see *AAW98130*), an enzyme that catalyses the conversion of linoleic acid to gamma-linolenic acid (GLA). Delta-6 desaturase cDNA was isolated from a borage membrane-bound polysomal cDNA library using a partial clone, obtained from an EST database search, as probe. The borage delta-6 desaturase nucleic acid can be operably linked to the seed-specific 5' regulatory region (see *AAZ4916*) of the Arabidopsis thaliana oleosin At521 gene in claimed expression cassettes of the invention. Transgenic plants, e.g. sunflower, soybean, maize, tobacco, cotton, peanut, oilseed rape or Arabidopsis are obtained that show increased levels of GLA or octadecatrienoic acid. The levels of desirable fatty acids in oilseed crops can be manipulated to provide seed oils of use in human health and industrial applications.

SQ Sequence 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 other;

Query Match	20.78;	Score 365.4;	DB 20;	Length 1684;
-------------	--------	--------------	--------	--------------

Matches 740; Conservative 0; Mismatches 581; Indels 6; Gaps 2;

QY	155	ATCTCTCCAAAGAGGCTCCGGCGCTCAGCGTTCCGGCGAGCACTCTGATATCTCATCTCC	214
Db	67	ATTACCTCAGATGAACTTCAAGAACCAAGATTAACCCGAGATCTATGATATTCATTCA	126
QY	215	GCGCAGCTGTACGACGTCAAGCCCTGGCTGCTCCCAACCAACCGGGCGGAGCTCCGCTT	274
Db	127	GCGAAAGCCATATGATGTTTCGGATGGGGTGAAGAACATCCAGGTGGAGCTTCCCTTG	186
QY	275	CTCACCCTGGCGGGGAGAGAGCGCACCGACGCTTTCGCGCTACACCGGCTCTCGGGC	334
Db	187	AAGAGTCTTGCTGGTCAAGAGGTAATCTGATTTGTCATTTCAATCCGCTCTAC	246
QY	335	CGCGGCTCTCCGGCGGCTTTCTTGTTG - - CGGCTCTGACTACGCGCTCTCCCC	391
Db	247	TGGAAGATCTTGATATGATTTTCACTGGATTTATCTTAAAGATACCTGTTTCTGAG	306
QY	392	GCCTCCGCGACTACCGCGGCTCTCTCGGACGATCTCCGCGGGCTCTTGACAGC	451
Db	307	GTTTCTTAAGATTTATAGAAAGCTGTGTGATTTTCTAAATGGGTTGTATGACAA	366
QY	452	GTCGCCCCAACCCCAAGTCCAGCTCGTCTGATGGCGGTCTTCTACCGCGCTG	511
Db	367	AAGGTCATATTATGTTTCTCAACTTGTGCTTTATAGCAATGCTGTTTGCTATGAGTT	426
QY	512	TACTGTGCTCTGCAATGCGGCAGCGCTCGGGGCACTCTCGGGGGGCTCATTTGCG	571
Db	427	TATGGGATTTGTTTGTGTAGAGGTGTTTGTGATCAATTTGTTTCTGGGTGTTTGATGGG	486
QY	572	TTGCTGTGATCCAGTCCCGCTGSAATGGGCCAGACTCGGGCCACCAACCGCATACGGC	631
Db	487	TTTCTTTGATTCAGAGTGTGTTGATGTGACATAGTGTGGCATTTATATGTATGTCT	546
QY	632	CATCCGCTCTGCAACCGGCTGTGCAAGGTCTCTCGGAACTGCTTACCGGCTCAGC	691
Db	547	GATTCAGGCTTAATATAGTTTATGGGATTTTTCGTGCAAAATGCTTTCAGGAATAGT	606
QY	692	ATGCGCGGTGAAGTGAACCAACAACGCAACATGCGCTGCACAGCTCGAGACAT	751
Db	607	ATTGTTGTGGAAATGAAACCATATGCAATCAATGCTCTGTAATAGCTTGAATAT	666

QY	752	GACCCGGACCTCCAGCACAATGCGGCTTTTGCGCTCTCCCAAGCTGTCGGCACAATA	811
Db	667	GACCTGATTTACAAATATATACCATTCCTCTGTTGTGTCTTCCAAAGTTTTTGGTTCACTC	726
QY	812	TGCTCTACTTCTTACCAACGGACCTGCGCTGTGATGCGCGCTCGAAATTCCTCATCAGC	871
Db	727	ACCTCTCATTTATATAGAAAGAGTTGACTTTTGTGACTCTTATCAAGATTCCTTGTAAGT	786
QY	872	TACAGACATCGACCTCTTACCCGGTAAATGTCATGSCCAGATTAATCTTTCGCCAG	931
Db	787	TATTAACATTTGAAATTTTACCCCTATATATGTGTGTCTATGAGCTCAGAACTTTGGGA	846
QY	932	TCCGCCCTGTTCGTTCTCAACGAGAAAGAGGTGCCGACGCGTTTGCTTGAGATGCGCGGG	991
Db	847	TCTCTCATATGTTGTGTGACCAAGAAATGTGTCTATGAGCTCAGAACTTTGGGA	906
QY	992	GTCGCACATTCCTGGGCTGTGACCCGCTGCTGGTGGCTTCCCTGCCAAATGTGTGGAG	1051
Db	907	TGCTCATGTTCTTCGATTTTGGTACCCGCTGCTGTCTTGTTCCTTATGTGGGAGTGA	966
QY	1052	AGGTCGCCGTTTGTGCTTTTCACTTCCATCTGGGGATTTAGACAGTTCGAATTCGC	1111
Db	967	AGAAATATGTTGTATTTAGCAAGTTATCACTGATCTGGAATGCAACAAGTTCAAGTTCTCC	1026
QY	1112	CTGAACCATTCCTCTCGTCGACGCTGATGTGCGGCAACCAAGGGCAATGACTGGTTGAG	1171
Db	1027	TTGACACACTTCTCTTCAAGTGTATATGTTGAAAGGCTTAAGGAATATATGTTTGGAG	1086
QY	1172	AAGCAGACGCGACGACGCTGCAATCTGTGCTCTCTTGATGATGTGGTTCCACGCT	1231
Db	1087	AAACAAACGGATGGGACACTTTCATTTCTGTCTCTCTTGATGATGTGGTTTCATGCT	1146
QY	1232	GGCTGTGAGTTCCAGATTTGAGCAACATCTGTTTCCCGGCTTACTGGTGGCACCTTCGC	1291
Db	1147	GGATTCGAATTCCAAAATTGAGCAATCATTTGTTTCCAAAGATGCTTAAATGCAACCTTAGG	1206
QY	1292	AAGGTTGACACCGGCGCTCCGCGACCTTTGCAAGAGCATGGGCTCACTTATTTGCAACC	1351
Db	1207	AAATCTCGGCTTACGATGATGAGTTATGCAAGAAATATATTTGCCCTTCAATTAATGCA	1266
QY	1352	ACATTTGGGGGTGCAATGTGCTTACATGGAAGACACTCAGGCGCTGCTGCATTTGCAAGCC	1411
Db	1267	TCTTTCTCCAAAGCCCAATGAAATGACACTCAGAAACATTTGAGAAACACAGCATTTGCAAGCT	1326
QY	1412	AGGACCGCTTCAAGTGGTGTGCTCCGAGAAATTTGGTATGGAGGCTGGAACACCCAT	1471
Db	1327	AGG--GATATTAACCAAGCGCTCCGAGAAATTTGGTATGGGAAGCTCTTCAACATCAT	1383
QY	1472	GGATTAAT 1478	
Db	1384	GGTTAAAT 1390	
RESULT 15			
AAT30395			
ID	AAT30395 standard; DNA; 1685 BP.		
XX	AAT30395;		
AC	AAT30395;		
XX	15-SEP-1996 (first entry)		
DT	XX		
XX	XX		
DE	Borage delta-6-desaturase gene.		
XX	XX		
KW	Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;		
KW	polyunsaturated fatty acid; octadecatrienoic acid;		
KW	chilling resistance; oilseed; ss; ds.		
XX	XX		
OS	Borage officinalis.		
XX	XX		
Key	Location/Qualifiers		
FT	44..1390		
CD	/*tag= a		
FT			

XX MO9621022-A2.
 XX 11-JUL-1996.
 XX 28-DEC-1995; 95WO-1B01167.
 XX 30-DEC-1994; 94US-0366779.
 XX (RHON) RHONE POULENC AGROCHIMIE.
 XX Freysinet GL, Nuccio M, Nunberg AN, Reddy AS, Thomas TL;
 XX WPI; 1996-333997/33.
 XX P-PSDB; AAR98455.
 XX Transgenic plants comprising the borage delta-6-desaturase gene -
 XX show increased production of gamma linolenic acid and having
 XX increased resistance to chilling
 XX Claim 2; Page 51-52; 75pp; English.
 XX A DNA clone (AAT0395) codes for borage delta-6-desaturase (AAR98455),
 XX which catalyzes the conversion of linoleic acid to gamma-linolenic
 XX acid (GLA). It was isolated from a borage membrane-bound polyosomal
 XX library using probes based on abundantly expressed seed storage
 XX protein cDNAs and with an isolated partial cDNA clone. The gene
 XX can be incorporated into a vector, pref. incorporating a
 XX tissue-specific promoter, for the expression of delta-6-desaturase
 XX in transgenic plants, esp. sunflower, soybean, maize, tobacco,
 XX peanut, carrot or oilseed rape, resulting in increased GLA prodn.
 XX Alteration of plant lipids may also lead to improved chilling
 XX resistance.
 XX Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 other;

Query Match 20.7%; Score 365.4; DB 17; Length 1685;
 Best Local Similarity 55.8%; Pred. No. 1.8e-64;
 Matches 740; Conservative 0; Mismatches 581; Indels 6; Gaps 2;

QY 155 ATCTCTCCAGAGAGCTCCGCTCAGCTTCGCGGAGAGACTTGTGATCTCCATCTCC 214
 DB 68 ATTACCTCAGATGAATCAAGAAACAGATTAACCCGAGATCATGATCTGCATTCAA 127
 QY 215 GGGGAGCTGACAGAGCTGAGCCCTGCTCCCGACAGCCGCGGCGAGACTCCGCTT 274
 DB 128 GGGAAAGCTATGATGTTTGGATGGGTAAAGACCATCCAGGTGCACTTCCCTTG 187
 QY 275 CTCACCTGAGCGGGGAGAGAGCCAGCCGCTTCGCGCTACACCGCCCTCGGGG 334
 DB 188 AAGAGCTTGTGCTGACAGAGGTGATGATGATGATGATGATGATGATGATGATGAT 247
 QY 335 CGCGCGCTCTCGCGCGCTTCTTGCTG---CGGCTCTGATGAGCGGCTCTCCCG 391
 DB 248 TGAAGAGATCTGATTAAGTTTTCACGTGGATTAATCTTAAAGATGCTGTTTCTGAG 307
 QY 392 GCGTCCGCGACATACCGCGCGCTCTCGCGAGATATCTCCGCGGCTCTTGAAGC 451
 DB 308 GTTCTTAAAGATTAAGAAAGCTTGTGATGTTTCTTAAAGATGAGGTTGTATGACAA 367
 QY 452 GTGCGGCGGCGGCGGCGGCGGCTGCTGATGAGCGGCTCTTCTTACGCGGCGCTG 511
 DB 368 AAGAGTATATATATATGTTGCAACTTGTGCTTATTAAGCAATGCTGTTGCTATGAGTGT 427
 QY 512 TACCTGCTCTCGATGCGGAGCGGCTGAGCGGCACTCTCGGCGGCGGCTCTATGAGC 571
 DB 428 TATGGGCTTTTGTGTTGAGGGGTTTGGTACATTTGTTCTGGGTGTTGATGAGGG 487
 QY 572 TTGCTGATGATCCAGTCCGCTGATGAGGCGACGATCGGCGGCGGCGGCGGCGG 631
 DB 488 TTTCTTTGATGATGAGTGGTGGTGGTGGATGAGATGATGATGATGATGATGATGATGAT 547
 QY 632 CATCCGCTCTCGAGCGGCTGAGGCTGCTCTCGGGAAGTGGCTCACCGGCTGAGC 691

DB 548 GATTCAAGGCTTAATAGTTATGAGTATTTTGTGCAAAATGCTTTCAGAAATAGT 607
 QY 692 ATGCGCTGTGAGAGGTAAACCAACAGCAACCAATGCGCTGCAAGCGCTGAGCAT 751
 DB 608 ATGTTGTTGGAAAGAAAGCAATTAAGCAATCAATGATGCTGATATGCTGATAT 667
 QY 752 GACCGGAGCTCCAGACATGCGGCTCTTTCGCGCTCCCGCAAGCTGTTCGCAATTA 811
 DB 668 GACCTGATTTACAAATATATACCATCTTGTGTGTCTTCCAAAGTTTTTGGTTCACTC 727
 QY 812 TGGTCTACTTCTACCAAGGAGCTGCGGTGATGAGCGGCTGCAATTTCTTCAAGC 871
 DB 728 ACCTCATTTCTATGAGAAAGGTTGACTTTTGACTTTTATCAAGATTTCTTGAAGT 787
 QY 872 TACCAAGACTGAGACTTCTTACCGGTAATGATGATGATGATGATGATGATGATGAT 931
 DB 788 TATCAACATTTGACATTTTACCTATTAATGATGATGATGATGATGATGATGATGAT 847
 QY 932 TCCGCGCTGTTGCTCAAGGAGAGGAGGCGGAGGCTGATGATGATGATGATGATGAT 991
 DB 848 TCTCTATATATGTTGTTGACCAAGAAATGCTTATGAGCTGAGAACTTCTTGGGA 907
 QY 992 GTGCGCAATTCAGGCTTGTGTAACCGGTGCTGCTGCTTCCCTGCGAATGCTGAG 1051
 DB 908 TGCCTAGTGTTCGATTTGTAACCGGTGCTGCTGCTTCTGTTGCTTATGAGGTTGA 967
 QY 1052 AGGCTGCTGTTGCTTCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 1111
 DB 968 AGAATATATGTTGTTTTCAGAGTTTATAGTACGTGAATGCAAGTTTCAGTTCTCC 1027
 QY 1112 CTGACCACTTCTGTCGACGAGTATGTCGGGCAACCAAGGCAATGACTGTTGAG 1171
 DB 1028 TTAAACCACTTCTTCTTCAAGTATGTTATGTTGAAAGCTTAAGGAAATATGTTGAG 1087
 QY 1172 AAGCAGAGCGAGGAGCGCTGACATCTGTGCTCTCTTGAATGATGATGATGATGATGAT 1231
 DB 1088 AAGCAAGGAGTGGAGCACTTGAATTTCTGCTCTCTGATGATGATGATGATGATGAT 1147
 QY 1232 GGCCTGAGTTCAGATTAAGCAACATCTGTTTCCCGGCTTACTGCTGCTGCTGCTGCT 1291
 DB 1148 GATTTCAATTCGAAATTAAGCAATCTTGTGTTCCCAAGATGCTTATGATGATGATGAT 1207
 QY 1292 AAGTTGACCGGCGGCTGCGGAGCTTTCGAAAGATGAGGCTGATTTCTGAGCC 1351
 DB 1208 AATATCTGCGCTTACGATGATGAGTTATGCAAGAAACATTAATTTGCTTATGATGAT 1267
 QY 1352 ACATTTCTGGGTTGCAATGCTTATGATGAAAGACATGAGGCTGCTGATTTGAGGCC 1411
 DB 1268 TCTTTCTCAAGGCAATGAAATGACATCAGAAATGAGAAACAGATTTGAGGCT 1327
 QY 1412 AGGACGCTTAAGTGTGTGCTCCGAAAGATTTGATGAGGCTGTAACACCAT 1471
 DB 1328 AGG---GATATTAACCAAGCGCTCCGAAAGATTTGATGAGGAGCTTTCACACTCAT 1384
 QY 1472 GATATAA 1478
 DB 1385 GGTATAA 1391

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 Job time : 339.729 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:48:07 ; Search time 2688.35 Seconds
(without alignments)
15947.709 Million cell updates/sec

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Perfect score: 1764
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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27: em_estvrt:*
28: gb_est1:*
29: gb_est2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1764	100.0	1764	11	AY103762 Zea mays
2	662.4	37.6	825	BZ730996	OGEDJ37TM
3	588.8	33.4	744	14	CD463185 ETH1.42.C
4	559.4	31.7	634	12	BI075898 IPI_22_F1

5	546.6	31.0	609	12	BM322472
6	523.2	29.7	744	13 <td>BQ281359</td>	BQ281359
7	509.4	28.9	585	14 <td>CB381262</td>	CB381262
8	495.4	28.1	497	29 <td>BZ730988</td>	BZ730988
9	492.8	27.9	499	14 <td>CD484486</td>	CD484486
10	486	27.6	497	14 <td>CD484487</td>	CD484487
11	462.8	26.2	489	28 <td>BH785221</td>	BH785221
12	462.6	26.2	691	14 <td>B465389</td>	B465389
13	456.8	25.9	679	13 <td>CD230348</td>	CD230348
14	455.8	25.8	679	13 <td>B0788546</td>	B0788546
15	441	25.0	575	9 <td>AI691910</td>	AI691910
16	433.4	24.6	665	14 <td>CA502522</td>	CA502522
17	432	24.5	488	12 <td>BM323877</td>	BM323877
18	429.2	24.3	528	18 <td>BI075599</td>	BI075599
19	417	23.6	465	28 <td>BH229897</td>	BH229897
20	417	23.6	465	28 <td>BH230086</td>	BH230086
21	414	23.5	462	14 <td>CB278101</td>	CB278101
22	410.6	23.3	465	28 <td>BH229656</td>	BH229656
23	410	23.2	593	14 <td>CA498944</td>	CA498944
24	405.6	23.0	663	12 <td>B446983</td>	B446983
25	404.6	22.9	558	14 <td>CD230432</td>	CD230432
26	403.8	22.9	655	12 <td>B0309365</td>	B0309365
27	399.6	22.7	699	12 <td>B0321063</td>	B0321063
28	386	21.9	563	13 <td>BQ606843</td>	BQ606843
29	382.2	21.7	640	12 <td>BJ230767</td>	BJ230767
30	381.8	21.6	554	14 <td>CA501548</td>	CA501548
31	381.4	21.6	477	10 <td>BI158520</td>	BI158520
32	381	21.6	555	9 <td>AL818304</td>	AL818304
33	378.2	21.4	469	28 <td>BH229707</td>	BH229707
34	376.6	21.3	628	12 <td>B0309966</td>	B0309966
35	374.8	21.2	573	6 <td>AL810658</td>	AL810658
36	372.6	21.1	576	29 <td>CC344270</td>	CC344270
37	371.2	21.0	429	28 <td>BH229798</td>	BH229798
38	370.2	21.0	718	14 <td>CD453035</td>	CD453035
39	369.2	20.9	490	10 <td>BG158511</td>	BG158511
40	364	20.6	526	10 <td>BE445712</td>	BE445712
41	353.8	20.1	501	10 <td>BE446353</td>	BE446353
42	350.4	19.9	412	28 <td>BH229657</td>	BH229657
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44	346	19.6	400	10 <td>BG158998</td>	BG158998
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ALIGNMENTS

RESULT 1
LOCUS AY103762 1764 bp mRNA linear HTC 16-OCT-2002
DEFINITION Zea mays PCO087385 mRNA sequence.
ACCESSION AY103762
VERSION AY103762.1 GI:21206840
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE
AUTHORS Hake, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitlitt, M.S.,
Arthur, L.W., Hanfey, M., Morgante, M. and Tingey, S.V.
TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE
AUTHORS Coe, E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones
these are publicly available from ZmDB and may be found by BL
searching at MSU, maizegap.org; ZmDB, www.zmdb.iastate.edu;
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source

maize cDNA sequences is either Virginia Walbot, Stanford or Patricia Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES

Source

Location/Qualifiers

1. 1764

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/mol_type="mrn"

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/db_xref="taxon:4577"
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/clone_lib="Maize Mapping Project/DuPont Cornsensus
Library"
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/note="This sequence is part of a project of ESR assemblies resulting from the application of public configs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the MaizeG Mapping Project"

BASE COUNT	310 a	602 c	456 g	396 t
ORIGIN				

ORIGIN

Query Match	Score	DB	Length
100.0%	1764	11	1764
100.0%	1764	11	1764
100.0%	1764	11	1764

Matches 1764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1764; Conservative

QY	1	GCACGAGTCCCTCTCTCTCCCAATCTCCCGGCTCCCGCTACCAATAGCACACC	60
Db	1	GCACGAGTCCCTCTCTCTCCCAATCTCCCGGCTCCCGCTACCAATAGCACACC	60
QY	121	CGGAGCGCCGCGGGGGCGCGCGAGCTGCGGATGATCTCTCCAGAGAGCTCCGGCTCA	180
Db	121	CGGAGCGCCGCGGGGGCGCGCGAGCTGCGGATGATCTCTCCAGAGAGCTCCGGCTCA	180
QY	181	CGCTTCGCGCAGACACTCTGGAATCTCATCTCCGAGCAGTGATGCAAGTCAAGCCCTG	240
Db	181	CGCTTCGCGCAGACACTCTGGAATCTCATCTCCGAGCAGTGATGCAAGTCAAGCCCTG	240
QY	241	GCTCCGCCACACCCCGGGCGGAGCTTCGCTTCTCACTCTGCGGGGACAGACGCAC	300
Db	241	GCTCCGCCACACCCCGGGCGGAGCTTCGCTTCTCACTCTGCGGGGACAGACGCAC	300
QY	301	CGAGCGCTTCGCGCGCTACACACCGGCTTCGCGCGCGCTCTCTCGCGCTTCTTGCT	360
Db	301	CGAGCGCTTCGCGCGCTACACACCGGCTTCGCGCGCGCTCTCTCGCGCTTCTTGCT	360
QY	361	TGGCGGCTCTGACTAGCGCGATTCGCCCGCGCTCCCGGACATACCGCGCTCTCGC	420
Db	361	TGGCGGCTCTGACTAGCGCGATTCGCCCGCGCTCCCGGACATACCGCGCTCTCGC	420
QY	421	GCACTATCTCTCGCGGGCTCTTTCGAAGCGGTCCGACCACCCCAAGTTCAGCTGCT	480
Db	421	GCACTATCTCTCGCGGGCTCTTTCGAAGCGGTCCGACCACCCCAAGTTCAGCTGCT	480
QY	481	CTGATGGCGTCTCTTCTTACGCGCGGCTGTACTCTGCTCTGCGATGCGCAGGCGCTG	540
Db	481	CTGATGGCGTCTCTCTTCTTACGCGCGGCTGTACTCTGCTCTGCGATGCGCAGGCGCTG	540
QY	541	GGCGCACTCTCTCGCGGGGGGTCTCATTTGGCTTGTCTGATTCAGTCCGGCTGATGGG	600
Db	541	GGCGCACTCTCTCGCGGGGGGTCTCATTTGGCTTGTCTGATTCAGTCCGGCTGATGGG	600
QY	601	CCAGAGCTCCGGGACACACCGGATACCGGGCATCCGGTCCCGACCGCGTGTGCAAGT	660
Db	601	CCAGAGCTCCGGGACACACCGGATACCGGGCATCCGGTCCCGACCGCGTGTGCAAGT	660
QY	661	GCTCTCGGGAATGCTCTCACCGGCTCAGCATCGCTGTGGAAGTGAACCAACAC	720
Db	661	GCTCTCGGGAATGCTCTCACCGGCTCAGCATCGCTGTGGAAGTGAACCAACAC	720
QY	721	GCACCAATGCTTGACAAGCTTGACATGACCGGACCTTCAGCAGATGCGCTCTT	780

Db	721	GCACCAATCGCCCTGCACAAAGCCTGCAGACATATGACCCGGACCTCCAGACATAGCCGCTTT	780
Qy	781	TGCCGTCCCCCAAGCTGTTGGGCAACATATGGTCTTACTTTACACGAGACCTGGC	840
Db	781	TGCCGTCCCCCAAGCGTTCGGCAACATATGGTCTTACTTTACACACGAGCCTGGC	840
Qy	841	GTTGATAGCGCCCTCGAAATTCTTCATCAGGTACACAGACTGAGACCTTCTACCCGGTAT	900
Db	841	GTTGATAGCGCCCTCGAAATTCTTCATCAGGTACACAGACTGAGACCTTCTACCCGGTAT	900
Qy	901	GTCATCGCCAGATTAATCTTCTCGCGCAGTCCGCCCTGTTCTGCTTCACGAGAAAG	960
Db	901	GTCATCGCCAGATTAATCTTCTCGCGCAGTCCGCCCTGTTCTGCTTCACGAGAAAG	960
Qy	961	GGTCCGAGCGGTTGCTTGAATCGCGGGGTCGCCAATTCGGGCTTGGTACC	1020
Db	961	GGTCCGAGCGGTTGCTTGAATCGCGGGGTCGCCAATTCGGGCTTGGTACC	1020
Qy	1021	GCTGTGAGCTTCCCTGCGAAATGTGTGAGAGGGTGCAGTTGTGCTTTCACTTAC	1080
Db	1021	GCTGTGAGCTTCCCTGCGAAATGTGTGAGAGGGTGCAGTTGTGCTTTCACTTAC	1080
Qy	1081	CATCTGCGGATTCAGACGTCCTAATTCGCTGTCGACCACTTCTGTCGACGTATGT	1140
Db	1081	CATCTGCGGATTCAGACGTCCTAATTCGCTGTCGACCACTTCTGTCGACGTATGT	1140
Qy	1141	CGGCGCACCCAGGGCAATGACTGGTTTGAGAACACACGCGACGACGCTCGACATCT	1200
Db	1141	CGGCGCACCCAGGGCAATGACTGGTTTGAGAACACACGCGACGACGCTCGACATCT	1200
Qy	1201	GTCGTCCTTTGATGATATGGTATTCACCGGTGCGTGCAGTTGCAGATTTGAGACCAATCT	1260
Db	1201	GTCGTCCTTTGATGATATGGTATTCACCGGTGCGTGCAGTTGCAGATTTGAGACCAATCT	1260
Qy	1261	GTTTCCCCCGCTACCTCGGTGCGACTTTCGCAAGTTGACCGGCGCTGCGACCTTTG	1320
Db	1261	GTTTCCCCCGCTACCTCGGTGCGACTTTCGCAAGTTGACCGGCGCTGCGACCTTTG	1320
Qy	1321	CAGAGACATGGGCTCACTTATTTGCAGCCCAATTCGGGGTCGAAATGTGCTTACATG	1380
Db	1321	CAGAGACATGGGCTCACTTATTTGCAGCCCAATTCGGGGTCGAAATGTGCTTACATG	1380
Qy	1381	GAAACACTACGAGGCTGTGATTCGACGACCAATTCGGGGTCGAAATGTGCTTACATG	1440
Db	1381	GAAACACTACGAGGCTGTGATTCGACGACCAATTCGGGGTCGAAATGTGCTTACATG	1440
Qy	1441	GAAATTTGGTATGGAGGCTGTGAAACCCCATGTGATTAATGGAGTGAAGATACGGGCTAT	1500
Db	1441	GAAATTTGGTATGGAGGCTGTGAAACCCCATGTGATTAATGGAGTGAAGATACGGGCTAT	1500
Qy	1501	GCGCACTTCTGGTGTTCAGCTTGGTGCATGTATGTCTGATGCTTCAGTATTT	1560
Db	1501	GCGCACTTCTGGTGTTCAGCTTGGTGCATGTATGTCTGATGCTTCAGTATTT	1560
Qy	1561	AGAGATATTGATCACTTCAACCTGCTGACAGTCAAGTTGGAATTTTCGTGTGACAAAGTGC	1620
Db	1561	AGAGATATTGATCACTTCAACCTGCTGACAGTCAAGTTGGAATTTTCGTGTGACAAAGTGC	1620
Qy	1621	TGCTATTCAGATTGAGAGTTCAGTCTTCATATGCTGTGTTCACGCGATGTTCTGTT	1680
Db	1621	TGCTATTCAGATTGAGAGTTCAGTCTTCATATGCTGTGTTCACGCGATGTTCTGTT	1680
Qy	1681	CTCCCTATTCACGATTAATATATGATATGATCCTTGCTTAAATCAATGAACTATGTTTC	1740
Db	1681	CTCCCTATTCACGATTAATATATGATATGATCCTTGCTTAAATCAATGAACTATGTTTC	1740
Qy	1741	AAAGTTAAAAAATTTTTTTTTTTT 1764	
Db	1741	AAAGTTAAAAAATTTTTTTTTTTT 1764	

RESULT 2

BZ730996/c 825 bp DNA linear GSS 03-MAR-2003
 LOCUS BZ730996
 DEFINITION OGBDJ377M ZM 0.7-1.5 KB Zea mays genomic clone ZMMBma237H02,
 genomic survey sequence.
 ACCSSION BZ730996
 VERSION BZ730996.1 GI:28704535
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 825)
 Whitehead, C.A., Quackenbush, J., Van Aken, S., Utecher, T., Resnick
 A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek
 R.W., Nunberg, A., Robbins, D. and Lakey, N.
 TITLE Unpublished
 JOURNAL Consortium for Maize Genomics
 COMMENT Other GSSs: OGBDJ377C
 Contact: Cathy Whitehead
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitehead@cigr.org
 Seq primer: TR
 Class: sheared ends.
 FEATURES
 source
 1..825
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMMBma237H02"
 /clone_1lb="ZM 0.7-1.5_KB"
 /note="Vector: pBCKS-; Site 1: HindIII; 0.7-1.5 kb
 methylation filtered genomic DNA library"
 BASE COUNT 245 a 221 c 191 g 168 t
 ORIGIN
 Query Match 37.6%; Score 662.4; DB 29; Length 825;
 Best Local Similarity 98.5%; Pred. No. 1.4e-105;
 Matches 701; Conservative 0; Mismatches 6; Indels 5; Gaps 3;
 QY 1041 ATTGGGAGAGAGGCGGCTTTGCTTTCAGCTTCAACATTCGCGGATTCAGC 1099
 DB 813 AATGGGAGAGAGGCGGCTTTGCTTTCAGCTTCAACATTCGCGGATTCAGC 754
 QY 1100 GTCAATTCTGCTGAACCACT--TCTGCTCGAGCTGATGTGGGCGACCAAGG- 1155
 DB 753 GTCAATTCTGCTGAACCACTTTCTTCTCCGACGCTGATGTGGGCGACCAAGGCG 694
 QY 1156 CAATGACTGTTTGAAGACAGACGCGCAGCAGCTCGACATCTGTGCTTCTTGGAT 1215
 DB 693 CAATGACTGTTTGAAGACAGACGCGCAGCAGCTCGACATCTGTGCTTCTTGGAT 634
 QY 1216 GATTGCTTCCACGCGGCTTCAAGATTGAGCCATCTGTTTCCCGGCTTACC 1275
 DB 633 GATTGCTTCCACGCGGCTTCAAGATTGAGCCATCTGTTTCCCGGCTTACC 574
 QY 1276 TCGGTGCGACCTTTCGCAAGTTGACCGGCGCGCGACCTTTGCAAGACATGGGCT 1335
 DB 573 TCGGTGCGACCTTTCGCAAGTTGACCGGCGCGCGACCTTTGCAAGACATGGGCT 514
 QY 1336 CACTATTCTGACGACCATTTCTGGGGTCAATGTGCTTACATGAGACACTCAGGCG 1395
 DB 513 CACTATTCTGACGACCATTTCTGGGGTCAATGTGCTTACATGAGACACTCAGGCG 454
 QY 1396 TCGTGCATTCGAGCGCAGACCGCTCAAGTGTGCTTCCGAGAAATTTGGTATGGA 1455
 DB 453 TCGTGCATTCGAGCGCAGACCGCTCAAGTGTGCTTCCGAGAAATTTGGTATGGA 394
 QY 1456 GGCTGTGAACACCATGATTAATGGAGTGAAGATACGGGCTAATGGCAACTTGTGT 1515

DB 393 GGCTGTGAACACCATGATTAATGGAGTGAAGATACGGGCTAATGGCAACTTGTGT 334
 QY 1516 TCAGCTTGCTGCCATGTGATGTCTGATGTGCTTTCAGTTATTTAGATATTTGATCT 1575
 DB 333 TCAGCTTGCTGCCATGTGATGTCTGATGTGCTTTCAGTTATTTAGATATTTGATCT 274
 QY 1576 TCAACCTGCTGAGTCAGGTTGGAATTTTCGTTGACAGTGGCTGTCTATCCAGTTGG 1635
 DB 273 TCAACCTGCTGAGTCAGGTTGGAATTTTCGTTGACAGTGGCTGTCTATCCAGTTGG 214
 QY 1636 AGAGTTCACTTCAATAGTCTGTTGTTACAGGAGTGTCTTCTCCATACAGGTA 1695
 DB 213 AGAGTTCACTTCAATAGTCTGTTGTTACAGGAGTGTCTTCTCCATACAGGTA 154
 QY 1696 ACTAATGATGATGATCTCTGCTTAAATTCATGAACACTTGTTCAGATTA 1747
 DB 153 ACTAATGATGATGATCTCTGCTTAAATTCATGAACACTTGTTCAGATTA 102
 RESULT 3
 CD463185 744 bp mRNA linear EST 04-JUN-2003
 LOCUS ETH1_42_C07_g1_A002 Ethylene-treated seedlings Sorghum bicolor cDNA
 DEFINITION clone ETH1_42_C07_A002 5', mRNA sequence.
 ACCSSION CD463185
 VERSION CD463185.1 GI:31384453
 KEYWORDS EST.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 744)
 Cordomier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S., Klein
 R., Liang, C., Sun, F., Sullivan, R., Shah, M., Salzman, R., Chua Tan
 N., Gonzalez, M., Lane, S., Miller, V., Nanda, P., Olaseinde, O.,
 Eastman, A. and Pratt, L.H.
 An EST database from Sorghum: 1-aminocyclopropane-1-carboxylic acid
 (ACC)-treated seedlings
 TITLE Unpublished
 JOURNAL Other ESTs: ETH1_42_C07_b1_A002
 COMMENT Contact: Cordomier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Km. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu
 Library constructed by Dr. Yuraka Suzuki and Dr. Sumio Sugano in
 the Human Genome Center, University of Tokyo Institute of Medical
 Science; plant material and RNA prepared at Texas A & M University;
 sequencing done in the Laboratory for Genomics and Bioinformatics,
 University of Georgia. Sequence ends have been trimmed to exclude
 vector and regions below Phred quality 16. Three-prime sequences
 are presented as their reverse complement and have been trimmed to
 exclude polyA.
 Seq primer: Sugs (CTTCTGCTTAAAGCTGCG).
 FEATURES
 source
 1..744
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /cultivar="BTK623"
 /db_xref="taxon:4558"
 /clone="ETH1_42_C07_A002"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /clone_1lb="Ethylene-treated seedlings"
 /note="Vector: pMT18S-PL3; Site 1: XhoI; Site 2: XhoI; The
 library was prepared from polyA+ RNA from seedlings grown
 in hydroponic culture. At 8 days of age, medium was
 supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic
 acid (ACC) to induce endogenous ethylene (ETH) production.
 Roots and shoots were harvested after 27 and 72 hr and

material from both time points was combined prior to RNA isolation. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-PL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."

BASE COUNT 102 a 325 c 201 g 116 t

Query Match 33.4%; Score 588.8; DB 14; Length 744;
Best Local Similarity 91.6%; Pred. No. 9,4e-93;
Matches 636; Conservative 0; Mismatches 52; Indels 6; Gaps 1;

71 CCAGAGCCAGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGC-----124
4 CCCCCTCGGGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 63
125 GAGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 184
64 GAGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 123
185 TCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 244
124 TCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 183
245 CCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 304
184 CCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 243
305 GCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 364
244 GCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 303
365 GCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 424
304 GCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 363
425 CCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 484
364 CCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 423
485 GCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 544
424 GCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 483
545 GCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 604
484 GCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 543
605 GCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 664
544 GCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 603
665 GCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 724
604 GCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 663
725 GCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 788
664 GCGCGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 724

RESULT 4
LOCUS B1075898 634 bp mRNA linear EST 20-JUN-2001
DEFINITION IP1.22.F11.b1.A002 Immature pannicle 1 (IP1) Sorghum bicolor cDNA,
mRNA sequence.

ACCESSION B1075898
VERSION B1075898
KEYWORDS EST, Sorghum bicolor (sorghum)
SOURCE Sorghum bicolor
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
AUTHORS
Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and Pratt
"L.H." database from Sorghum: developing preanthesis pannicles
unpublished
Contact: Cordonnier-Pratt, M.M.
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Km. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmp@pratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions
below phred quality 16. The threshold for high quality sequence is
20. Three-prime sequences, which are obtained with POLYTAIL or 17
sequencing primer, are presented as the reverse complement.
Seq primer: JEN REV
High quality sequence stop: 598
POLYA=No.

FEATURES
source
Location/Qualifiers
1..634
/organism="Sorghum bicolor"
/mol_type="mRNA"
/cdate="19980623"
/db_xref="taxon:4558"
/clone_lib="Immature pannicle 1 (IP1)"
/note="Organ: Developing preanthesis pannicles; Vector:
pBluescript II SK(-) from Lambda Zap II; Site 1: XhoI;
Site 2: EcoRI; The library was made from polyA RNA in the
cloning vector lambda Zap II. Clones to be sequenced were
prepared by mass excision."

BASE COUNT 71 a 297 c 171 g 95 t

Query Match 31.7%; Score 559.4; DB 12; Length 634;
Best Local Similarity 94.1%; Pred. No. 1.3e-87;
Matches 594; Conservative 0; Mismatches 31; Indels 6; Gaps 1;

72 CGAGCCAGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA-----G 125
4 CGAGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 63
126 CGAGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 185
125 CGAGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 123
186 CGAGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 245
124 CGAGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 183
246 CGAGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 305
184 CGAGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 243
306 CGAGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 365
244 CGAGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 303
366 CGAGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 425
304 CGAGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 363
426 CGAGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 485
364 CGAGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 423
486 CGAGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 545
424 CGAGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 483
546 CGAGCGCGCGCGCGCGCAATGCGCCCTGTGATGCAATGCGGCGCCCGCAGAGGA 605

|||||
 Db 484 ACCTCTCGGGGGGGCTCATCGGCTTGTGATTCAGTCCGGCTGGATGGGACAG 543
 QY 606 ACTCGGGCCACACCCGATATCCGGCTCTCTCGACCCGCTGTGTACAGTGTCT 665
 Db 544 ACTCGGGCCACACCCGATATCCGGCTCTCTCGACCCGCTGTGTACAGTGTCT 603
 QY 666 CCGGGAAGTCTCTACCGGCTCTGAGTGGC 696
 Db 604 CCGGCAACTGCTCTACCGGCTCTGAGTGGC 634

RESULT 5
 BM322472 609 bp mRNA linear EST 04-JAN-2002
 LOCUS PIC1_5_C04.b1_A002 Pathogen-infected compatible 1 (PIC1) Sorghum
 DEFINITION bicolor cDNA, mRNA sequence.
 ACCESSION BM322472
 VERSION BM322472.1 GI:18059465
 KEYWORDS EST.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 609)
 Cordonnier-Pratt,M.-M., Gingle,A., Fang,G.C., Dean,R., Wing,R.,
 Sudman,M. and Pratt,L.H.
 An EST database from Sorghum: plants infected with a compatible
 pathogen
 Unpublished
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu

SEQUENCES have been trimmed to exclude PolyA, vector, and regions
 below Phred quality 16. The threshold for highest quality sequence
 is 20. Three-prime sequences, which are obtained with PolyT/Mix or
 17 sequencing primer, are presented as the reverse complement.
 Seg primer: JEN REV
 High quality sequence stop: 595
 PolyA-No.

FEATURES
 source

1. 609
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /cultivar="BTx623"
 /db_xref="taxon:4558"
 /tissue_type="Leaves"
 /dev_stage="4-week-old seedlings infected with
 Colletotrichum graminicola"
 /clone_lib="Pathogen-infected compatible 1 (PIC1)"
 /note="Vector: pBluescript II SK(-) from Lambda Zap II;
 Site1: XhoI; Site2: EcoRI; Four-week-old sorghum
 seedlings were sprayed with spore suspension prepared from
 3-week-old PM421, a sorghum isolate of the antheranose
 pathogen Colletotrichum graminicola. Inoculated plants
 were kept in a 25 C dark growth chamber with 100% relative
 humidity for 24 hr, followed by 12/12 hr of light/dark
 cycle at 25 C with 90% relative humidity for another 24
 hr. All leaves were harvested and quick frozen with liquid
 nitrogen and stored in a -80 C freezer. The library was
 made from poly-A RNA in the cloning vector lambda Zap II.
 Clones to be sequenced were prepared by mass excision.
 WARNING: While most or all ESTs are expected to derive
 from the host plant, no effort was made to eliminate ESTs
 deriving from the pathogen."

BASE COUNT
 ORIGIN

108 a 211 c 152 g 138 t

Query Match 31.0%; Score 546.6; DB 12; Length 609;
 Best Local Similarity 94.3%; Pred. No. 2,2e-85;
 Matches 567; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 694 CCGCTGTGGAAAGTGAACCAACACGACCATCGCTTGCACAGCTTGACCATGA 753
 Db 9 CCGCTGTGGAAAGTGAACCAACACGACCATCGCTTGCACAGCTTGACCATGA 68
 QY 754 CCGGACCTCCAGACATGCGGCTTTGGCCGTCGCCCAAGCTTGTGGGCAATATG 813
 Db 69 CCGGACCTCCAGACATGCGGCTTTGGCCGTCGCCCAAGCTTGTGGGCAATATG 128
 QY 814 GTCTTACTTCTACCAACGACCTGCGTTCAGATGCGGCTCGAAATTTCTACGCTA 873
 Db 129 GTCTTACTTCTACCAACGACCTGCGTTCAGATGCGGCTCGAAATTTCTACGCTA 188
 QY 874 CCAGCACTGAGACCTTCTACCCGGTATGTGATCGGCAGATTAATTTCTCGCGAGTC 933
 Db 189 CCAGCACTGAGACCTTCTACCCGGTATGTGATCGGCAGATTAATTTCTCGCGAGTC 248
 QY 934 CCGCCGTGTCGTTCTACGAGAGAGGGGTGCGGAGCGGTTGCTTGAATGCGGGGGT 993
 Db 249 CCGGCTCTTCTGTTCTACCGAGAGAGGGGTGCGGAGCGGTTGCTTGAATGCGGGGGT 308
 QY 994 CCGCACAATCTGGAGCTTGTGATCCGTTGGTGTGCTTCCCTGCGAATTTGTGGAGAG 1053
 Db 309 CCGCGAATCTGGAGCTTGTGATCCGTTGGTGTGCTTCCCTGCGAATTTGTGGAGAG 368
 QY 1054 GGTGGGTTTGTGCTTTTACGCTTACCATCTGCGGATTTACAGACGTTCAATTTGCTCT 1113
 Db 369 GGTGGGTTTGTGCTTTTACGCTTACCATCTGCGGATTTACAGACGTTCAATTTGCTCT 428
 QY 1114 GAACCACTTCTGTCTCGAGATGTATGTGGGCGCACCCAGGCGCAATGCTGTTTGA 1173
 Db 429 CAACCACTTCTGTCTCGAGATGTATGTGGGCGCACCCAGGCGCAATGCTGTTTGA 488
 QY 1174 GCAGACGAGGAGCAGCTGACATCTGTGCTCTCTTGGATGATTTGTTCCAGCGTGG 1233
 Db 489 GCAGACGAGGAGCAGCTGACATCTGTGCTCTCTTGGATGATTTGTTCCAGCGTGG 548
 QY 1234 CTTGCAATTCAGATTTGACACCATCTGTTTCCCGCTTACCTTGGTGCCACTTGGCAA 1293
 Db 549 TCTGCAATTCAGATTTGACACCATCTGTTTCCCGCTTACCTTGGTGCCACTTGGCAA 608
 QY 1294 G 1294
 Db 609 G 609

RESULT 6
 B0281359 744 bp mRNA linear EST 13-MAY-2002
 LOCUS WHE3020_D06.H12S wheat unstressed seedling shoot normalized cDNA
 DEFINITION library Triticum aestivum cDNA clone WHE3020_D06.H12, mRNA
 sequence.
 ACCESSION B0281359
 VERSION B0281359.1 GI:20548798
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticaceae; Triticum.
 1 (bases 1 to 744)

REFERENCE
 Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
 P.S., Heia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
 Rauech,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
 The structure and function of the expressed portion of the wheat
 genomes - Normalized shoot cDNA library

TITLE
 JOURNAL
 COMMENT
 Unpublished
 Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center

800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: canderstn@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer:
Location/Qualifiers

FEATURES

Source

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/organism="Triticum aestivum"
/mol_type="rRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE3020_D06_H12"
/tissue_type="Etisolated shoot"
/dev_stage="Five day old seedling"
/lab_host="E. coli DH10B"
/clone_lib="Wheat unstressed seedling shoot normalized
cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK+, Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A)+ RNA were prepared, a cDNA library was made in the
TU C10se lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pBluescript phagemid before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares'. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

```

Query Match	Similarity	Score	DB	Length
Best Local	81.9%	2.5e-81		
Matches	603	Conservative	0	Mismatches 133; Indels 0; Gaps 0;
Qy	595	GATGGGCGACGACTCGGGCCACACCGCATACCGGCGATCCGGCTCTCGACCGCGTGT	654	
Db	9	GATTGGCCATBACTCGGGCCACCAATATCACAGGACCCCGGCTCAACCGGCTCCT	68	
Qy	655	GCAGGTGCTCTCGGGAACTGCTTACCGGCTTACGATGCGCTTGTAAGTTAACCA	714	
Db	69	GCAGGTGCTCTCGGGAACTGCTTACCGGCTTACGATGCGCTTGTAAGTTAACCA	128	
Qy	715	CAACACGCACACATCGCTTGCAACAGCTTGGAACATACCCGGAACCTTCAGCATATCC	774	
Db	129	CAACACACACACATCTCTTGCAACAGCTTGGAACATACCCGGAACCTTCAGCATATCC	188	
Qy	775	GCTCTTGCGCGTCTCCGCCAAGCTGTTGGGAACATATGTCCTACTTCTACCAAGGAC	834	
Db	189	GCTCTTGCGCGTCTCCGCCAAGCTTCTTAACAACCTTTGGTGGCTTGCTACGAGCGAC	248	
Qy	835	CTGGCGCTTGAGTCCGCGCTTGAAATCTTCATCAGTACGACAGACTGGAACCTTCTACCC	894	
Db	249	CTTGCGCTTGATGCAATTCGAAGTTCTTGTCAGCTACAGCATGGAACATTTACCC	308	
Qy	895	GGTATGTGCATCGCCACAGATTAATCTTCTCGCGCATCGGCGCTTGTCGTTCTACGGA	954	
Db	309	GGTATGGGAATTTCAAGATTAATCTTCTTGGAAGTCANCGGTTCTGTATCAGCA	368	
Qy	955	GAAGAAGGTGCGGACAGCGGTGCTTGAGATCGCGGAGTGGCACATTTCTGGGCTTGTA	1014	
Db	369	AAAGAAGGTGCGGACAGCGGTGCTTGAGATCGCGGAGTTGACAGGTTCTGGGTTGGTA	428	
Qy	1015	CCCGTCTCGTGGCTTCCCTGCGGAATGGTGGGAAGGGTGGCGTTTGCTTTTACG	1074	
Db	429	CCCGTCTCGTCTCTTGCGCGGAATGGTGGGAAGGGTGGCGTTTGCTTTTACG	488	

QY	1075	CTTCACCATCTGCGGGATTGAGCAGTCCATTCTGCGCTGAACACATCTCTGTCGAGCT	113
Db	489	CTTTGTGTATCAGGGGATTACGCAATGTTCAAGTTCTGCTGAAACACTTCTATCCGCGCT	548
QY	1135	GTATGTCTGGGCGACCCAAAGGGCAATGACTGTGTTTGAGAAAGCAGACGGAGGCACGCTCGA	1197
Db	549	GTATGTGGGGCCACCAAAAGGGGAAACGACTGTTTGAGAGGCAAAACAGCGGGACACTTGA	608
QY	1195	CATCTGTGCTCTCTTGATGATGATTTGGTTCCAGGTGCGCTGCAGTTCAGATTGAGCA	125
Db	609	TATCAAGTGTCTCCCGTGATGATTTGGTTTCCATGTGTGTCTGCAGTTCAGATTGAACA	668
QY	1255	CCATCTGTGTTCCCGGCTAACCCTGCGTGCACCTTCGCAAGGTTGCACCGGCGGTCCGCGA	1314
Db	669	CCATTGTGTTCTCTGCGCTGCTCGCTGCACATATAGAGATGTGTGCGCGCATGTGTGCGTGA	728
QY	1315	CCTTTGCAAGAGCAT	1330
Db	729	CCTTTGCAGAGACAT	744

RESULT 7	
CB381262	
LOCUS	
DEFINITION	CB381262 585 bp mRNA linear EST 16-MAY-2003
ACCESSION	3529_145.1.B08.Y.1 3529 - 2 mm ear tissue from Schmidt and Hake
VERSION	CB381262
KEYWORDS	labe Zea mays cDNA, mRNA sequence.
SOURCE	CB381262.1 GI:29130558
ORGANISM	EST.
	Zea mays
	Zea mays

REFERENCE	1 (bases 1 to 585)
AUTHORS	Walbot, V.
TITLE	Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL Unpublished
COMMENT Contact: Walbot V

Stanford University
855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Place: 3529_1_45_1 row: B column: 08

FEATURES

Source

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/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
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/dev_stage="2 mm"
/lab_host="E. coli XLOR"
/clone_1ib="3529 - 2 mm ear tissue from Schmidt and Hake
labs"
/note="Organ: ear; Vector: PAD-GAL4-2.1; Site: 1; EcORI,
Site 2: XhoI; RNA isolated by Hake. lab. 1 million ptu
amplified. Ampicillin is the selection marker."
BASE COUNT      118 a      151 c      167 g      146 t
ORIGIN

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Query Match	28.9%	Score 509.4	DB 14	Length 585
Best Local Similarity	98.8%	Pred. 6.7e-79		
Matches 565	Conservative 0	Mismatches 2	Indels 5	Gaps 5

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Db 16 GGGGGCTTCCCTCCGAAATTGG-GGGAAGGGGCGCGTTTGCTTTACGCTTACCAT 74

QY 1084 CTGCGGATTCAGCAGCTCCAAATTCGCTGAAACCACTTCTGTCGACGCTGATGTCGG 1143
 DB 75 CTGCGGATTCAGCAGCTCCAAATTCGCTGAAACCACTTCTGTCGACG-GRATGTCGG 133
 QY 1144 GCCACCCAAAGGCGATGACTGTTTGAAGAGCAGACGCGACGCTTGACATCTCTTG 1203
 DB 134 GCCACCCAAAGGCGATGACTGTTTGAAGAGCAGACGCGACGCTTGACATCTCTTG 193
 QY 1204 CTCTCTGATGATGATGTTGTCACAGGTCGCGCTGCAAGTTCCAGATTGACACCATCTGT 1263
 DB 194 CTCTCTGATGATGATGTTGTCACAGGTCGCGCTGCAAGTTCCAGATTGACACCATCTGT 253
 QY 1264 TCCCGCCTTACCTCGGTGCAACCTTCGCAAGTTGACCGCGCTGCGACCTTTGCAA 1323
 DB 254 TCCCGCCTTACCTCGGTGCAACCTTCGCAAGTTGACCGCGCTGCGACCTTTGCAA 313
 QY 1324 GAAGCATGGGCTCATTATTCTGACGCAACATTCTGGGCTGCAATGTGCTTACATGAA 1383
 DB 314 GAAGCATGGGCTCATTATTCTGACGCAACATTCTGGGCTGCAATGTGCTTACATGAA 373
 QY 1384 GACACTCAGGCTGCTGCAATTCGAGGCCAG-GACCGCTCAAGTGTGCTG-CTCCGAG 1441
 DB 374 GACACTCAGGCTGCTGCAATTCGAGGCCAGGCCCTCAAGTGTGCTGCTCCGAG 433
 QY 1442 AATTGCTATG-GAGGCTGTGAACACCATGATTAATGAGTGAAGATACGGCTTAAT 1500
 DB 434 AATTGCTATGAGGCTGTGAACACCATGATTAATGAGTGAAGATACGGCTTAAT 493
 QY 1501 GGCACCTTGTGTTGCTGACCTGTCGCCATGATGTTCTGAGTCCCTTTCAGTTAAT 1560
 DB 494 GGCACCTTGTGTTGCTGACCTGTCGCCATGATGTTCTGAGTCCCTTTCAGTTAAT 553
 QY 1561 AGAGATATGATCATCAACCTGCTGAACTCA 1552
 DB 554 AGAGATATGATCATCAACCTGCTGAACTCA 585

RESULT 8
 BZ730988 497 bp DNA linear GSS 03-MAR-2003
 LOCUS OGEDJ377C.ZM_0.7.1.5_KB_Zea_mays_genomic_clone.ZMBA0237H02,
 DEFINITION genomic survey sequence.
 ACCESSION BZ730988
 VERSION BZ730988.1 GI:28704527
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 497)
 White, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick,
 A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek,
 R.W., Nurnberg, A., Robbins, D. and Lakey, N.
 Consortium for Maize Genomics
 Unpublished
 Other_GSSs: OGEDJ377M
 CONTACT: Cathy White, Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitec@maize.igs.org
 Seg primer: TF
 Class: sheared ends.
 Location/Qualifiers
 1..497
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 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMBA0237H02"
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FEATURES
 source

/note="Vector: pBSCS-; Site 1: HincII; 0.7-1.5 kb
 methylation filtered genomic DNA library"
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 ORIGIN

Query Match 28.1%; Score 495.4; DB 29; Length 497;
 Best Local Similarity 99.8%; Pred. No. 1.9e-76;
 Matches 496; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 752 GACCCGACCTTCACACATATGCGCTCTTTGCGCTCTCCCACTGTGGCAACATA 811
 DB 1 GACCCGACCTTCACACATATGCGCTCTTTGCGCTCTCCCACTGTGGCAACATA 60
 QY 812 TGGTCTCTTCTACCAACGACCTGCGGTTCAGATGCGCGCTCGAAATTTCTCATACG 871
 DB 61 TGGTCTCTTCTACCAACGACCTGCGGTTCAGATGCGCGCTCGAAATTTCTCATACG 120
 QY 872 TACACGACCTGACCTTCTACCCGTAATGTGCATGCGCAGGATTAATCTTCTCGCGAG 931
 DB 121 TACACGACCTGACCTTCTACCCGTAATGTGCATGCGCAGGATTAATCTTCTCGCGAG 180
 QY 932 TCCGCTCTGTTCTGCTCAGGAGAGAGGTGCGCAGCGGTTCGTGAGATCGCGAGG 991
 DB 181 TCCGCTCTGTTCTGCTCAGGAGAGAGGTGCGCAGCGGTTCGTGAGATCGCGAGG 240
 QY 992 GTGCGCACATCTGGGCTTGGTGAACCGGTGCTGAGGCTTCCCTGCGAATGTTGGAG 1051
 DB 241 GTGCGCACATCTGGGCTTGGTGAACCGGTGCTGAGGCTTCCCTGCGAATGTTGGAG 300
 QY 1052 AGGCTGCGGTTTGTGCTTTTACAGTTCACATCTGCGGATTCACACGCTCCAAATTTCTGC 1111
 DB 301 AGGCTGCGGTTTGTGCTTTTACAGTTCACATCTGCGGATTCACACGCTCCAAATTTCTGC 360
 QY 1112 CTGAACCACTTCTGCTCGAGCTGATGTGGGCGCACCCAGGCGCAATGACTGTTGAG 1171
 DB 361 CTGAACCACTTCTGCTCGAGCTGATGTGGGCGCACCCAGGCGCAATGACTGTTGAG 420
 QY 1172 AAGCAGAGGCGAGGAGCGCTGACATCTGCTGCTGATGATGATGTTCCACGGT 1231
 DB 421 AAGCAGAGGCGAGGAGCGCTGACATCTGCTGCTGATGATGATGTTCCACGGT 480
 QY 1232 GGCCTGCACTTCCAGAT 1248
 DB 481 GGCCTGCACTTCCAGAT 497

RESULT 9
 CD484486/c 499 bp mRNA linear EST 04-JUN-2003
 LOCUS 3529_1.115_1.A01.X_1 3529 - 2 mm ear tissue from Schmidt and Hake
 DEFINITION 1ab5 Zea mays cDNA, mRNA sequence.
 ACCESSION CD484486
 VERSION CD484486.1 GI:31405754
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 499)
 Walbot, V.
 Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 Unpublished
 CONTACT: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 3529_1.115_1 row: A column: 01.

FEATURES
 location/Qualifiers

source 1. .499
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 /cultivar="B73"
 /db_xref="taxon:4577"
 /tissue_type="ear"
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 /lab_host="E. coli XL0LR"
 /clone_1lb="3529 - 2 mm ear tissue from Schmidt and Hake
 labs"
 /note="Organ: ear; Vector: PAD-GAL4-2.1; Site_1: EcoRI;
 Site_2: XhoI; RNA isolated by Hake lab. 1 million pfu
 amplified. Ampicillin is the selection marker."
 BASE COUNT 150 a 131 c 112 g 106 t
 ORIGIN

Query Match 27.9%; Score 492.8; DB 14; Length 499;
 Best Local Similarity 99.6%; Pred. No. 5.4e-76;
 Matches 494; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1252 GCACCACTGTTCCCGGCTACTCGGTCGACCACTTCGGAAGTGGCAACGGCCGCG 1311
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 DB 439 CGACCTTTCGAAGAAGCATGGCTCACTTATTCGACGACCACTTCGGGGTCCAAATG 380
 QY 1372 GCTTACATGGAAGACACTCAGGCTGTGCAATTCAGGCGGACGAGACCGCTACAAAGTGTG 1431
 DB 379 GCTTACATGGAAGACACTCAGGCTGTGCAATTCAGGCGGACGAGACCGCTACAAAGTGTG 320
 QY 1432 TGCTCCGAAGAAATTTGGTATGGAGAGCTGTGAACACCCATGATTAATGGAGTGAAGATA 1491
 DB 319 TGCTCCGAAGAAATTTGGTATGGAGAGCTGTGAACACCCATGATTAATGGAGTGAAGATA 260
 QY 1492 CGGGCTAATGGCAACTTCGTGTTCAGTGTGAGTGGTCCCATGATTCGTGATGCTTT 1551
 DB 259 CGGGCTAATGGCAACTTCGTGTTCAGTGTGAGTGGTCCCATGATTCGTGATGCTTT 200
 QY 1552 CAGTTAATTAAGAAATTTGATTCATTCACCTGCTGAGTCAAGTGGAAATTTTGTGTTG 1611
 DB 199 CAGTTAATTAAGAAATTTGATTCATTCACCTGCTGAGTCAAGTGGAAATTTTGTGTTG 140
 QY 1612 ACAAGTGGCTGTATTCAGTATTCAGAGTTCATGCTTCATATCTGTTTCAACGGGA 1671
 DB 139 ACAAGTGGCTGTATTCAGTATTCAGAGTTCATGCTTCATATCTGTTTCAACGGGA 80
 QY 1672 TGTTCGTTCTCCCTATCAGGTAATACTATATGATGATGATCCTTGTATTAATCATGAAC 1731
 DB 79 TGTTCGTTCTCCCTATCAGGTAATACTATATGATGATGATCCTTGTATTAATCATGAAC 20
 QY 1732 ACTTGTTCAGATTA 1747
 DB 19 GCTTGTTCAGATTA 4

RESULT 10
 CD484487 497 bp mRNA linear EST 04-JUN-2003
 LOCUS 3529.1.115.1.A01.Y.1.3529 - 2 mm ear tissue from Schmidt and Hake
 DEFINITION lab's Zea mays cDNA, mRNA sequence.
 ACCESSION CD484487
 VERSION CD484487.1 GI:31405755
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 497)
 AUTHORS Walbot V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL University
 COMMENT Unpublished
 CONTACT Walbot V
 DEPARTMENT Department of Biological Sciences
 INSTITUTION Stanford University
 ADDRESS 855 California Ave, Palo Alto, CA 94304, USA
 TEL 650 723 2227
 FAX 650 725 8221
 EMAIL walbot@stanford.edu
 PLATE 3529.1.115.1 row: A column: 01.
 LOCATION/Qualifiers

FEATURES
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 labs"
 /note="Organ: ear; Vector: PAD-GAL4-2.1; Site_1: EcoRI;
 Site_2: XhoI; RNA isolated by Hake lab. 1 million pfu
 amplified. Ampicillin is the selection marker."
 BASE COUNT 78 a 197 c 123 g 99 t
 ORIGIN

Query Match 27.6%; Score 486; DB 14; Length 497;
 Best Local Similarity 99.8%; Pred. No. 8.3e-75;
 Matches 497; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 413 CTCCTCGGAGAGTATCTCCGGGGCTCTTCGGAACGGGTGGCCCAACCCCAAGATC 472
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 QY 473 CAGCTGTCCTGAATGGCCGCTCTTCTTACCGCGGCTGTACCTGCTCTCGATGCGC 532
 DB 60 CAGCTGTCCTGAATGGCCGCTCTTCTTACCGCGGCTGTACCTGCTCTCGATGCGC 119
 QY 533 AGGCGCTGGGGCGCACTCTCTCGGGGGGTCTCATTTGCTTGTGATCCAGTCCGGC 592
 DB 120 AGGCGCTGGGGCGCACTCTCTCGGGGGGTCTCATTTGCTTGTGATCCAGTCCGGC 179
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 DB 180 TGGATGGGCGAGACTCGGGGCAACCAACCGCATCACCGGCTCCGCTCGACCGGTC 239
 QY 653 GTGCAAGTCTCTCCGGGAATGCTTCAACCGGCTTCAGATGCTGTGGAAGTGTAA 712
 DB 240 GTGCAAGTCTCTCCGGGAATGCTTCAACCGGCTTCAGATGCTGTGGAAGTGTAA 299
 QY 713 CACACACGACCAATCGCTGTGCAACAGCTGTGACATGACCCGGAACCTCCAGCATG 772
 DB 300 CACACACGACCAATCGCTGTGCAACAGCTGTGACATGACCCGGAACCTCCAGCATG 359
 QY 773 CGGCTCTTGGCGTCCCGCAAGCTTCCGGAACATATGATGCTTCTTACCAACGG 832
 DB 360 CGGCTCTTGGCGTCCCGCAAGCTTCCGGAACATATGATGCTTCTTACCAACGG 419
 QY 833 ACCCTGGCTGTGATGCGGCTCGAAATCTTATCATGCTACCAAGCATGACCTTCTAC 892
 DB 420 ACCCTGGCTGTGATGCGGCTCGAAATCTTATCATGCTACCAAGCATGACCTTCTAC 479
 QY 893 CCGGTATATGATCGCC 910
 DB 480 CCGGTATATGATCGCC 497

RESULT 11
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 LOCUS fzm013f038h11k0 fzm013f038h11k0 fzm013f038h11k0
 DEFINITION fzm013f038h11 5', genomic survey sequence.

ACCESSION BH785221 GI:19789571
 VERSION BH785221.1
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 489)
 REFERENCE Budiman,M.A., Freese,R.G., Bedell,J.A., Nunberg,A.N. and Lakey,N.D. Gene/shresher methylation filtered genomic sequences from maize
 AUTHORS TITLE Unpublished
 JOURNAL COMMENT Contact: Bedell JA
 Origin Genomics, LLC
 4041 Forest Park Ave, St. Louis, MO 63108, USA
 Tel: 314 615 6879
 Fax: 314 615 5975
 Email: jbedell@oriolongenomics.com
 Plate: f2mb013f038 row: h column: 11
 Seq primer: SK reverse
 Class: shotgun
 High quality sequence stop: 489.
 Location/Qualifiers
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 /db_xref="taxon:4577"
 /clone="f2mb013f038h11"
 /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells."
 BASE COUNT 87 a 156 c 130 g 116 t
 ORIGIN
 Query Match 26.2%; Score 462.8; DB 28; Length 489;
 Best Local Similarity 99.0%; Pred. No. 9.1e-71;
 Matches 487; Conservative 0; Mismatches 2; Indels 3; Gaps 2;
 QY 724 CCACATCGCTGCAAGAGCTGAGCAATGACCCGAGCTCCAGACATGCGGCTTTTGG
 DB 1 CCACATCGCTGCAAGAGCTGAGCAATGACCCGAGCTCCAGACATGCGGCTTTTGG 58
 QY 784 CGTCTCCCCAGAGCTGTTGGCAACATATGCTTACTTACCAACGACCTGGCGTT 843
 DB 59 CGTCTCCCCAGAGCTGTTGGCAACATATGCTTACTTACCAACGACCTGGCGTT 117
 QY 844 CGATGCGGCTCGAATTTCTTATCAGCTACAGCACTGACCTTACCCGTAATGTG 903
 DB 118 CGATGCGGCTCGAATTTCTTATCAGCTACAGCACTGACCTTACCCGTAATGTG 177
 QY 904 CATGCGAGGATTAATCTTCTCGCGAGTCGCGCTGTTCTTCACGGAAGAGGT 963
 DB 178 CATGCGAGGATTAATCTTCTCGCGAGTCGCGCTGTTCTTCACGGAAGAGGT 237
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 QY 1024 GGTGGCTTCTTCCGCAATTTGTGGAGAGAGGTTCGGTTGTCTTTCAGCTTACCAT 1083
 DB 298 GGTGGCTTCTTCCGCAATTTGTGGAGAGAGGTTCGGTTGTCTTTCAGCTTACCAT 357
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QY 1204 CTCTCCTTGAT 1215
 DB 478 CTCTCCTTGAT 489
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 DEFINITION BJA65389 691 bp mRNA linear EST 23-MAY-2002
 BJA65389 K. Sato unpublished cDNA library, cv. Haruna Nijo
 bag939K05 5', mRNA sequence.
 BJA65389
 ACCESSION BJA65389.1 GI:21143896
 VERSION BJA65389
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
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 1 (bases 1 to 691)
 REFERENCE Sato,K., Saitoh,D. and Takeda,K.
 AUTHORS Barley EST sequencing project in NIG and Okayama Univ
 TITLE Unpublished
 JOURNAL COMMENT Contact: Tadaeu Shin-1
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.
 Location/Qualifiers
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 BASE COUNT 118 a 224 c 183 g 165 t 1 others
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 Query Match 26.2%; Score 462.6; DB 12; Length 691;
 Best Local Similarity 80.9%; Pred. No. 8.8e-71;
 Matches 551; Conservative 0; Mismatches 129; Indels 1; Gaps 1;
 QY 431 TCCGGGGGCTTGAAGAGCGTCCGCCACCCCAAGTCCAGCTGCTGATGGCC 490
 DB 12 TCCGGAGAGGCTTGAAGAGCGTCCGCCACCCCAAGTCCAGCTGCTGATGGTG 70
 QY 491 GTCTCTTTACGCGCGCTGACTCGTCTGATGCGGAGCGGCTGGGCGCACTC 550
 DB 71 GTCTCTTTGCTGCGCTTCTTACGCGCTGACTCGTCTGATGCGGAGCGGCGCACTG 130
 QY 551 CTGCGGGGGGTCTCATTTGCTTCTGATTCAGTCCGCTGATGGGCCACGACTCG 610
 DB 131 TTGCGCGGGGCTCATTTGCTTCTGATTCAGTCCGCTGATGGGCCATGACTCC 190
 QY 611 GGCACACACCGGATACCGGCGCATCCGCTTCGACACCGGCTGTCAGAGTCTTCGCGG 670
 DB 191 GGCACACACCGGATACCGGCGCATCCGCTTCGACACCGGCTGTCAGAGTGTTCGCGG 250
 QY 671 AACTGCTCAGCGGCTCAGATCCGCTGATGGAAGTGAACCAACACGACCAATC 730
 DB 251 AACTGCTCAGCGGCTCAGATCCGCTGATGGAAGTGAACCAACACGACCAATC 310
 QY 731 GCTTGAACAGCTTGACCATGACCCGACCTTCAGACATGCGCTTTTCCGCTTCC 790
 DB 311 TCTGCAACAGCTTGACCATGACCCGACCTTCAGACATGCGCTTTTCCGCTTCC 370

Qy	791	CCCAAGCTGTGGGAACATATGGCTTACTTCTACCAAGGACCTTGAGCTTCATGCC	850
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Qy	851	GCTTCGAATTCCTTCATCAGCTACAGGACCTGACCTTACCCGGTATGTGATCGCC	910
Db	431	ATATCCAAAGTCTTGTGTACGCTACAGACATCGACATTTTACCGGTATGGGATTTGCA	490
Qy	911	AGGATAAATCTTCTCGCGCAGTCCGCTGTTCGTTCTTCACGGAGAGAGGTGCGCAG	970
Db	491	AGGATAAATCTTCTAGTGCAGTCAATCGTGTTCCTCATCACAAAGAGGTGCGCAG	550
Qy	971	CGGTTCCTTGAGATCGCGGGGTGCGCCACATTTGCGCTGTGATCCGTTGCTGTGCT	1030
Db	551	CGTTGGCTGGAGATCGCGGTGTGCGCCGCTTCTGGTGTGGTACCCCTTGCTGTGCT	610
Qy	1031	TCCCTGCCGAATGTGTGGAGAGGGTGCAGTTGTGCTTTTCAGGTTTCAACATCTGCGGG	1090
Db	611	TGCTTCGCCGAATGTGTGGAGAGGGTGTGCTTTGTGTTCAGAGCTTTGTGTATCACGGGG	670
Qy	1091	ATTGAGCAGTCATCTTGC 1111	
Db	671	ATTGAGCATGTGCATTTGCTGC 691	

RESULT 13	LOCUS	CD330348	CD330348	DEFINITION	CD330348	562 bp	mrna	linear	EST 21-MAY-2003
		SS1_43_D08_b1	A012	Salt-stressed seedlings	Sorghum	bicolor	CDNA		
		clone SS1_43_D08_A012 3'		mrna sequence.					

ACCESSION	CD230348	
VERSION	CD230348.1	GI:30973782
KEYWORDS	EST.	
SOURCE	Sorghum bicolor (sorghum)	
ORGANISM	Sorghum bicolor	

REFERENCE

1 (bases 1 to 562)

Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S., Klein

AUTHORS

TITLE R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Summer, B. J., Eastman, A. and Paez, L. H.
JOURNAL An EST database from Sorghum: salt-stressed seedlings
COMMENT Unpublished
Other_Ests: SSI_43_D08_g1_A012

Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel.: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University,
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sug3 (CGACCTGCAGCTCGAGCACA)
POLYA=yes.

```

FEATURES
    source
        Location/Qualifiers
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                /mol_type="mRNA"
                /cultivar="IS3620C"
                /db_xref="taxon:4558"
                /clone="SS1_43_D08_A012"
                /lab_host="DH10B-T1 phage-resistant E. coli"
                /clone_lib="Salt-stressed seedlings"
                /note="Vector: pME18-FUJ, Site_1: XhoI, Site_2: XhoI, The
library was prepared from polyA+ RNA from 9-day-old

```

seedlings grown in hydroponic culture. Seedlings were transferred to a 150 mM NaCl solution and harvested at 3, 6, 12 and 24 hr following transfer. Roots and leaves were pooled from all time points and RNA isolated. Double-stranded cDNA was cloned unidirectionally into DraIII sites of the pMD18-FL3 vector (5-prime DraIII site is CACTGTGG, 3-prime DraIII site is CACCATGTG

Query Match	25.9%	Score 456.8	DB 14	length 562
Best Local Similarity	90.7%	Pred. No. 6	6e-70	
Matches 510, Conservative	0	Mismatches 47	Indels 5	Gaps 2

QY 1149 CCAAGGGCAATGACTGGTTTGAGAGCAGACGGCAGGACGCTGCACATCCCTGTGCTTC 1208

1209 CTTGATATGAAATTGCTTCCACCGGTGGCCGACGTTCCAGATTGAGCCATCTGTTTCCCC 1268
Db 1 CCAGGGCATTGACTGCTGTTGAGNAGACAGACGGAGGACGCTGCACATCCTGTGCCCC 60

61 CCTGATGAGTTGGTTCATGGTGTCTGCAGATTCAGATTGAGCACCATCTGTTCCCC 120

Q7 1269 GCCTACCTCGGTGCACTTGCAGGTGCAACGGCGCTCCGCACTTTGCAAGAAGC 1328

Db 121 GCCTACCTCGGTGCCACTTTCGCAGGTGCGCGCGCGCTGCGTGAACCTTTGCCAAGC 180

Db 132 ATGGCTCACTATTTCGACGCTCATTTGGGGCGCAATGTCTTACATGGAAACAC 240

1389 TCAGGCTGCTGCATTGCAGGCCAGACCGCTACAGTGTGTCTCCGAGAATTTCG 1448

Db 241 TCAGGAGCTGCTGCATTGCAGGCGCAGGAGCGCCACAGCGCGTGCCTCCGCCCGGAGAAATTTGG 300

Db 301 TCTGGAGGCTTTGAAACACCATGTGATGATGGATATATGAACTGAAGCAGC 360

1507 TTCTGGTGTTCAGCTTGCTGGTCCCATGTGATTGCTGATGCTTTCAGTTATTTAGAGA- 1565

Db 361 TTGTGTTGTCAGCTTTGTGTCCATGCGATTGTCGATTGCTTCAGTTATTAGAT 420

1566	--TATGATCAATCAACTGCGGAGAGCAGGTTGGAAATTTTCGTGTGACAAGTGGCCTGT	1623
0y		
Db	421 ACATATGATCATTTAAACCCGACTGAGTCGGGTGGAAATTTTCGTGTGACAAGTGA	480

1624 CTATCCAGTTGAGAGCTTCATGCTTCATAGTCTGTTGTTCACGGGATGTTCTGTTCTC 1683

Db 481 CTATCCAGTTGAAGAGTGTGATGCTTCAATGTGTGGTGTTCGCCGGCGTGTCTC 540

dy 1684 CCTATCAGCGTAACTATATGAT 1705
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 db 541 CCTATCATGGTAACTATATAT 562
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[illegible]

LOCUS	679 bp	mrna	linear	EST 26-JUL-2002
BQ788546				
BQ788546				
RESULT 14				

Accession	Definition
WHE4151_B02_C03ZS	wheat CS whole plant cDNA library Triticum aestivum cDNA clone WHE4151_B02_C03, mRNA sequence.
D0788645	

ACCESSION	B0700270
VERSION	B0788546.1
KEYWORDS	GI:21997018
	EST.

SOURCE	ORGANISM
Triticum aestivum (bread wheat)	
Triticum aestivum	
Embryophyta: Streptophyta: Eukaryota: Viridiplantae	Tracheophyta:

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.

REFERENCE
AUTHORS
1 (cases 1 to 6/5)
Anderson, O.D., Akhunov, E., Chao, S., Crossman, C., Deal, K., Dvorak, J.,
Lazo, G.R., Rausch, C.J., Wilson, C. and Woo, J.

TITLE. The structure and function of the expressed portion of the wheat

JOURNAL
COMMENT

genomes - Chinese Spring whole plant cDNA library
Unpublished
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818

Email: oanderson@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer.

FEATURES

source

Location/Qualifiers

1..679

/organism="Triticum aestivum"

/mol_type="mRNA"

/cultivar="Chinese Spring"

/db_xref="taxon:4565"

/clone="WHE4151_B02_C03"

/tissue_type="Roots, leaves, crown, stem and sheath"

/dev_stage="Adult"

/lab_host="E. coli SOLR"

/clone_lib="Wheat CS whole plant cDNA library"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid
plasmid SK(-); Site 1: EcoRI; Site 2: XhoI; Plant
tissues from wheat cv. CS grown to full tillering stage in
greenhouse were collected at University of California,
Davis (Jan Dvorak's lab, K. Deal and E. Akhunov). Total
RNA was prepared from leaves (young leaf and third leaf),
whole roots, crown, stem and sheath tissues, and then
equal quantities of RNA were pooled from the these
samples. PolyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo excised
to give plasmid SK(-) phagemids in J. Dvorak's lab (E.
Akhunov, J. Dvorak) at the University of California,
Davis. Colony plating, plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
other authors)."

BASE COUNT 95 a 300 c 176 g 107 t 1 others
ORIGIN

Query Match 25.8%; Score 455.8; DB 13; Length 679;
Best Local Similarity 81.4%; Pred. No. 1,4e-69;

Matches 542; Conservative 0; Mismatches 118; Indels 6; Gaps 1;

QY 27 CTTCCCGCTCCCTCCCAATACAGACACCAAGGCGCATCCGACGAGCCGCG 86
DB 20 CCCCTCTCCGCTCCCAATACAGACACCAAGGCGCATCCGACGAGCCGCG 79

QY 87 CAATGCCGCTCTGTGATGCAATGCGGCGCCCGCGGCGAGCGCGGCGGCGAG 146
DB 80 CAACGCGCGGGAAGCGGCAATGCGGCGCGGCGGCGGCGGCGGCGGCGGCGG 133

QY 147 TGGCGATGATCTCTCCAGAGGCTCCGCTCAAGCTTCGCGGAGAGACTTGATCT 206
DB 134 TCGGATGATCTCCAGAGGCTCCGCTCAAGCTTCGCGGAGAGACTTGATCT 193

QY 207 CCACTTCGCGGAGAGTGTACAGGCTCAGGCTTCGCGGAGAGACTTGATCT 266
DB 194 CCACTTCGCGGAGAGTGTACAGGCTCAGGCTTCGCGGAGAGACTTGATCT 253

QY 267 TCCGCGCTTCACCTTCGCGGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGG 326
DB 254 TCCGCGCTTCACCTTCGCGGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGG 313

QY 327 CTTCCGCGGAGAGGCTTCCTCCGCGGCTTCGTTGAGCGGCTTCGATAGCGGCT 386
DB 314 CTTCCGCGGAGAGGCTTCCTCCGCGGCTTCGTTGAGCGGCTTCGATAGCGGCT 373

QY 387 CCGCGCGGCTTCGCGGAGAGGCTTCCTCCGCGGCTTCGTTGAGCGGCTTCG 446
DB 374 CCGCGCGGCTTCGCGGAGAGGCTTCCTCCGCGGCTTCGTTGAGCGGCTTCG 433

QY 447 AACGCGTCCGCCCCACACCCCAAGTCCAGTCTCTGTATGAGCCGCTCTTTACGCCG 506
DB 434 AGCGCGTCCGCCCCACACCCCAAGTCTCTGTATGAGCCGCTCTTTACGCCG 493

QY 507 CGGTGATCTCTGCTTCGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTCA 566
DB 494 CCGTTCATGCGGCTTCGCTTCGATGCGGCGGCGGCGGCGGCGGCGGCGGCTCA 553

QY 567 TTGGCTTCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 626
DB 554 TTGGCTTCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 613

QY 627 CCGGCGATCCGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 686
DB 614 CCGGCGATCCGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 673

QY 687 TCAGCA 692
DB 674 TCGGCA 679

RESULT 15
A1691910 575 bp mRNA linear EST 02-FEB-2000
LOCUS
DEFINITION
mays cDNA, mRNA sequence.

ACCESSION
A1691910 GI:4967237
VERSION
A1691910.1

KEYWORDS
EST.
SOURCE
Zea mays
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 575)

REFERENCE
Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University

AUTHORS
TITLE
JOURNAL

COMMENT
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 606012 row: P column: 04.

FEATURES
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/mol_type="mRNA"
/cultivar="Ohio43"
/db_xref="taxon:4577"
/tissue_type="mixed"
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/clone_lib="606 - Ear tissue cDNA library from Schmidt
lab"
/note="Organ: Immature ear; Vector: pBK-CMV; Site 1: EcoRI
Site 2: XhoI; Mixed ear tissue cDNA library from Schmidt
lab"

BASE COUNT 180 a 143 c 108 g 142 t 2 others
ORIGIN

Query Match 25.0%; Score 441; DB 9; Length 575;
Best Local Similarity 99.8%; Pred. No. 5,4e-67;

Matches 441; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1366 AATGTGCTTACATGGAAGACACTCAGGCGCTCTGATTCAGGCGAGGAGCGCTACAG 1425

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Qy	1486	AAGATACGGGCTAATGSCAACCTTCTGTGTTTCAGCTGTGSCCATGTGATTTGTCTGGAT	1545
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Qy	1546	GCCTTTCAGTTATTTAGATATTTGATCATTTCAACCTGCTGAGTCAGGTTGGAAATTTTC	1605
Db	335	GCCTTTCAGTTATTTAGATATTTGATCATTTCAACCTGCTGAGTCAGGTTGGAAATTTTC	276
Qy	1606	GTTGTGACAAAGTGGCTGTCTATCCAGTTGGAGAGTTCACTGCTTCAATATGTCTGGTTGTC	1665
Db	275	GTTGTGACAAAGTGGCTGTCTATCCAGTTGGAGAGTTCACTGCTTCAATATGTCTGGTTGTC	216
Qy	1666	AACGGATGTCGTCTTCCCTATCACGGTACTATATGATATGATCTCTTCTTAATTC	1725
Db	215	AACGGATGTCGTCTTCCCTATCACGGTACTATATGATATGATCTCTTCTTAATTC	156
Qy	1726	ATGAACACTTGTGTTCAAGATTA	1747
Db	155	ATGAACACTTGTGTTCAAGATTA	134

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Job time : 2693.35 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:49:12 ; Search time 87.5326 Seconds
(without alignments)
8894.970 Million cell updates/sec

Title: US-09-857-524B-3

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	491.2	27.8	1702	4 US-08-934-254-26	Sequence 26, Appl
2	365.4	20.7	1684	2 US-08-831-570-1	Sequence 1, Appl
3	365.4	20.7	1684	2 US-08-831-575-1	Sequence 1, Appl
4	365.4	20.7	1685	1 US-08-366-779-4	Sequence 4, Appl
5	365.4	20.7	1685	1 US-08-789-936-4	Sequence 4, Appl
6	365.4	20.7	1685	4 US-08-934-254-4	Sequence 4, Appl
7	275.6	15.6	221	4 US-09-313-294A-1966	Sequence 1966, Ap
8	275.6	15.6	221	4 US-09-313-294A-3256	Sequence 3256, Ap
9	120	6.8	1926	4 US-09-249-585A-4	Sequence 4, Appl
10	120	6.8	1931	2 US-09-130-114-2	Sequence 2, Appl
11	77.6	4.4	7218	1 US-08-232-463-14	Sequence 14, Appl
12	77.2	4.4	1221	1 US-08-343-428-1	Sequence 1, Appl
13	75.6	4.3	1221	6 5212296-16	Patent No. 5212296
14	75.6	4.3	1879	6 5212296-5	Patent No. 5212296
15	72.8	4.1	4411529	3 US-09-103-840A-1	Sequence 1, Appl
16	72.6	4.1	4403765	3 US-09-103-840A-2	Sequence 2, Appl
17	71.6	4.1	1249	4 US-09-674-741-7	Sequence 7, Appl
18	71.6	4.1	4466	4 US-09-410-551B-20	Sequence 20, Appl
19	71.6	4.1	4478	4 US-09-410-551B-16	Sequence 16, Appl
20	71.6	4.1	4547	4 US-09-410-551B-22	Sequence 22, Appl
21	71.6	4.1	4571	4 US-09-410-551B-18	Sequence 18, Appl
22	71.6	4.1	77536	4 US-09-410-551B-1	Sequence 1, Appl
23	71.6	4.1	77536	4 US-09-410-551B-1	Sequence 1, Appl
24	71.2	4.0	1248	3 US-09-105-537-7	Sequence 7, Appl
25	70.4	4.0	13613	3 US-09-105-537-3	Sequence 3, Appl
26	70.4	4.0	1671	4 US-09-252-991A-8261	Sequence 8261, Ap
27	70.4	4.0	1944	4 US-09-252-991A-8062	Sequence 8062, Ap

28	70	4.0	1717	4 US-09-048-888-2	Sequence 2, Appl
29	69.6	3.9	4689	3 US-09-105-537-34	Sequence 34, Appl
30	69.6	3.9	36778	3 US-09-105-537-5	Sequence 5, Appl
31	69.6	3.9	38506	3 US-09-320-878-19	Sequence 19, Appl
32	69.6	3.9	38506	4 US-09-141-908-1	Sequence 1, Appl
33	69.6	3.9	38506	4 US-09-657-440-19	Sequence 19, Appl
34	69.4	3.9	320	3 US-09-165-264-13	Sequence 13, Appl
35	68.6	3.9	1926	4 US-09-249-585A-2	Sequence 2, Appl
36	68.6	3.9	1926	4 US-09-410-399-3	Sequence 3, Appl
37	68.6	3.9	1965	3 US-09-178-252-26	Sequence 26, Appl
38	68.6	3.9	2580	3 US-09-050-863-2	Sequence 2, Appl
39	68.6	3.9	2580	4 US-09-359-081-2	Sequence 2, Appl
40	68.6	3.9	5452	2 US-09-130-114-1	Sequence 1, Appl
41	68.6	3.9	8705	4 US-09-647-344A-14	Sequence 14, Appl
42	68.6	3.9	9600	3 US-08-910-647-1	Sequence 1, Appl
43	68.6	3.9	9600	4 US-09-620-925-1	Sequence 1, Appl
44	68.6	3.9	10596	1 US-07-884-811-15	Sequence 15, Appl
45	68.6	3.9	10596	1 US-07-885-971-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-934-254-26
Sequence 26, Application US/08934254
Patent No. 6155861
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSES: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1702 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1406
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1406
US-08-934-254-26
Query Match 27.8%; Score 491.2; DB 4; Length 1702;
Best Local Similarity 62.0%; Pred. No. 1.2e-96;

Matches 832; Conservative 0; Mismatches 498; Indels 12; Gaps 3;

QY 155 ATCTCCCAAGAGGCTCCGGCTCAAGCTTCCGGCCGACGACCTTGATTCATCTCC 214
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 QY 569 GGGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 628
 DB 492 GGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 551
 QY 629 GGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 688
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 QY 689 AGGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 748
 DB 612 AGGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 671
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 QY 1169 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1228
 DB 1092 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1151

QY 1229 GGTGAGCTGAGTTCAGATTGAGACCATCTGTTCCCGGCTACCTCGGTGACCTT 1288
 DB 1152 GGTGGGCTGAGTTCAGATTGAGACCATCTGTTCCCTAGGCTGCGGCTGGGACCTT 1211
 QY 1289 CGGAGGTTGACCGGCGCTCGGAGCTTTGCAAGAGAGTGGCTCACTTATTTGCA 1348
 DB 1212 AGGAGATTGCGGCTTGGCTCGGAGCTTGTGAAGAGGAGGAGGAGGAGGAGGAGG 1271
 QY 1349 GCCACATTTGG--GCTGAAATGCTTACATGAGAGCACTCAGGCTGCTGCAATTG 1405
 DB 1272 TTGGGTTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1331
 QY 1406 CAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1462
 DB 1332 CAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1391
 QY 1463 AACACCATGATGAATGGGAT 1484
 DB 1392 AACACCATGATGAATGGGAT 1413

RESULT 2
 US-08-831-570-1
 ; Sequence 1, Application US/08831570
 ; Patent No. 5959175
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; APPLICANT: Number, Andrew N.
 ; APPLICANT: Beremand, Phillip D.
 ; TITLE OF INVENTION: A SUNFLOWER ALBUMIN 5' REGULATORY REGION
 ; TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; City: Garden City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/831,570
 ; FILING DATE: 09-APR-1997
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Digililo, Frank S.
 ; REGISTRATION NUMBER: 31,346
 ; REFERENCE/DOCKET NUMBER: 10545
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 743-4366
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1684 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 43..1387
 ; US-08-831-570-1

Query Match 20.7%; Score 365.4; DB 2; Length 1684;
 Best Local Similarity 55.8%; Pred. No. 1,2e-69;
 Matches 740; Conservative 0; Mismatches 581; Indels 6; Gaps 2;

QY 155 ATCTCTCCAGAGAGCTCCGCGCTCAGCTTCGCGCAGACCTCTGATCTTCATCTCC 214
 DB 67 ATTACCTCAGATGAATCAAGAAACACGATTAACCCGAGATCTATGATCTCGATTCAA 126
 QY 215 GCGGAGCTGATGAGAGCTCAGCGCTTGGCTTCCCAACACCCGGGCGGACCTCCGCTT 274
 DB 127 GGGAAAGCCTATGATTTTCGATTTGGTAAAGACATCAGTGGCAGCTTTCCTTGG 186
 QY 275 CTCACCTGGCGGGGAGGAGCGCCACGACGCTTCGCGGCTACCAACCGCGCTCGGGG 334
 DB 187 AAGAGCTCTGCTGCTCAAGAGGATCTGATGATTTGTCATTCATCTGCTCTTCAA 246
 QY 335 CGCCGCTCTCCGCGCT 391
 DB 247 TGGAAAGATCTGATTAAGTTTTCAGTGGGATTAATCTTAAGATTAATCTCTGTTCTGAG 306
 QY 392 GCGCTCCGCGACTACCGCGCGCTCTCTCGGAGCTATCTCGCGGGGCTCTTTCGAGCC 451
 DB 307 GTTCTTAAGATTAAGAAAGCTTGTGTTGAGTTTCTAAAGTGGGTTGTATGACAAA 366
 QY 452 GTGCGCCCAACCCCAAGCTCCAGCTCTCTCTGATGCGCGTCTCTCTACCGCGCGCTG 511
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 QY 512 TACCTGCTCTCGCATGCGCAGCGCGCTGCGCAGCTCTCTCGCGGGGCTCTCATTTGCG 571
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 QY 572 TTGCTGTGATTCAGTCCGCTGATGAGGCGCAGCAGCTCGGCGCAGCAGCAGCTACCGCG 631
 DB 487 TTTCTTTGATTCAGAGTGGTTGATTTGAGCATGATGCTGGGAGATTAATGATGATGCT 546
 QY 632 CATCCGCTCTCGACCGCGCTCTGAGGCTCTCGCGGAACTGCTCTACCGCGCTCAGC 691
 DB 547 GATTCAAGCTTAATTAAGTTTATGAGTATTTTGTGCAAAATTTCTTCAGAAATAAT 606
 QY 692 ATGCGCTGTGAGAGTGAACCAACACGACACCATGCGCTCGAAGAGCTCGAGCAT 751
 DB 607 ATTGTTGTTGAGAAATGAGAACATTAATGACATCAATTTGCTGTAATAGCTTGAATAT 666
 QY 752 GACCGGAGCTTCAGACATGCGCTCTTTCGCGCTCTCCCAAGCTGTTTCGCAACATA 811
 DB 667 GACCTGATTTACATATATATACATTCCTTGTGTGCTCCAAAGTTTTTGGTTCACTC 726
 QY 812 TGGTCTACTCTTACCAAGAGAGCTGCGGCTTGAATGCGCGCTCGAATTTCTCATCAGC 871
 DB 727 ACCTCTCATTTCTATAGAAAGATGACTTTTGAATCTTTTATCAAGATTTCTTTGAGT 786
 QY 872 TACCAAGCTGAGCTTTACCGGTAATGTCATGCGCAGATTAATCTTCTCGCGAG 931
 DB 787 TATCAACATTTGACATTTTACCTTATTTAGTGTGCTGCTAGGCTCAATATGATATCAA 846
 QY 932 TCCGCGCTGCTCTCTCAAGAGAGAGGCTCCGACAGGCTTGTGATTCGCGGAG 991
 DB 847 TCTCTATATATGTTGATGACAAAGAAATGTTCTCTATGAGCTCAGGAACTTTGGGA 906
 QY 992 GTGCGCAATTTGCGCTTGTGATCCGCTGCTGCTGCTGCTTCTCTCGCAATGTTGGAG 1051
 DB 907 TGCCTAGTGTTCGATTTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAA 966
 QY 1052 AAGGTGCGGTTGCTTTTCACTTCAACATCTGCGGAGTTTACAGACGTTCAATCTCAGC 1111
 DB 967 AGAATTAATGTTGTTTATGCAATTTATATGATGATGCAATGCAAGTTCTCTCC 1026
 QY 1112 CTGAACCACTTCTGCTCCAGCTGATGCTCGGCGCAGCAGGAGGCAATGATGTTTGGAG 1171
 DB 1027 TTGAACCACTTCTCTTCAAGTGTATATGTTGAGAAAGCTAAAGGAAATATGTTTGGAG 1086
 QY 1172 AAGCAAGCGGAGGAGAGCTGCAATCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1231
 DB 1087 AAACAAACGATGAGGAGCACTTGAATTTCTGCTCTCTGAGATGATGATGATGATGATGAT 1146
 QY 1232 GCGCTGAGTTTCAAGATGAGCAATCTGTTTCCCGGCTACTGCGGCGCACTTTCGC 1291

DB 1147 GGAATGCAATTCGAATGAGATCATTTGTTCCCAAGATGCTAGATGCAACCTTAGG 1206
 QY 1292 AAGTTGACCGGCGCGCTCCGAGCCTTTGCAAGAGCATGAGGCTCATATTCTCGAGCC 1351
 DB 1207 AAAATCTGCGCTTACGATTAATGATGAGGAAACATTAATTTGCTTACATTAATGCA 1266
 QY 1352 ACATCTGGGGGTCGAATGCTGCTTACATGAGAACACTCAGGCTGCTGATTTGAGCGCC 1411
 DB 1267 TCTTTCTCCAGGCGCAATGAATGACATCTCAGAACATTTGAGGAAACAGACATTTGAGGCT 1326
 QY 1412 AGACCGCTACAGTGTGCTGCTCGAAGAAATTTGATGAGGAGCTGTGACACCAT 1471
 DB 1327 AGG---GATATTAACAGAGCGGCTCCGAAAGATTTGATGGAAGCTTTCACACTCAT 1383
 QY 1472 GGAATAA 1478
 DB 1384 GGTAA 1390

RESULT 3
 US-08-831-575-1
 ; Sequence 1, Application US/08831575
 ; Patent No. 5977436
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; TITLE OF INVENTION: AN OLEOSIN 5' REGULATORY REGION FOR THE
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/831,575
 ; FILING DATE: 09-APR-1997
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Digilio, Frank S.
 ; REGISTRATION NUMBER: 31,346
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1684 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 43..1387
 ; US-08-831-575-1
 Query Match 20.7%; Score 365.4; DB 2; Length 1684;
 Best Local Similarity 55.8%; Pred. No. 1,2e-69;
 Matches 740; Conservative 0; Mismatches 581; Indels 6; Gaps 2;
 QY 155 ATCTCTCCAGAGAGCTCCGCGCTCAGCTTCGCGCAGACCTCTGATCTTCATCTCC 214
 DB 67 ATTACCTCAGATGAATCAAGAAACACGATTAACCCGAGATCTATGATCTCGATTCAA 126

QY 215 GCGAGCTGTACAGCTACGCGCCCTGCTCCCGACACCGCGCGCGACCTCCGCTT 274
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 QY 452 GTGCGCCCAACCCCAAGTTCAGCTGTCTGATGCGCGCTCTTCTACGCGCGCTG 511
 DB 367 AAGGTCATATATATGTTGCAACTTGTGCTTTATACCAATGCTGTTGCTATAGTGT 426
 QY 512 TACTGCTCTCGATGCGCGAGCGCTGGCGGACCTCTCGCGGGGGCTCATTTGGC 571
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 QY 572 TTGCTGTGATTCAGTCCGCTGATGAGCGACACTCGGGCCACACCGCATCACCGCG 631
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 QY 692 ATGCGCTGTGAGTAACTACCAACAGCAGACACACACACACACACACACACACACAT 751
 DB 607 ATGCTTGTGAGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 666
 QY 752 GACCGGACCTCCAGCAGATGCGCGCTTGTGCGCTCTCCCGCAAGCTTGTGCGGACATA 811
 DB 667 GACCTGATTTAGAT 726
 QY 812 TGTCTCTATCTTACCAACGAGACCTGCGCTGATGATGATGATGATGATGATGATGATG 871
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 QY 872 TACGAGACCTGACCTTACACCGGTAATGATGATGATGATGATGATGATGATGATGATG 931
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 QY 932 TCCGCGCTGTTCTCTACGAGAAAGAGTGCAGAGCGGTTGCTTGAATGCGGGG 991
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 DB 907 TGCTTATGTTCTGATTTGTTGATGATGATGATGATGATGATGATGATGATGATGATG 966
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 DB 967 AGAATTAATGTTTGTATGCAAGTTTATCAGTGAATGCAACAAAGTTCACTTCTCC 1026
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 DB 1147 GGAATTCAGATTCAGAAATTTGAGACATTTGTTTCCCAAGATGCTTAAGTGAACCTTAAG 1206
 QY 1292 AAGGTGACACGGCGCTGCGGACCTTTGCAAGAAAGATGAGGCTCACTTATTTGACAGCC 1351

DB 1207 AAAATCTCCCGCTACGATGATGATGATGATGATGATGATGATGATGATGATGATG 1266
 QY 1352 ACATTCGAGGTCGAAATGCTTACATGAGAGACCTGAGGCTGTCTGATTTGAGGCG 1411
 DB 1267 TCTTTCTCAAGGCCATATAAATGACATCAGAACATTAAGAAACACACATTTGAGGCT 1326
 QY 1412 AGGACGCTACAAAGTGTGTGCTCCGAGAAATTTGATGAGAGCTGTGAACACCAT 1471
 DB 1327 AGG---GATTAACAGACCGGCTCCGAGAAATTTGATGAGAGCTTTCACACTCAT 1383
 QY 1472 GGATTA 1478
 DB 1384 GGTAA 1390
 RESULT 4
 US-08-366-779-4
 ; Sequence 4, Application US/08366779
 ; Patent No. 5614393
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; APPLICANT: Reddy, Avutu S.
 ; APPLICANT: Nuccio, Michael
 ; APPLICANT: Freysinet, Georges L.
 ; APPLICANT: Nunberg, Andrew N.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; TITLE OF INVENTION: DELTA 6-DESATURASE
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; City: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/366,779
 ; FILING DATE: 30-DEC-1994
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 83832YXX
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELBX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1685 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-366-779-4
 Query Match 20.7%; Score 365.4; DB 1; Length 1685;
 Best Local Similarity 55.8%; Pred. No. 1,2e-69;
 Matches 740; Conservative 0; Mismatches 581; Indels 6; Gaps 2;
 QY 155 ATCTCTCAAGAGCTCCGCGCTCAAGCTTCCGCGAGACCTCTGATTTCTCATCTCC 214
 DB 68 ATTAACCTCAGATGAATCAAGAACACAGTAACCCGAGATCTATGATCTGATTCAA 127
 QY 215 GCGAGCTGTACAGTCAAGCGCTGCTCCCGACACCGCGGCGGACCTCCGCTT 274
 DB 128 GGAAGAGCTATGATTTTCGATTTGGTGAAGAACCATTCAGTGGGAGCTTCCCTTG 187

QY 275 CTCACCTGGCGGGGAGAGACGCGACCGAGCGCTTGGCGGCTTACGACCGCGCGGGG 334
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 DB 248 TGGAGAAATCTTATTAAGTTTTTCTACGTGGTATTAATCTTAAGATTAATCTGTCTGAG 307
 QY 392 GCGTCCGCGAGCTACCGCGCGCTCTCTCGCGAGCTATCTCGCGCGGCTCTTGAACG 451
 DB 308 GTTCTTAAGATTAAGAGCTGTGTGTGATTTCTAATAATGGGTTGTATGACAA 367
 QY 452 GTGCGGCCACCGCCCAAGGTCAGCTGTGTGATGGCGGTCTCTTCAACCGCGGCTG 511
 DB 368 AAGAGCTATTAATGTGTCATCTTGTGTATAGCAATGCTGTGTGATGATGTT 427
 QY 512 TACCTGTCTGTGATGCGGACGCGCGCTGGCGCACCTCTCGCGGGGCTCTCATTTGC 571
 DB 428 TATGGGTTTTTGTGTGTAGGGTGTGTGTGATCAATTTGTGTGTGTGTGTGTGAGGG 487
 QY 572 TTGCTGTGATTCAGTCCGCTGTGATGGGTCACGACTGGGCGCAACGCGATCACCGC 631
 DB 488 TTCTTTGTGATTCAGAGTGGTGTGATGGACATGATGCGGATTAATGTAGTGTCT 547
 QY 632 CATCGGCTCTGACCGCGCTGTGAGGTGTCTCGCGGAACTGCTCAACCGCGCTCAG 691
 DB 548 GATTCAGGCTTAATTAAGTTTATGGGTATTTTGTGCAATGTCTCTTCAAGAAATAGT 607
 QY 692 ATGCGCTGTGTAAGTATTAACCAACAGCAGCAGATCGCTGCAACAGCCTGACCAT 751
 DB 608 ATTTGTTGTGTAAGTATTAACCAACAGCAGCAGATCGCTGCAACAGCCTGATAT 667
 QY 752 GACCCGAGCTCTGACAGCATGCGCTCTTGTGCGTCTCTCCCAAGCTGTGGCAACA 811
 DB 668 GACCTGATTAACAAATATATACCATTCCTGTGTGTCTTCAAGTTTTTGTGATCCTC 727
 QY 812 TGGTCTACTTCAACCAAGAGCCTGTGATGCGCGCTCGAAATTTTCAATCAGC 871
 DB 728 ACCTTCATTAATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGT 787
 QY 872 TACCAAGCTGACCTTCTTACCGGTAATGTGATGCGCGAGTAATCTTCTCGCGCAG 931
 DB 788 TATCAACATTTGACATTTTACCTTATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 847
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QY 1352 ACATTTCTGGGATGCAATGT 1411
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 QY 1412 AGAAGCGCTCAAGATGT 1471
 DB 1328 AGG---GATATTAACCAAGCGCTCCCGAAGAAATTTGTATGGAAGCTTCTCAACTCAT 1384
 QY 1472 GGATATA 1478
 DB 1385 GGTTAAA 1391

RESULT 5
 ; Sequence 4, Application US/08789936
 ; Patent No. 5789220
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; APPLICANT: Reddy, Avutu S.
 ; APPLICANT: Nuccio, Michael
 ; APPLICANT: Freybelnet, Georges L.
 ; APPLICANT: Nunberg, Andrew N.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; TITLE OF INVENTION: DELTA 6-DESATURASE
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/789,936
 ; FILING DATE: 28-JUN-1997
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/366,779
 ; FILING DATE: 30-DEC-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 8383ZYXW
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1685 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-789-936-4
 Query Match 20.7%; Score 365.4; DB 1; Length 1685;
 Best Local Similarity 55.8%; Pred. No. 1.2e-69;
 Matches 740; Conservative 0; Mismatches 581; Indels 6; Gaps 2;
 QY 155 ATCTCTCCAAGAGCTCCGCGCTCAGCGTTCCGCGAGAGCACTGTGATCTCCATCTCC 214
 DB 68 ATTACTCAGATGAATCAAGAACCAAGTAACCCGAGATCTATGATCTCGATTCAA 127
 QY 215 GCGAGGTGTACAGGTACGCGCTGTGCTCCCAACCAACCGCGGCGGAGCACTCCGCGCTT 274
 DB 128 GGGAAAGCCTATGATGTTTGGGATTTGGGTGAAGAACATCCAGGTGGCAGCTTTCCCTTG 187

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Qy 275 CTACACCTGGGGGAGAGAGCCACCGACCTTCCGCGCTACACCGCCCTCGGGC 334
Db 188 AAGAGCTTGTGTGTCAAGAGTACATGATGATTTGTGATTCATCTGCTCTACA 247
Qy 335 CGCCCGCTCTCGCGCGCTTCTGTTGG--CGGCTCTCTGACATACCGCTGCCCC 391
Db 248 TGAAGAGATCTGATTAAGTTTTCATGCGGATATATCTTAAAGATTAATCTGTTTCTGAG 307
Qy 392 GCGTCCCGACATACCGCCGCTCTCGCGAGATATCTTCGCGGGGCTCTTGAACGC 451
Db 308 GTTCTAAAGATTATAGAAAGCTGTGTGATTTCTAAAGATGAGTTGTATGACAAA 367
Qy 452 GTGCGCCCAACCCCAAGCTCAGCTGCTGATGAGCGGCTCTCTTACGCGCGCTG 511
Db 368 AAGAGCTATATATATGTTTGAACATTTGTGCTTATAGCAATGCTGTGTGATGAGTGT 427
Qy 512 TACCTGCTCTCGATCGCCAGCGCTGCGGCGACCTCTCGCGGGGGTCTCATTTGC 571
Db 428 TATGGGGTTTGTGTTGTGAGGGGTGTTGTGATCATTTGTTTCTGGGTGTTGATGGG 487
Qy 572 TTGCTCTGATCAGTCCGCTGATGAGGCGACGACTCGGCGCACACCGCATACCGGC 631
Db 488 TTTCTTGTGATCAGAGTGTGATTTGACATGATGCTGGGCAATTAATGATGCTCT 547
Qy 632 CATCCGGCTCTCGACCGCTGCTGTCAGAGTGTCTCCGGAAGTGTCTCACCGCGCTGAG 691
Db 548 GATTCAAGGCTTAATAGTTTATGAGTATTTTGTGCAATTTGTCTTACAGAAATAGT 607
Qy 692 ATGCGCTGTGAGAGTGTAAACACACGACGACCATGCTGTCACACGCTGAGCAT 751
Db 608 ATTGTTGTGTGAAGTGAACCATTAATGACATCATGCTGCTGTAATAGCTTGAATAT 667
Qy 752 GACCCGAGCTCCAGACATGCGCGCTTGTGCGCTCTCCGCAAGCTGTTCGGAACATA 811
Db 668 GACCTGATTTACAAATATATACATCTTGTGTGTCTTCAAGTTTGTGTTCACTC 727
Qy 812 TGGTCTACTTCTACCAAGGAGCCCTGCGCTGATGCTCGCGCTGAAATCTTCATCAGC 871
Db 728 ACCTCTCATTTCTTATGAGAAAGTTTACCTTTTATACATCTTTTATAGT 787
Qy 872 TACACGACGTGACCTTCTACCGGTAATGTGATTCGCGAGATTAATCTTCTGCGCAG 931
Db 788 TATCAACATTTGACATTTTACCATTAATGATGCTGAGGCTCATATATGATGATCA 847
Qy 932 TCGCGCTGTCTCTCAAGGAGAGAGGCTCGGAGGCTTGTGATGCGCGG 991
Db 848 TCTCTATATATGTTGTGACCAAGAAATGTCTATGAGCTCAGGAATCTTGGGA 907
Qy 992 GTGCGCACATTTGCGGCTGTGACCGGCTGTGCTGCTTCCGCGGAATGGTGGAG 1051
Db 908 TGCCTAGTGTCTGATTTGTGATCCGCTGTGTTCTTGTGCTTAATGGGCTGAA 967
Qy 1052 AGGCTGCGGTTTGTCTTTCAGCTTTCACATTCGCGGATTCAGACGTCATTTCTGC 1111
Db 968 AGAATTAATGTTTGTATTTGCAAGTTTATCAGTGATCGAATGCAAGATTCAGTTCTCC 1027
Qy 1112 CTGAACCATTTCTGTCTGAGAGTATGTGCGGACCAAGGCAATGACTGTTTGA 1171
Db 1028 TTGAACCATCTCTTCAAGTGTATGTTGAAAGCTTAAGGGAATTAATGGTTTGA 1087
Qy 1172 AAGCAGCGGAGGACGCTGACATCTGTGCTCTCTTGAATGATGGTTTCAAGT 1231
Db 1088 AAGCAAGGATGAGGACATTTGACATTTCTTCTCTTGAATGATGGTTTCAAGT 1147
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Qy 1352 ACATCTGGGTCGCAATGTGCTTACATGAGAGACATGAGGCTGCTGATTTGAGGCC 1411
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Db 1328 AGG---GATATACCAAGCGCTCCGAAAGATTTGTATGGAAGCTCTTCACTACAT 1384
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RESULT 6

US-08-934-254-4

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; Sequence 4, Application US/08934254
; Patent No. 635861
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; TITLE OF INVENTION: DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,254
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 83832XXWVU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELETYPE: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1685 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-934-254-4

```

Query Match 20.7%; Score 365.4; DB 4; Length 1685;
Best Local Similarity 55.8%; Pred. No. 1.2e-69;
Matches 740; Conservative 0; Mismatches 581; Indels 6; Gaps 2;

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Qy 155 ATCTCTCCAGAGAGCTCGCGCTCAAGCTTCCGCGAGACCTCTGATCTTCATCTCC 214
Db 68 ATTAAGCTCAGATTAATCAAGAAACGATTAACCGAGATCTATGATCTGATTCAA 127
Qy 215 GCGAGGTGATGACATGACGCGCTGCTGCCACACCGGCGGCGGACCTCCGCTT 274
Db 128 GGGAAAGCTATATATTTTCGATTTGGTGAAGACATTCAGTGCAGCTTCTCCCTTG 187
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Qy 335 CGCCCGCTCTCGCGCGCTTCTGTTGG--CGGCTCTCTGACATACCGCTGCCCC 391

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Db 248 TGAAGATCTTATAGTTTTCACCTGGTATTTCTTAAGATTACTCTGTTTCAG 307
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 QY 452 GTGCGCCCGCCCGCAAGGTCCAGCTGCTGATGGCCGCTCTCTTCTACGCGCGCTG 511
 Db 368 AAGAGTCATATTATGTTTGAACAATCTTGTGCTTATAGCAATGCTTGTGATAGAGTT 427
 QY 512 TACCTGCTCTCGCATGCGCGACGCGCTGGCGCACCTCTCGCGGGGGCTCTCATTTGC 571
 Db 428 TATGGGATTTGTTTGTGAGGGGTGTTGTGACATTTGTTTCTGGGTGTTGATGGGG 487
 QY 572 TTGCTGATTCAGTCCGCTGATGGGCGCAAGCTCGGGCCACCAAGCCCATCACCGGC 631
 Db 488 TTTCTTGTGATTCAGAGTGTGATTTGACATGATGCTGGGATATATATAGTGTCT 547
 QY 632 CATCCGGTCTCGACCGCGTGTGACAGTGTCTCTCCGGAACTGCTCACCGGCTGAGC 691
 Db 548 GATTCAAGGCTTATTAAGTTATAGGTAATTTTGTGCAAAATGCTCTTTCAGGAATAGT 607
 QY 692 ATGCGCTGTGAGATGTAAACAACAACGACCAATGCGCTGCAACAGCTTGACAT 751
 Db 608 ATTGGTTGTGGAATGGAACCATTAATGACATACATGCTGTAATAGCTTTGAATAT 667
 QY 752 GACCCGGACCTCCAGCATGCGCGCTTTGCGGTCTCCCGCAAGCTTGTGCGCAATA 811
 Db 668 GACCCGTATTTACATATATATACATCTCTGTGTGTCTTCCAGATTTTGTGTCATC 727
 QY 812 TGGCTACTTCTTCAACAGGACCGCTGCGTGTGATGCGCGCTGCAAAATCTTCATGAGC 871
 Db 728 ACCTCTATTTCTATGAGAAAGGTGATGACTTTGATCTTTATCAAAATCTTTGTAAGT 787
 QY 872 TACCAGACATGACCTTCTACCGGTATGTGATGCGCGAGATTAATCTTCTGCGCAG 931
 Db 788 TATCAACATTTGACATTTTACCTATATGCTGCTAGAGCTCAATATGATGATCA 847
 QY 932 TCGCGCTGTCTTCAAGGAGAGAGGTGCGCGAGCGGTGCTTGAGATGCGCGG 991
 Db 848 TCTCTCAATATGTTGTGACCAAGAAATGTGCTATGAGTCAAGGAACTCTTGGGA 907
 QY 992 GTGCGCAATCTTGGGCTGTGTAACCGGTGTGCTGCTCTCCGCAATTTGGTGGAG 1051
 Db 908 TGCTAGTGTCTGATTTGTGTAACCGGTGTGCTTCTTGTGCTTAATGGGAG 967
 QY 1052 AGGCTGCGTGTGTCTTTCAGCTTCAACATGCGGGATTCAGACGTCAATTTGCG 1111
 Db 968 AGATTTATGTTTGTATTTGCAAGTTTATCACTGACTGGAATGCAACAAGTTCAGTCTCC 1027
 QY 1112 CTGAACCACTTCTGTCGAGAGTATGTGCGGCCACCAAGGCAATGACTGTTGAG 1171
 Db 1028 TTGAACCACTTCTTCAAGTGTATGTTGAAAGCTTAAAGGAATTAATTTGTTGAG 1087
 QY 1172 AAGCAGACGCGAGCAGCTGACATCTGTGCTCTCTTGGATGATGTTGTTCCAGGT 1231
 Db 1088 AACAAGCAGATGAGACACTTGAATTTCTTGTCTCTCTTGGATGATGTTGTTCCAGGT 1147
 QY 1232 GGCCTGCAATTCAGATTTGACACCATCTGTTTCCCGCACTACCTGCTGACCTTGC 1291
 Db 1148 GGATTTGCAATTTCAATTTGACATCTTGTGTTCCAAAGATGCTTAAGATGCACTTAAG 1207
 QY 1292 AAGTTGCAACGCGCGCTGCGGACCTTTGCAAGAGATGAGGCTCATTTATTCGAGCC 1351
 Db 1208 AAAATCTGCGCTTACGTATGATGATGCAAGAAATTAATTTGCTTTAATAATTATGCA 1267
 QY 1352 ACATTTGGGGTGCAGATGTCTTATAGCAAGACACTCAGGGCTGTGCTCAGGCC 1411
 Db 1268 TCTTTCTCAAGGCAATGAATGACATCTCAGAACATTTGAGAAACAGCATTTGAGGCT 1327
 QY 1412 AGGACCGCTACAGTGTGTGCTCGAAGATTTGTATGAGAGGCTGTGAACCCAT 1471
 Db 1328 AGG---GATATTAACAAGCCGCTCCGAAAGATTTGTATGGGAAGCTCTTCAACATCAT 1384

QY 1472 GGATAAA 1478
 Db 1385 GGTAAA 1391
 RESULT 7
 US-09-313-294A-1966
 ; Sequence 1966, Application US/09313294A
 ; Patent No. 6476212
 ; GENERAL INFORMATION:
 ; APPLICANT: Lalundi, Raghunath V.
 ; APPLICANT: Ito, Laura Y.
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 ; FILE REFERENCE: PL-0017 US
 ; CURRENT APPLICATION NUMBER: US/09/313,294A
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 7600
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1966
 ; LENGTH: 291
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 6476212 700551823H1
 ; NAME/KEY: unsure
 ; LOCATION: 256
 ; OTHER INFORMATION: a, t, c, g, or other
 ; US-09-313-294A-1966
 Query Match 15.6%; Score 275.6; DB 4; Length 291;
 Best Local Similarity 98.2%; Pred. No. 1.5e-50;
 Matches 278; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1014 ACCCGTGTGCTGTGCTGCTTCCCTGCGCAATTTGTGAGAGAGGTGCGGTTGTCTTTCA 1073
 Db 1 ACCGTTGTGCTGTGCTGCTTCCCTGCGCAATTTGTGAGAGAGGTGCGGTTGTCTTTCA 60
 QY 1074 GCTTCAACATCTGCGGATTCAGACGTGCTCAATTTGCTGCTGCACTTCTGCTCGAGC 1133
 Db 61 GCTTCAACATCTGCGGATTCAGACGTGCTCAATTTGCTGCTGCACTTCTGCTCGAGC 120
 QY 1134 TGTATGTCGGGGCCACCAAGGGCATGACTGTTTGAAGACAGAGGCGACGCTCG 1193
 Db 121 TGTATGTCGGGGCCACCAAGGGCATGACTGTTTGAAGACAGAGGCGACGCTCG 180
 QY 1194 ACATCTGTGCTCTCTTGTGATGATTTGTTCCAGCGTGGCTGCAATTTGAGC 1253
 Db 181 ACATCTGTGCTCTCTTGTGATGATTTGTTCCAGCGTGGCTGCAATTTGAGC 240
 QY 1254 ACCATCTGTTTCCCGCTTACCTCGGTGCTGCACTTGGCAAGT 1296
 Db 241 ACCATCTGTTTCCCGCTTACCTCGGTGCTGCACTTGGCAAGT 283
 RESULT 8
 US-09-313-294A-3256
 ; Sequence 3256, Application US/09313294A
 ; Patent No. 6476212
 ; GENERAL INFORMATION:
 ; APPLICANT: Lalundi, Raghunath V.
 ; APPLICANT: Ito, Laura Y.
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 ; FILE REFERENCE: PL-0017 US
 ; CURRENT APPLICATION NUMBER: US/09/313,294A
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 7600
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 3256
 ; LENGTH: 266

QY		37	TGACTACGGCGTCTCCCGCGAGCAGCATCACGCCGCCTCCGCGAGCATCTC	432
Db		487	CGTCCTCCCCGTCTCCCGCTGTGCTCTCTCCCGCTCTCTCTCTCTCTCTCT	546
QY		433	CGCGGGGCTTTTGAA CGCGT CGGCCCACCCCAAGGT CAGCT GCTGTATGACGT	492
Db		547	CCCCGCTCTGTCCTCTCCCGCTCTCCCGCTCTCCCGCTCTCCCGCTCTCT	606
QY		493	CCTCTTTACGCGCGCTGTACTGCTGTCTGSCATATGCCACGCTGAGCACTCT	552
Db		607	CTCTGCTCTCCCGCTCTCCCGCTCTCCCGCTCTCTCTCTCTCTCTCTCTCT	666
QY		553	CGCGGGGGGTCTCATGTGCTTGTGTGTGATCCAGTCCGGCTGATGAGGACA	612
Db		667	CCCCGCTCTCCCGCTCTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCT	726
QY		613	CCAACAACCGATFACCGGCAATCGGCTCTGACCGCGGTGTGAGTGTCTTC	672
Db		727	CTCTCCCGCTCTGTCCTCTCCCGCTCTCCCGCTCTCTCTCTCTCTCTCT	786
QY		673	CTGCTTCACCGGCTTCAGATGCTGTGTGTGAAGTGTAAACAACAACGACAT	722
Db		787	CGTCTCTCCCGCTCTCTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCT	846
QY		733	CTGCAACAGCCTGACATGACCAGAACCTCCAGACATGCGCTTTGGCGCTCC	792
Db		847	CCCCGCTCTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	906
QY		793	CAAGCTGTTGGGACATATGTGCTTAATTCTTACCAACGACCTCGGCGTAT	852
Db		907	CGTCT	966
QY		853	CTCGAATCTTTCATCAGCTACACAC	880
Db		967	CTCTGCTCTCACCTCGGCCCCAGCTC	994
 RESULT 11 US-08-232-463-14				
/	Sequence 14, Application US/08232463			
/	Patent No. 5670367			
/	GENERAL INFORMATION:			
/	APPLICANT: DORNER, F.			
/	APPLICANT: SCHEIFLINGER, F.			
/	APPLICANT: FALKNER, F. G.			
/	TITLE OF INVENTION: RECOMBINANT FOAMBOX VIRUS			
/	NUMBER OF SEQUENCES: 52			
/	CORRESPONDENCE ADDRESS:			
/	ADDRESSEE: Foley & Lardner			
/	STREET: 1800 diagonal Road, Suite 500			
/	City: Alexandria			
/	STATE: VA			
/	COUNTRY: USA			
/	ZIP: 22313-0299			
/	COMPUTER READABLE FORM:			
/	MEDIUM TYPE: floppy disk			
/	COMPUTER: IBM PC compatible			
/	OPERATING SYSTEM: PC-DOS/MS-DOS			
/	SOFTWARE: Patent Release #1.0, Version #1.25			
/	CURRENT APPLICATION DATA:			
/	APPLICATION NUMBER: US/08/232,463			
/	FILING DATE:			
/	CLASSIFICATION: 435			
/	PRIOR APPLICATION DATA:			
/	APPLICATION NUMBER: US/07/935,313			
/	FILING DATE:			
/	APPLICATION NUMBER: EP 91 114 300.6			
/	FILING DATE: 26-AUG-1991			
/	ATTORNEY/AGENT INFORMATION:			
/	NAME: BENT, Stephen A.			
/	REGISTRATION NUMBER: 29,768			
/	REFERENCE/DOCKET NUMBER: 30472/114 IMMU			

```

      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (703)836-9300
      TELEFAX: (703)683-4109
      TELEX: 899149
      INFORMATION FOR SEQ ID NO: 14:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 7218 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
      IMMEDIATE SOURCE:
        CLONE: PTZ9pt-Fis
      US-08-232-463-14

Query Match          4.4%; Score 77.6; DB 1; Length 7218;
Best Local Similarity 4.9%; Pred.No. 1.1e-07;
Matches    20; Conservative 242; Mismatches 146; Indels   0; Gaps   0;

QY      119  CCGGCGACGCCGGCGCGCGCGAGCTGCATGTCTTCACGAAGACTCCGCGCT 178
           ||| | | | | | | | | | | | | | | | : : : : : : : : : : : :
DB      1033 CCAGAGCTTGCTCAGTCAAGGAGAGCTTCGATGTTTTTTTTTTTTTTTTTTT 1092
QY      179  CACGCTTCGCGCAGCACCTCTGGAATCCATCTCCGGCAGCGTACAGATCAGCCC 238
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1093 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1152
QY      239  TGGCTCCCCACACC CGGCGGCGACCTCCGCTTTCACCTGGCGGGCAGACGCC 298
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1153 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1212
QY      299  ACGGAGCGCTTCGCGCGCTACACCGCCCTCGGCGGCGCCGCTCTCCGCGTCTCTC 358
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1213 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1272
QY      359  GTTGGCGGCTCTCTGACTACGCGGTCTCCCGCGTCCCGCAGTACCGCGCTCTCTC 418
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1273 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1332
QY      419  GCGCAGCTATCTCCGCGGCGCTTTCGAAGCGCTCGGCCACCCCAAGTCCAGCTC 478
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1333 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1392
QY      479  GTCTGATGCGGCTCTCTTCTAAGCGCGCTGACTCGTCTCGCA 526
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      1393 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYGTACA 1440


RESULT 12
US-08-343-428-1
; Sequence 1, Application US/08343428
; Patent No. 5665586
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Etsuo
; APPLICANT: Tazunuki, Hiroshige
; APPLICANT: Kitadokoro, Kengo
; APPLICANT: Shin, Naasaru
; APPLICANT: Teraoka, Hiroshi
; TITLE OF INVENTION: No. 5665586el Protease
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720KB storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS Dos 5.0
; SOFTWARE: Wordperfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,428

```

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1      FILING DATE: 18-NOV-1994
2      CLASSIFICATION: 435
3      PRIOR APPLICATION DATA:
4      APPLICATION NUMBER: PCT/JP93/00592
5      FILING DATE: 30-APR-1993
6      APPLICATION NUMBER: JAPAN 4-126511
7      FILING DATE: 19-MAY-1992
8      ATTORNEY/AGENT INFORMATION:
9      NAME: Haley, Jr., James F.
10     REGISTRATION NUMBER: 27794
11     REFERENCE/DOCKET NUMBER: SHGN-7
12     TELECOMMUNICATION INFORMATION:
13     TELEPHONE: (212) 596-9000
14     TELEFAX: (212) 596-9030
15     INFORMATION FOR SEQ ID NO: 1:
16     SEQUENCE CHARACTERISTICS:
17     LENGTH: 2064
18     TYPE: nucleic acid
19     STRANDEDNESS: double
20     TOPOLOGY: linear
21     MOLECULE TYPE: genomic DNA
22     ORIGINAL SOURCE:
23     ORGANISM: Streptomyces fradiae
24     FEATURE:
25     NAME/KEY: -35 signal
26     LOCATION: 359..364
27     IDENTIFICATION METHOD: by experiment
28     NAME/KEY: -10 signal
29     LOCATION: 378..383
30     IDENTIFICATION METHOD: by experiment
31     NAME/KEY: CDS
32     LOCATION: 435..1505
33     IDENTIFICATION METHOD: by experiment
34     NAME/KEY: sig peptide
35     LOCATION: 435..944
36     IDENTIFICATION METHOD: by experiment
37
38     OS-08-343-428-1

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Query Match 4.4%; Score 77.2; DB 1; Length 2064;

Qy	1	CCTCTCTCCCAATCCCTCCCGGCTCCCGCTACCAATGAGCAACCCAAAGGCGAT	70
Dp	460	CCGGTCTGTCCGCTTGTCTCTGCGGCTCTCTGGCTCGGCGCGCCCGGCGGAG	519
Qy	71	CCGAGCCACGGCGCGCAATGCGGCTCTGTGATGCAATGCAATGCG--GCCCGGCGAG	128
Dp	520	CCGAGCGCCCCCAGAGGCGCGGCCCAACCCGGGCTCCGACTCGGCGCGGCTCTCAAG	579
Qy	129	CCGGGGGGGGCGGACGTGCGCAATGATCTCTCCAGGAGCTCCGGCGTCAAGCTTCCG	188
Dp	580	CCCTCGAGCGCGCCCTCGAGCGAGCCCTCGGAGACAGCGCGCGCACATACGTGAGAG	639
Qy	189	CCGAGCACTCTGATCTTCATCTTCGGGCGAGTGTACGACGTCAAGCCTTAGTCCCC	248
Dp	640	CCGGAGCGGGAAATCGTCTGTCAACGTATACCAACGAGGCGCCCGCGCAAGGTCCGG	699
Qy	249	ACCAACCGGGGGGCGACCTCCGCTTTCTTCACTTCGGCGGGGAGAGACGCCACCGACT	308
Dp	700	CGGCGGGGCGCACGCGCCCGGCGGGGTTCAGCGGGGCGCGCCGACGCTCGACGCGGGCATGG	759
Qy	309	TGCGCGCTTACCAACCGGCGCTCGGGGCGCGCGCTCTCCGCGGCTTTGTTGGCGCGC	368
Dp	760	CCGCGCTTGAAGGCAAGGCGCAAGATCCCGGACCTCGTGGGGGCTGGAACCGCGGACTCA	819
Qy	369	TCTGTGACTACGCGGCTCTCCCGCGGTGCGGCAATACCGCGCGCTCTGTGCGGAGTAT	428
Dp	820	ACCGGATCGCGGTGAGGCGGACTCTCGGTCTCGGCGCGGACCACTGAGCGCGGCTTCGGA	879
Qy	429	CCTCGCGGGGCTCTTTCGACGCGGTGCGGCCCAACCCCAAGTCCAGCTGTCTGTAGTG	488
Dp	880	AGGTGCGCGCTCTCGACGCGCGGCTGTACAGTACACCGCACTCCCGGCGGTTTCCAC	939

Qy	489	CCGACCTCTTCTAAGCGCGCGCTGACCTCGCTCTCGCATGCGCAGCGCCTCGGGCGCAC	548
Db	940	GCGAGTGTGCGCGCGCGGACCGCCATCTACGGCGCGGCTCGCGCTGCTCGGCGGCTTCA	999
Qy	549	TCCTCGCGGGGGTCTCATTTGCTTCGTCTGATTCAGTCCGGCTGGATGGGCCACGACT	608
Db	1000	ACGTACACCAAGAACGGCGTTCTGGTACTTCCGACCGCGGGCACTGACCAACTCTTCGT	1058
Qy	609	CGGGCCACACCGCATACCGGGCCATCGGCTCGCTCGACCGCGGTGATGAGGTGCTTCGG	668
Db	1060	CCACTTGGTGGTCCACTTCGGCGGGCACGTTCATGGGCTTCGGGAGGGACCAAGTTTC	1119
Qy	669	GGAACTGCTTACCGGCGCTCAGCATCGCTGGTGGAAGTGTAAACACAACGACCA	728
Db	1120	CGACCAAGACTACGGCATGGTCCGCTAACAGACACGACCAAGTGAACGGCGGGGTCA	1179
Qy	729	TGCGCTGCAACAGCGCTGGAACCATACCCGGACCTTCAGACATGCGCTCTTTGCGGCT	788
Db	1180	ACCTGTACAAAGGGGGCTACAGGACATGCGCTCCGGCGGACGCGCTCTGGGCGCAGG	1239
Qy	789	CCCCAAGCTGTTGGCAACATATGTACTTACTTACCAAGGAGCCCTGGCTTTCGATG	848
Db	1240	CCATTCAGAGAGGGGCTCCACAGACCAAGGTACACAGCGGACCGCTCAGCGCCGTCAACG	1299
Qy	849	CCGCGTGGAAATTTCTATCAGCTACGACGACGTGACCTTCTACCCGGTAATGTGCATCG	908
Db	1300	TCACCTGTCACTACAGCGAGCGGCCCCGTCTACGCGCATATGTCCGACGACCGCCTGTCGG	1359
Qy	909	CCAG 912	
Db	1360	CCGG 1363	

```

RESULT 13
5212296-16
Patent No. 5212296
APPLICANT: DEAN, CAROLINE; HARDER, PATRICIA A.; LETO, KENNETH
J.; O'KEEFE, DANIEL P.; OMER, CHARLES A.; ROMESSER, JAMES A.
TEPPERMAN, JAMES M.
TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
CYTOCHROMES
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/569,781
FILING DATE: 23-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 405,605
FILING DATE: 11-SEP-1989
SEQ ID NO:16
LENGTH: 1221
5212296-16

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Query Match	4.3%;	Score 75.6;	DB 6;	Length 1221;
Best Local Similarity	44.1%;	Pred. No. 1.9e-07;		
Matches 315;	Conservative 0;	Mismatches 399;	Indels 0;	Gaps 0;

Qy	127	CGCGCGGGGCGCGGCAGCGCGCAGATCTCTCCAAAGGATTCGGCGCTCAAGCTTC	186
Db	369	CCCCGAGGTGAGGAGGTGTGTGCACGGCTTCTTGACAGATGTGTGGCCCGCGCCGAC	428
Qy	187	CGCGCAGCACTCTGGAATCTTCATCTCCGGGACGTGTACGACGCTCAAGCCCTGAGCTCC	246
Db	429	CGCGACCTGTGATCAGTTCAGTTCGGCTGCGCGGTGACCTCCATGTGTGATCTGCGACATCTT	488
Qy	247	CCACCAACCCGGGGCGCGCACTTCCCGCTTTCACCTGGCGGGGAGAGACGCCACCAAGCG	306
Db	489	CGCGGTGCCCTTACGCCCAACCGATCTTCTTCAGAGACGCGCAAGCGGCTGTGTGCACTC	548
Qy	307	CTTGGCGGCTTACCAACCGCCCTTGAGGGCGCCGCTCTCGACCGCTTCTTCTGTGGCGG	366

Db 549 CACGAGACGGGACGGGCTCAACGGGAGAAACAACCTCGGGATTACTGGACGGCCT 608
Qy 367 CCTCTGTAGTACGCGCTCTCCCGCGTCCGACACTACGCGCTCTCTCGCGAGCT 426
Db 609 CATACCCAGATTCCAGACCCAAACCGGGCGGGGCTGTGGGCGCTCTGTCTCCCAACA 668
Qy 427 ATCTCCGGGGGCTCTTGGAGCGGTCGAGCCCAACCCCAAGTCCAGTCTGCTGAT 486
Db 669 GCTGGCCAAAGGAGATGACGCTGAGAACTGATTTCCACCGCATGCTGCTCTCAT 728
Qy 487 GGCCTCTCTTCTACGCGCGCTGTACTCTCTCTCGCATGCGCAAGCCCTCGGCGCA 546
Db 729 CGCGGCGACAGACCAACGCGCTGTGATGATCCTCCTGAGGTATACCTGCTGAGCA 788
Qy 547 CTTCTCTCGGGGGGCTCTATTGGCTTGTCTGTGATCAATCCGGCTGATGGCCACA 606
Db 789 CCCCAGCATAGACGCGCGCTGCGCGCGCAACCGAGCTGTGCGCGCGCGGTGGAGA 848
Qy 607 CTGGGGCCACACCGCATACCGGCGCATCGGCTCTGACCGGCTGCGTGGAGTCTC 666
Db 849 ACTGCTCGTACTCTGCGCATGCGCGCATGCGGCGCGCGGCTGCCACGCGGACAT 908
Qy 667 CGGGAATGCTCTACCGGCTCTACGATCGCTGTGGAGTGAACCAACAACGACCA 726
Db 909 CGAGTCTGAGGGGACCTCATCCGGGCGGGGAGGGGTGATGCTGTCACTGATAGC 968
Qy 727 CATGCTCTGAACAGCTGTGACATGACCGGACCTTCAGACATGCGCTTTTGGCGT 786
Db 969 CAACCGGAGCGGACGCTGTACGAGACCGGACGCTCTGACATCCACGCTCGCGCG 1028
Qy 787 CTCCCCAAGCTGTTCGGCAACATATGTCCTTACTTACCAACGAGCCTTGGC 840
Db 1029 CCACCACTTGGCTTGGCTTGGCGGTGACACAGTGTGCGGCGAGAACTTGG 1082

RESULT 14
5212296-5
; Patent No. 5212296
; APPLICANT: DEAN, CAROLINE, HARDER, PATRICIA A., LENO, KENNETH
; J. O'KEEFE, DANIEL P., OMER, CHARLES A., ROMESSER, JAMES A.
; TEPERMAN, JAMES M.
; TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
; CYTOCHROMES
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/569, 781
; FILING DATE: 23-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 464,499
; FILING DATE: 12-JAN-1990
; APPLICATION NUMBER: 405,605
; FILING DATE: 11-SEP-1989
; SEQ ID NO: 5
; LENGTH: 1879
5212296-5

Query Match 4.3%; Score 75.6; DB 6; Length 1879;
Best Local Similarity 44.1%; Pred. No. 2.1e-07;
Matches 315; Conservative 0; Mismatches 399; Indels 0; Gaps 0;
Qy 127 CGCGCGGGCGCGCGGACGTCGCGCATGATCTCTCCAGAGAGTCCGCGCTCAGCTTC 186
Db 496 CCCCAGAGTCAAGAGGTGTGACGCGCTTCTGACGAGATGCTGCGCGCGCGCGAC 555
Qy 187 CGCGGACGACCTCTGATCTCTCATCTCCGCGGACGCTGACGACCTCAGCGCTGCC 246
Db 556 CGCGGACCTGTCTAGTACTGTCTGCGGCTCGCGGTGCTCCATGATGATGCGACACTCT 615
Qy 247 CCACCAACCGGGCGGACCTCTCGCTTCTGACCTTGGCGGGGAGAGACGCGACGACGC 306
Db 616 CGGGGTGCTTACCGCGGACGAGATCTTCCAGAGACGAGGAGCGGCTGTGACGTC 675
Qy 307 CTTGGCGGCTTACCAACCGCGGCTTGGCGGCGCGCGCTCTCTCGCGGCTTCTTGGCGG 366

Db 676 CACGAGCGGACGAGCGGCTCACCGCGGAGAAACAACCTCGGGATTACTGGACGGCCT 735
Qy 367 CCTCTGTAGTACGCGCTCTCCCGCGTCCGCGCACTACGCGCTCTCTCGCGAGCT 426
Db 736 CATACCCAGATTCCAGACCCAAACCGGGCGGGGCTGTGGGCGCTCTGTCTCCCAACA 795
Qy 427 ATCTCCGGGGGCTCTTGGAGCGGTCGAGCCCAACCCCAAGTCCAGTCTGCTGAT 486
Db 796 GCTGGCCAAAGGAGATGACGCTGAGAACTGATTTCCACCGCATGCTGCTCTCAT 855
Qy 487 GGCCTCTCTTCTACGCGCGCTGTACTCTCTCTCTCGCATGCGCAAGCCCTCGGCGCA 546
Db 856 CGCGGCGACAGACCAACGCGCTGTGATGATCCTCCTGAGGTATACCTGCTGAGCA 915
Qy 547 CTTCTCTCGGGGGGCTCTATTGGCTTGTCTGTGATCAATCCGGCTGATGGCCACA 606
Db 916 CCCCAGCATAGACGCGCGCTTGGCGCGCGCAACCGAGCTGTGCGCGCGCGGTGGAGA 975
Qy 607 CTGGGGCCACACCGCATACCGGCGCATCGGCTCTGACCGGCTGCGTGGAGTCTC 666
Db 976 ACTGCTCGTACTCTGCGCATGCGCGCATGCGGCGCGCGGCTGCCACGCGGACAT 1035
Qy 667 CGGGAATGCTCTACCGGCTCTACGATCGCTGTGGAGTGAACCAACAACGACCA 726
Db 1036 CGAGTCTGAGGGGACCTCATCCGGGCGGGGAGGGGTGATGCTGTCACTGATAGC 1095
Qy 727 CATGCTCTGAACAGCTGTGACATGACCGGACCTTCAGACATGCGCTTTTGGCGT 786
Db 1096 CAACCGGAGCGGACGCTGTACGAGACCGGACGCTCTGACATCCACGCTCGCGCG 1155
Qy 787 CTCCCCAAGCTGTTCGGCAACATATGTCCTTACTTACCAACGAGCCTTGGC 840
Db 1156 CCACCACTTGGCTTGGCTTGGCGGTGACACAGTGTGCGGCGAGAACTTGG 1209

RESULT 15
US-09-103-840A-1/C
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103, 840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 441529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 4.1%; Score 72.8; DB 3; Length 441529;
Best Local Similarity 46.2%; Pred. No. 5.8e-06;
Matches 279; Conservative 0; Mismatches 322; Indels 3; Gaps 1;
Qy 85 CGCATATGCGGCTCTGTGATGACATGCGGCGCGCGGACGCGCGGCGCGGCA 144
Db 1218147 CGTACAGCAACCGCGGAGTGGCGCGCTGTCCGCAATGCGGCAATGCGCGCTTGC 1218088
Qy 145 CGTGGCAGATATCTCTCAAGAGAGCTCCGCGCTACAGCTTCCGCGGAGACCTGTGAT 204
Db 1218087 CATTGGCGCGCTTCCGCGGACCGCGGCTTGGCGCGGCGCGCGCGCGG 1218028
Qy 205 CTCATCTCGGCGGACGATGACAGCTGACGCGCTTGTCTCCCAACACCGGCGGCGCA 264

Db 1218027 CCCCAGCGTTCCGCGCAGCCCGCCATGCGAAGCAGCACCAGGCGGGCCGCGGCC 1217968
Qy 265 CTTCCCGCTTCTACCCCTGAGCGGGCAGAGCCAGACCGACCTTCCGCCCTTACCAACC 324
Db 1217967 CGCCCGCGCGTACACACCGCTGCGCACCGCTGCGCCGCGCGCAGCGCGCAGCGC 1217908
Qy 325 GCGCTCGGCGCGCGCGCGCTCCCTCCGCGCTTCTTGTGGCGCGCGCTCTGTGACTACGCGT 384
Db 1217907 CGCGGATGCCCGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1217848
Qy 385 CTCGCCCG 444
Db 1217847 CCGCGCGCGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1217788
Qy 445 CGAAGCGCTGGCG 501
Db 1217787 CG 1217728
Qy 502 CGCGCGCGTGTACCTGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 561
Db 1217727 CGCTGAGGCGCAGAGCCCGCTTTGCGCGCGCGCGCGCGCGCGCGCGCGCG 1217668
Qy 562 TCTCATTTGGCTTCTGCTGTGATCCAGTCGGCGTGGATGAGGCCAGACTCGGGCCACACCG 621
Db 1217667 CGCGGCGCGCACCGACCGCCCAAGCCTGAGGCTTCCCGCGCGCGCGCGCG 1217608
Qy 622 CATCACCGGCGCATCCGCTCTCGACCGCGCTGTGAGAGTGTCTCCGGGAATGCTCAC 681
Db 1217607 CCCACCGGCG 1217548
Qy 682 CGGC 685
Db 1217547 CCGC 1217544

Search completed: January 1, 2004, 00:05:24
Job time : 99.5326 secs

LENGTH: 1702 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 48..1406
 NAME/KEY: CDS
 LOCATION: 48..1406
 SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 us-10-029-756-26

Query Match 27.8%; Score 491.2; DB 14; Length 1702;
 Best Local Similarity 62.0%; Pred. No. 2,5e-124;
 Matches 832; Conservative 0; Mismatches 498; Indels 12; Gaps 3;

155 ATCTCTCAAGAGAGCTCCGCGCTCACGCTTCCGCGCAGACCTGTGATCTCCATCTCC 214
 Db ATACGCGGAGAGAGCTCCGCGCGCACACAGTCCGCGCATCTGTGATCTCCATCTCCAG 131

215 GCGGACCTGTACGACGTACAGCCCTGGCTCCCAACACCCGCGCGGACCTCCGCTT 274
 Db GCGAAGGCTACGACCTCTCGGTGGCGCGGAGAGACCCCGCGCGGAGTCCGCTC 191

275 CTCACCTCTGCGGGGCGAGAGCGGACGCGCTTCCGCGCTACACACCCGCTCCGCG 334
 Db CTCAGTGTGCGCGCGGAGAGAGTACCGACCTTTCATGTGATCCACCCGCGGACGCG 251

335 CGCGCGCTCTCCGCGCGCTTCTTGTGTG-----CGGCTCTGTGACTACGCGCTTCC 388
 Db TGGCGGATGTGATCGGCTCTTACCGGCTACTACTCAAGACTTCAAGAGTGTG 311

389 CCGCGCTCGCGGACCTACCGCGCGCTCTCGCGGACGCTATCTCCGCGCGCTTCTGAA 448
 Db GAGATCTCCAGAGACTACCGGAGGCTTTGAACGAGATGTGCGCGGTCCGGATCTTGAG 371

449 CGGCTCGCGCGCGCGCGCGCGCTCTCTGATGTGCGCGCTCTTCTACGCGCG 508
 Db AAGAGGCGCGCACCATCATGTGAGCTGTGCGCGCTTCCGCGCTGATGAGCGCGCATC 431

509 CTGTACCTCTCTCTCGCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCTCAT 568
 Db GTCTACGCGCGCTGTGCGGTGAGATCGGTGGAATTCATGCTCTGCGCGCGCATCTG 491

569 GCGCTTGTGTGATTCAGTCCGCGGTGATGGCGGACGACTGTGGCGCACACCGCATACC 628
 Db GCGTGTGTGTGATTCAGACCGCGCGGTATGTGGCGCATCTCCGCGCATTTACAGGTGATG 551

629 GCGCATCGGCTCTCGACCGCGGTGTGAGGTGCTCTCGCGGAACTGCGCTCACCGGCTC 688
 Db CCAACCGGTGATACCAAGATATACGCACTCATAGCAGCAACATCTCAACCGGATC 611

689 AGCATGCGCTGTGAGAGTAAACACACAGCAGCAGCATCTGCGCTCAACAGCTTGAC 748
 Db AGCATGCGGTGTGAGAGTGAAGCCCAACAGCCACACACTGCGCTGCAACAGCTTGAC 671

749 CATGACCGGAGCTCTGACGACATGCGCGCTTTGCGGTCTCCGCAAGCTTTGCGGAC 808
 Db TACGACCGGAGCTCTGACGACATGCGGTATGCGCGCTCTCAACCGGATCTTCAACTGC 731

809 ATATGCTCTACTTCTTACCAAGGACCTGCGGTGATGATGCGCGCTGGAATTTCTTATC 868
 Db ATGACCTCGGTCTTCTTATGCGCGGATCTGAAATTTCAACAGAGGAGCGGTCTTATGTC 791

869 AGCTACGAGCAGTGAACCTTCTACCCGCTATGTGATGATGCGGAGGATTAATTTCTGCG 928
 Db AGCTACGAGCAGTGAACCTTCTACCCGCTATGTGATGATGCGGAGGATTAATTTCTTATC 851

929 CAGTCCGCGCTGTCTTCTTCAAGAGAGAGGTGCGGAGCGGTGCTTGAAGTCCG 988
 Db CAGACCTTTTATTTGCTCTCACAGGCGGAGAGTCTCTTACCGCGCTTAACTTATG 911

QY 989 GGGTCCGACATTTCTGAGCTGTGATCCGCTGTGAGCTTCCCTGCGCAATGTTGG 1048
 Db 912 GTATCGCGGTTTCTGAGAGTGTTCGCGCTCTGTGATCTTGTCTCCGAACTGGCT 974

QY 1049 GAGAGGTGCGGTTTGTGCTTTTCACTTCCACCATCTGCGGATTCAGACGTTCATTC 1108
 Db 972 GAACGTTGGGTTGCTGCTCATGCTTGTGCGGTACCGGATTCAGACGTTCAGTTTC 1031

QY 1109 TGCCTGAACCATTTCTGCTCCGACGTGATGTCGGCGCACCCGAGGCAATGACTGTTT 1168
 Db 1032 ACCTCAACCATTTCTGCTCCGACCATATGATGAGGCGCGCGCGCAAGGCACTGTTTC 1091

QY 1169 GAGAAGCAGACGCGGACGCTGACATCTGCTCTCTGATGATGATGTTGTTCCAC 1228
 Db 1092 GAGAGCAGACGAAAGGAGATGATATACGTGCTCCGACCGTGTGATGATGTTCTTT 1151

QY 1229 GGTGGCTGAGTTTCAGATTGAGCACCATCTGTTCCCGCTTACCTGCGTCCACTT 1288
 Db 1152 GTGGGCTGAGTTTCAGATTGAGCACCATCTGTTCCCTTACCTGCGTCCGCGTGGAGCTT 1211

QY 1289 CGAAGTTGACCGGCGCGCGCGCTTGTGAGAGAGATGAGTGGCTCATTTTCTGCA 1348
 Db 1212 AGGAAATGCGCGCTTGTGCTGAGACTGTGTAAGAGACGAGATGCGTATAGAGAGC 1271

QY 1349 GCCACATTTCTG--GATGCAATGTGCTTACATGAGACACTCAGGCGTGTGCAATTG 1405
 Db 1272 TTGGGTTTGGAGACACGCTATATGTCAGACAACTTGCAGCGTGTGAGGATGCGGCTT 1331

QY 1406 CAGGCGGAGACCGCTACAAAGTGTGTGCTCCGAGAAATTTGTAT--GGAGGCTGTG 1462
 Db 1332 CAGGCGGTGACCTTATTTGCGCGCGCTGCTTAAAGAACTTGGTATGAGGAACTTAT 1391

QY 1463 AACACCATGTGATTAATGGAT 1484
 Db 1392 AACACCATGTGATTTGTGT 1413

RESULT 2
 US-09-938-842A-558
 ; Sequence 558, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 558
 ; LENGTH: 1350
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-558

Query Match 24.9%; Score 439.2; DB 10; Length 1350;
 Best Local Similarity 59.8%; Pred. No. 4.4e-110;
 Matches 773; Conservative 0; Mismatches 513; Indels 6; Gaps 2;

QY 189 CCGACGACCTCTGATCTCCATCTCCGCGACGTGTACGACGTACGCGCTGCTCCCG 248
 Db 62 CTGAGATCATATGATGCGATTCAGGCAAGGTCTACAAAGTCTCGATGGATTAATA 121

QY 249 ACCACCCGGGCGGCGACCTCCGCTTCTACACCTTGGCGGGGAGAGCCGACCGACGCT 308
 Db 122 CTCATCCCGGAGGCGACAGGATATCTCAATCTCGTTGTAAGCAAAATGTGACCATTAACA 181
 QY 309 TCGCCGCGCTACACCC---GCCCTGGGCGGCGGCTCTCGGCGGCTTCTGTTGGCC 365
 Db 182 TCAATCCATTTTCATCCCGGAACGCTTGGACCATCTCGACCACTCTCTTCAACGCGTTAAC 241
 QY 366 GCCTCTGTGACGTAGCGGCTTCCCGCGGCTCGGCGCATACGCGCGGCTCTCGGCGAG 425
 Db 242 ACATCAGAGATTTTCAAGTCTCCGAAGTCTCAGCGAGTTACGCTGATGCGTGGAGT 301
 QY 426 TATCTCTCGGCGGCTCTTCTGAAAGCGTCCGCCACCCCAAGGTCAGCTGCTCTGA 485
 Db 302 TTGTAAATCGGCTCTTCTGAAAACAAAGTACAGTACTCTTACACTTACCTTGG 361
 QY 486 TGGCGCTCTTCTTACGCGGCGCTGACTGCTCTCGATGCGGAGCGCTGGGCGG 545
 Db 362 TCGCCGCGCATGTTCTCGAGTCTCTACGAGTGTGCTTGTGCTTACCTCGTCTGCTC 421
 QY 546 ACCTCTCGGCGGCGCTCTTCTGAAAGCGTCCGCCACCCCAAGGTCAGCTGCTCTGA 605
 Db 422 ACCAAATCGCGCGGCTCTGCTCTCTCTGATCCAGAGCGCTTACATAGTCAAG 481
 QY 606 ACTCGGCGCACACCGCATACCGGCGATCCGCTCTCGACGCGTCTGTCAGAGTCTCT 665
 Db 482 ATTCTGTCTATTACGTTATCATGTCGAACAAATCTTATTAACAGATTGCTGAGCTCTCT 541
 QY 666 CCGGGAATGCTCTACCGGCTGAGATGCTCTGTAAGTGAACCAACACGAC 725
 Db 542 CCGGTAATGCTCTACCGGAACTCAATCGGTGTAAGTGAACCAACATGCTCANTC 601
 QY 726 ACATCGCTGCAACAGCTGAGACCAAGACCGGACCTCCAGGACATGCGCTCTTGGCG 785
 Db 602 ATCTACTGTGTACAGCTCGATTAGATCAATCTCAACACATCCCTGCTTGGCGG 661
 QY 786 TCTCCCGCAAGCTGTTCGGGCAATATAGTCTACTTCTACCAAGGACCGTGGCGT 845
 Db 662 TCTCCACCAAAATCTTCTCTCTCATTTGACCTCGAGATTTCTACGATTCGAAACTCAGTTTG 721
 QY 846 ATGCGGCTCGAAATTTCTTCAAGCTACAGCACTGAGACTTCTTCAACCGGTAATGCA 905
 Db 722 ATCAGATCGGAGATTTCTTACGATCATCAACATTTACTTATTAATCCAGTATGCT 781
 QY 906 TCGCCAGATTAATCTTCTCGGCGAGTCCGCTGCTCTCTTCTCAAGGAGAGAGGTGC 965
 Db 782 TTGGAAGAAATCAATCTTCTTCAACAGTTTCTCTGCTCTTCTCAACGTAAGTAC 841
 QY 966 CGGAGCGGTTGCTTGAATGCGGCGGCTGCGCAATTTCTGGGCTTGTACCGGTTGCTG 1025
 Db 842 CAGATGTGCTTTAAACTTTCGCGGAATCTTACTTCTGAGCTTGGTTCCTCACTTTAG 901
 QY 1026 TGGCTTCCCTGCGGAATTTGTTGAGAGAGGCTCGGTTGCTTTTCAAGCTTCAACATCT 1085
 Db 902 TCTCATGTCTACCAACTGCGCGAGAGATTTCTTCTGCTTCTTCAAGGTTCAACGCTCA 961
 QY 1086 GCGGGAATCAGCAGTCAATTTGCTGTAACCACTTCTGTCGAGCGTATGTCGGG 1145
 Db 962 CGCGGCTTCAACATTTCAATTCAGCTTAAACATTTGCTGATGTCATAGTGTGTC 1021
 QY 1146 CACCAAGGCGCATGACTGTTTGAAGAGAGAGCGGAGGCAAGCTGCAATCTGTGCT 1205
 Db 1022 CACCAAGGCGCATGACTGTTTGAAGAGAGAGCGGAGGCAAGCTGCAATCTGTGCT 1081
 QY 1206 CTCCTTGAATGATTTGTTTCAAGGCTGCTGAGATTCAGATTGAGCACTGTGTTT 1265
 Db 1082 GATCATATCATGATGTTGTTTGTGAGATTACAGTTTCAAGTTCATTTGTTTCC 1141
 QY 1266 CCGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1325
 Db 1142 CTGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1201
 QY 1326 AGCATGGGCTCACTTATTTCTGAGCGCAATTTCTGGGCTGCAATGTCCTTACATGAAGA 1385

Db 1202 AGCATATCTTCCGATAGAGATATGTCGTTGTAAGCAAAATGTGACCATTAACA 1261
 QY 1386 CACTCAGGCTGTCTATTCAGGCGGAGACCGCTCAAGTGTGTGCTCCGAATTT 1445
 Db 1262 CTTTGAAGCAGCAGCTTATCAAGCTTGAAGAGAGTGTGCTTATCCGTTGTT---AAGACT 1318
 QY 1446 TGGTATGGAGGCTGTGAACCCATGATTA 1477
 Db 1319 TGGTTGGAGAGCTTGAATCTCATGCTTA 1350
 RESULT 3
 US-10-029-756-4
 ; Sequence 4; Application US/10029756
 ; Publication No. US20020108147A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; DELTA 6-DESATURASE
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/029,756
 ; FILING DATE: 21-Dec-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/934,254
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 8383ZYXWVU
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1685 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-10-029-756-4
 Query Match 20.7%; Score 365.4; DB 14; Length 1685;
 Best Local Similarity 55.8%; Pred. No. 8.9e-90;
 Matches 740; Conservative 0; Mismatches 581; Indels 6; Gaps 2;

QY 155 ATCTCTCCAGAGCTCCGCTCAGCTTCCGCGAGACCTTGTGATCTTCATCTCC 214
 Db 68 ATTACTCAGATGAGACTCAAGAACCAAGATTAACCCGAGATCTATGATCTCGATTCAA 127
 QY 215 GGGGAGCTGTAGAGATGACGCGCTCCGCCACCAACCGGCGGAGGAGCTCCGCGCT 274
 Db 128 GGGAAAGCTATGATGTTTGGATTGGGTAAGACATTCAGGTGGAGCTTCTCTTG 187
 QY 275 CTCACCTGCGCGGCGAGAGCCGACGAGAGCTTGGCGGCTTACCAACCGGCTCGGCG 334
 Db 188 AAGAGCTTCTGCTGCTCAAGAGTAATGATGATTTGTTGATTCATCTGCTCTTACA 247

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Qy 335 CGCCCGCTCCGCGCCGCTTCTTGTTG---CCGCTCTCTGACTAGCGCGTCCCCC 391
Db 248 TGGAGAAATCTGATTAAGTTTTCACCTGGGATATCTTAAAGATTAATCTGTTTTCAG 307
Qy 392 GCGTCCGCCCACTACCGCCGCTCTCGCGAGCTATCTCCGCGGCTCTTGAAGC 451
Db 308 GTTCTTAAAGATTAAGAAAGCTGTGTGATTTCTAAAGATTTGATGACAA 367
Qy 452 GTGGCCCCCAACCCCAAGTCCAGCTGTCTGATGAGCCGCTCTCTACCGCCGCTG 511
Db 368 AAGGATATATATATGTTTGAATCTTGTCTTATACAAAGCTGTGTCTATGAGTGT 427
Qy 512 TACCTCTCTCCGCTACGCGCAGCGCTGCGCGCAGCTCTCGCGGGGGCTCATTTGCG 571
Db 428 TATGGGTTTTTGTGTGAGGGTGTGTGTGATATTTGTTTCTGGGTGTGTGATGGG 487
Qy 572 TTGCTGTGATTCAGTCCGCGTGTGATGGCCACGACTCGGCGCACCGCATCCGCGC 631
Db 488 TTCTTTGATTCAGATGAGTGTGATTTGACATGATGCTGGGCAATATATGATGTCT 547
Qy 632 CATCCGCTCTCCAGCCGCGTGTGACAGTGTCTCCGCGAATGCTCACCGGCTCAGC 691
Db 548 GATTCAAGGCTTAAATTAAGTTATGAGTATTTGCTCAATGCTTTTCAAGAAATAGT 607
Qy 692 ATGCGCTGTGAAAGTGAATCAACACACGACGACATGCGCTGCAAGAGCTGAGCAT 751
Db 608 ATGCTGTGTGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 667
Qy 752 GACCCGAGCTTCGACGACATGCGCTGTGTGCGCTCTCCGCGCAAGCTGTTCGCAACA 811
Db 668 GACCTGATTTACATATATATACATCTTGTGTGTGCTTCAAGTTTGTGTGATCTC 727
Qy 812 TGGTCTACTTCTACCAAGGACCTGCGCTGTGATGCGCTGGAATTTCTTATCAGC 871
Db 728 ACCTCTATTTCTATGAGAAAGGTTGACTTTGACTTTATCAAAATTTTGTGTAAGT 787
Qy 872 TACGAGCACTGAGCACTTCTACCCGTAATGATGCAATGCGCAAGATTAATCTTCGCGCAG 931
Db 788 TATTAACATTTGACATTTTACCTATATATGTGTGTGTGTGTGTGTGTGTGTGTGT 847
Qy 932 TCCGCGCTGTGTCTTCAAGGAGAGAGGTGCGGAGCGGTGTGTGATGAGTCCGCGG 991
Db 848 TCTCTCATATATGTTGTGACCAAGAAATGTGTCTATGAGCTCAGAACTTTGGGA 907
Qy 992 GTGCGCACTTTGCGCTGTGTGATGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1051
Db 908 TGCTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 967
Qy 1052 AGGCTGCGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1111
Db 968 AGAATATATGTTTGTATTTGCAAGTTTATCACTGATGCAAGATGCAAGATTCCTTCC 1027
Qy 1112 CTGAACCACTTCTGTGCGAGCTGTATGTGCGGACCAAGGAGCAATGATGTTGAG 1171
Db 1028 TTGAACCACTTCTTCAAGTTTATGTTGAGAAAGCTTAAAGGAAATATGTTGAG 1087
Qy 1172 AAGCAAGCGGAGGAGCTGTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1231
Db 1088 AAACAAACGAGATGAGACATTTGATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1147
Qy 1232 GGCCTGAGTTTCAGATTGAGACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1291
Db 1148 GGAATGCAATTCCTCAATTTGACATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1207
Qy 1292 AAGGTCACACGCGCGCTTCGCGACTTTTGAAGAGATGAGGCTCACTTATTTGCGAGC 1351
Db 1208 AAATATCTGCGCTTACGATGATGATTAATGCAAGAAATTAATGCTTCAATTAATGCA 1267
Qy 1352 ACATTTCTGGGTGCAATGTGCTTACATGAGAGCACTCAGAGGCTGTGCTGATTCAGGCG 1411
Db 1268 TCTTTCTCAAGGCAATGAAATGACACTCAGAACTTGTGAGAACACAGCATTCAGGCT 1327

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Qy 1412 AGGACCGCTACAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1471
Db 1328 AGG---GATATACCAAGCGGCTCCGGAAGATTTGTATGGAAGCTCTTACACTCAT 1384
Qy 1472 GATATAA 1478
Db 1385 GATATAA 1391

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RESULT 4

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US-09-923-876-5116
; Sequence 5116, Application US/09923876
; Patent No. US2002013958A1
; GENERAL INFORMATION:
; APPLICANT: Ialjudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ico)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 5116
; LENGTH: 265
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURES:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700456385H1
US-09-923-876-5116

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Query Match 13.5%; Score 237.8; DB 9; Length 265;
Best Local Similarity 93.6%; Pred. No. 4, 6e-55;
Matches 248; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Qy 728 ATGCGCTGCAACGCTGGAACATGACCGGACCTTCAGACATGCGCGCTTGTGCGCTG 787
Db 1 ATGCGCTGCAACGCTGGAACATGACCGGACCTTCAGACATGCGCGCTTGTGCGCTG 60
Qy 788 TCCGCCAAGCTGTGCGCAACATATGCTCTACTTCTTACCAAGGACCTCGCGCTGAT 847
Db 61 TCCGCCAAGCTGTGCGCAACATATGCTCTACTTCTTACCAAGGACCTCGCGCTGAT 120
Qy 848 GCGCGCTGCAAAATCTTCACTACGCTACGACATGACCTTCAACCGGTAATGTCATC 907
Db 121 GCGCGCTGCAAAATCTTCACTACGCTACGACATGACCTTCAACCGGTAATGTCATC 180
Qy 908 GCCAGATTAATCTTCTGCGGAGTCCGCGCTGTGTGTCTCAGGAGAAAGAGGTCGCG 967
Db 181 GCCAGATTAATCTTCTGCGGAGTCCGCGCTGTGTGTCTCAGGAGAAAGAGGTCGCG 240
Qy 968 CAGCGGTGCTTGAGATTCGCGGCGG 992
Db 241 CAGCGGTGCTTGAGATTCGCGGCGG 265

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RESULT 5

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US-09-923-876-5116
; Sequence 5116, Application US/09923876
; Publication No. US20030237110A9
; GENERAL INFORMATION:
; APPLICANT: Ialjudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ico)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06

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;; PRIOR APPLICATION NUMBER: 09/298,329
 ;; PRIOR FILING DATE: 1999-04-21
 ;; PRIOR APPLICATION NUMBER: 60/085,331
 ;; PRIOR FILING DATE: 1998-05-05
 ;; NUMBER OF SEQ ID NOS: 6332
 ;; SOFTWARE: PERL Program

;; SEQ ID NO 5116
 ;; LENGTH: 265
 ;; TYPE: DNA
 ;; ORGANISM: Zea mays
 ;; FEATURE:
 ;; NAME/KEY: misc feature
 ;; OTHER INFORMATION: Incyte ID No. US20030237110A9 700456385H1
 US-09-923-876-5116

Query Match 13.5%; Score 237.8; DB 12; Length 265;
 Best Local Similarity 93.6%; Pred. No. 4,6e-55;
 Matches 246; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 728 ATGCGCTGCAACAGCTGAGCATGACCGGACCTCCAGACATGCGCGTCTTGGCGTC 787
 Db 1 ATGGCTGCAACAGCTGAGCATGACCGGACCTCCAGACATGCGCGTCTTGGCGTC 60
 Qy 788 TCCCCCAAGCTGTCGGCAACATATGCTCTTCTTACCAAGGACCTGCGTTCAT 847
 Db 61 TCCCCCAAGCTGTCGGCAACATATGCTCTTCTTACCAAGGACCTGCGTTCAT 120
 Qy 848 GCGCGCTCGAAATTTCTTATCAGCTACAGACATGACCTTCTTACCGCGTAAATGTCATC 907
 Db 121 GCGCGCTCGAAATTTCTTATCAGCTACAGACATGACCTTCTTACCGCGTAAATGTCATC 180
 Qy 908 GCCAGATAATCTTCTCGCGAGTCGCGCTGTTCTTCAACGGAAGAGGTCGCG 967
 Db 181 GCCAGATAATCTTCTCGCGAGTCGCGCTGTTCTTCTGCTGACGGAAGAGGTCGCG 240
 Qy 968 CAGCGTTCCTTGAATCGCGGCG 992
 Db 241 CAGCGTTCCTTGAATCGCGGCG 265

RESULT 6
 US-09-770-149-494/C
 ; Sequence 494, Application US/09770149
 ; Patent No. US20020059663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gorlach, Jörn
 ; APPLICANT: An, Yong-Qiang
 ; APPLICANT: Hamilton, Carol M.
 ; APPLICANT: Price, Jennifer L.
 ; APPLICANT: Raines, Tracy M.
 ; APPLICANT: Yu, Yang
 ; APPLICANT: Rameaka, Joshua G.
 ; APPLICANT: Page, Amy
 ; APPLICANT: Matthew, Abraham V.
 ; APPLICANT: Ledford, Brooke L.
 ; APPLICANT: Moesner, Jeffrey P.
 ; APPLICANT: Haas, William David
 ; APPLICANT: Garcia, Carlos A.
 ; APPLICANT: Krickler, Maja
 ; APPLICANT: Slader, Ted
 ; APPLICANT: Davis, Keith R.
 ; APPLICANT: Allen, Keith
 ; APPLICANT: Hoffman, Neil
 ; APPLICANT: Hurdan, Patrick
 ; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 ; FILE REFERENCE: 2024 (PABA-013PRV)
 ; CURRENT APPLICATION NUMBER: US/09/770,149
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 60/178,506
 ; PRIOR FILING DATE: 2000-01-27
 ; NUMBER OF SEQ ID NOS: 999
 ; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 494
 ;; LENGTH: 657
 ;; TYPE: DNA
 ;; ORGANISM: Arabidopsis thaliana
 US-09-770-149-494

Query Match 11.6%; Score 203.8; DB 9; Length 657;
 Best Local Similarity 62.2%; Pred. No. 1.5e-45;
 Matches 338; Conservative 0; Mismatches 202; Indels 3; Gaps 1;

Qy 984 TCGCGGGGTCGCCACATTCGCGCTTGGTACCCGTTGCTGCTGCTCCGCGCAATT 1043
 Db 642 TCGCGGAAATCTAGCTTCTGAGCTTGGTCCACTTATGCTATGCTATGCTATGCT 583
 Qy 1044 GGTGGAGAGGTCGCGTTTGTCTTTCAGCTTCCATCTCGCGGATTCAGCACTGC 1103
 Db 582 GGTGGAGAGGTCGCGTTTGTCTTTCAGCTTCCATCTCGCGGATTCAGCACTGC 523
 Qy 1104 AATTGCTGAAACCACTTCTGTCGAGCTGATGTCGGGCAACCAAGGCAATGACT 1163
 Db 522 AATTGCTGAAACCACTTCTGTCGAGCTGATGTCGGGCAACCAAGGCAATGACT 463
 Qy 1164 GGTGGAGAGGTCGCGTTTGTCTTTCAGCTTCCATCTCGCGGATTCAGCACTGC 1223
 Db 462 GGTGGAGAGGTCGCGTTTGTCTTTCAGCTTCCATCTCGCGGATTCAGCACTGC 403
 Qy 1224 TCCAGGTGCTGCAATTCAGATTCAGCACTGCTGCTCTCTTGGATGATGCT 1283
 Db 402 TCTTGGTGAATTAAGTTTCAAGCTTGAACATCTTCTGATGATGATGATGATG 343
 Qy 1284 ACCTTGCAAGGTGTCACCGGCTGCGGACCTTTCAGAAAGCAATGAGCTCACTAAT 1343
 Db 342 ATCTCGGAAAGTTTCTCGGCTGCTTCAAGAGCTTTCAGAAAGCAATCTTCCGTA 283
 Qy 1344 CTCAGCCACATTCGCGGTGCAATGCTTTCATGAGAACTCAGGCTGCTGAT 1403
 Db 282 GAGATGTCGTTGTTGAAGCAATGTTGATCACTTGAAGAGAGGAGCTT 223
 Qy 1404 TGCAGCCAGACCGCTACAGTGTGCTCCGAAAGTTTGGATGAGAGGCTGTA 1463
 Db 222 ATCAAGCTGAGACCGGCTAATCCGCTGTT---AAGAACTTGGTGGAGGCTTTGA 166
 Qy 1464 ACACCCATGATTAATGAGATGAGTACGGGCTATGAGCACTTGTGTTACGCTT 1523
 Db 165 ATACTAGCTTAATGATTTTATCAAAACAAATATCTTTGTTGGTTAAATTG 106
 Qy 1524 GTG 1526
 Db 105 ATG 103

RESULT 7
 US-09-878-574-3260
 ; Sequence 3260, Application US/09878574
 ; Patent No. US20020110548A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Byrum, Joseph R.
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Thompson, Michael D.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(15401)B
 ; CURRENT APPLICATION NUMBER: US/09/878,574
 ; CURRENT FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: 09/333,535
 ; PRIOR FILING DATE: 1999-06-14
 ; NUMBER OF SEQ ID NOS: 15775
 ; SEQ ID NO 3260
 ; LENGTH: 287
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; NAME/KEY: unsure


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; CURRENT APPLICATION NUMBER: US/09/770,444
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,502
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(476)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-444-39

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Query Match      7.3%; Score 129; DB 9; Length 476;
Best Local Similarity 55.8%; Pred. No. 4.5e-25;
Matches 265; Conservative 0; Mismatches 207; Indels 3; Gaps 1;

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QY 261 GGCAGCTCCGCTTCAACCTGCGGGGAGAGCCGACCGGCTTCCGCGCTAC 320
DB 1 GGCAGCGGTGATCTCAATCTGTTGTAAGACGTCACCGATGCTTTCATGCAATTC 60
QY 321 ACCC--GCCCTGCGCGCGCGCGCTCTCCGCGCTTCTTGTGCGCGCTCTGACT 377
DB 61 ATCCCGGAACCGTTGGACACATCTGACCATCTTTCACCGGTACACATCAGAGATT 120
QY 378 AGCGCTCTCCCGCGGTGCGCGGACTACCGCGCTCTCTGCGGAGCTATCTCGCGG 437
DB 121 TCCAACTCTCGAAGTCTCAACGAGATTACCGTGTGCTGCGGAGTTTCTAAACTG 180
QY 438 GCGCTTTCAGACCGGTGCGCGGCGGACCCGACCGTCCAGCTCTGCTGATGCGCTCT 497
DB 181 GTCTCTTCAAAACAAAGTCAAGTCACTCTTACACTTGAAGCTTGTGCGCGCATGT 240
QY 498 TCTACCGCGGTGATCTGCTGCTGCTGATGCGCGGCGGCGGCGGCGGCGGCGG 557
DB 241 TCTCTCGAGTCTCTACGAGTGTGTTGCTTGTACCTTCCGCTTCCACCAATGCGG 300
QY 558 GGGGTCTCATTTGCTTGTGATCCAGTCCGCGTGTGATGCGGCGGCGGCGGCGG 617
DB 301 CGCGGCTTCTCGGTCTCTCTGTGATCCAGGCGCTTACATAGGTCAAGATTGTGCTAT 360
QY 618 ACCGATCAACCGGCGGCGGCTCTGACCGCGGTGCGGAGTCTCTCGGGAATGCC 677
DB 361 ACCTTATCATGTGCAAAATCTTATTAACAGATTGCTCTCTTNNGGTAACTGTG 420
QY 678 TCACGCGGCTGACATGCGCTGTGAGAGTAAACCAACAGCAACCAATGCG 732
DB 421 TCACGGAATCTCAATGCGGTGAGAGTGAAGTCAACATGCTCATCATCTAGC 475

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RESULT 10
; US-10-156-761-2285
; Sequence 2285, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02

```

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; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2285
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1095)
US-10-156-761-2285

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Query Match      6.8%; Score 120.6; DB 15; Length 1095;
Best Local Similarity 46.8%; Pred. No. 1.3e-22;
Matches 457; Conservative 0; Mismatches 484; Indels 36; Gaps 1;

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QY 385 CTCCCGCGGCTCGCGAATACCGCGCTCTCGCGGAGCTATCTCGCGGCGCTTT 444
DB 54 CACCGCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 113
QY 445 CGAAGCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 504
DB 114 CGACCTGATCCCGGCTACTATAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 173
QY 505 CGGCTGATCTGCTCTGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 564
DB 174 CGGCTTCCGCGGCTTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 233
QY 565 CATGCTTCTGCTGATCCAGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 624
DB 234 GATGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 293
QY 625 CACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 684
DB 294 GTTCCGAGCAAGAAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 353
QY 685 CCTCAGCATGCGCTGTGAGAGTGAACCAACAGCAACAGCAACAGCAACAGCT 744
DB 354 GGTACGCTTCCGCTGTGAGTGAACCAACAGCAACAGCAACAGCAACAGCAAC 413
QY 745 GGAACATGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 804
DB 414 GGAACATGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 437
QY 805 CAACATGATGCTTCTTCAACAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 864
DB 438 GCGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 497
QY 865 CATCAGCTACGAGCACTGAGCTTCTTCAACAGGAGCGGCGGCGGCGGCGGCG 924
DB 498 CTTGCGCTTCAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 557
QY 925 CGGCGAGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 984
DB 558 GAAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 617
QY 985 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1044
DB 618 CTTGCTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 677
QY 1045 GTGAGAGAGGCTGCGGCTTGTGCTTTCAGCTTCAACATCTCGGAGATTACAG 1104
DB 678 CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 737
QY 1105 ATTGCTGTAACCACTTCTGCTGCGAGTGTATGTGCGGCGGCGGCGGCGG 1164
DB 738 CTTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 797
QY 1165 GTTGAAGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1224
DB 798 GCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 857
QY 1225 CCACGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1284
DB 858 CTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 917

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QY 1285 CCTTGGCAAGTTGCACCGGCGGCTTTCGACAGATGAGGCTTATTC 1344
 DB 918 CTTGGCGCGCGCGCGGCTTACCTTACCGGCTTACTGCGCGCGGCTTGTCA 977
 QY 1345 TGCAGCCACATCTTGGG 1361
 DB 978 CGAGGTGCGGTTCTGGG 994

RESULT 11

US-10-156-761-1/c
 ; Sequence 1, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; CURRENT FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 1
 ; LENGTH: 9025608
 ; TYPE: DNA
 ; ORGANISM: Streptomyces avermectilis
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (4187715)
 ; OTHER INFORMATION: a, t, c, g, other or unknown
 ; US-10-156-761-1

Query Match 6.8%; Score 120.6; DB 15; Length 9025608;
 Best Local Similarity 46.8%; Pred. No. 6.1e-21;
 Matches 457; Conservative 0; Mismatches 484; Indels 36; Gaps 1;
 QY 385 CTCTCCCGCGCTCCGCGACTACCGCGCTCTCTGCGGAGCTATCTCTCGCGGCTCTT 444
 DB 2801106 CACCGGCGCTTCCGCGACGTTCCCGCACTGCTCAACGCGTCAAGCGGAGGCTTCT 2801047
 QY 445 CGAAGCGGTGGGCGCCCAAGGTCAGCTGCTGTGATGAGCGGCTCTCTTCTAAGC 504
 DB 2801046 CGACCTGATCCCGGCTACTACTAGGCGGCTGGCGCTTAACAACAGCTGCTGTGT 2800987
 QY 505 CGGCTGTACTCTGCTCTGCTGATGCGGACGCGCTGGGCGCACCTCTCTCGCGGCGGTCT 564
 DB 2800986 CGGGTTGCGCGGCTTCTTGGCGGCGGCACTGTGTGTGCACTGTGTGTGCGCTGTG 2800927
 QY 565 CATGGCTTGTGTGATGCTGATGCTGCTGATGAGGCGCACTGCGGCGCAACCGCAT 624
 DB 2800926 GATGGGCTGTGTGCGGCGTACGCTTCTCATGTGCGACAGCGCGGCGCAAGGCGAT 2800867
 QY 625 CACGGGCAATCGGCTCTCTGACCGCGCTGCGAGGTCTCTCCGGGAACTGCTCAACCGG 684
 DB 2800866 GTTCCGAGCAAGAGCGCGCTCTCGCGGATTAATTTCAAGCAACTCTGTCAACGG 2800807
 QY 685 CCTCAGCATGCTCTGTGTGAAGTGAACCAACAGCAACGCAATGCGCTGTCAACAGCTT 744
 DB 2800806 GGTCACTTGT 2800747
 QY 745 GAGCATGACCGGACCTTCAGACATGCGGCTTTTGGCGGTCTCCCAAGCTGTTCGG 804
 DB 2800746 GGACATGACCGGACATC-----GGCGG 2800723

QY 805 CAACATATGCTCTACTTCTTACCAACGAGACCTTGCGGTTTCATGCGGCTCGAAATCTT 864
 DB 2800722 GCGCACCGCATTTTGAATCAAGATACCGGACCGCGGCGGACACAGATTCAT 2800663
 QY 865 CATACCTTACCAAGACTGACCTTCTTACCGGTAATGTGATGCGCAAGATTAATCTTCT 924
 DB 2800662 CGTGGCTTACAGAGGCTGTGTCTTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2800603
 QY 925 CGGAGTCCGCGCTTGT 984
 DB 2800602 GAGAGCGGCTGTCTTGT 2800543
 QY 985 CGCGGGGCTGCGACATTTCTGTGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1044
 DB 2800542 CTTGTCTTGT 2800483
 QY 1045 GTGGAGAGGCTGCGT 1104
 DB 2800482 CTTGCGGCTGCGCTTGT 2800423
 QY 1105 ATTCTGCTGAACTTCTCTGTCGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1164
 DB 2800422 CTTGCGGCTGAACTTCTCTGTCGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2800363
 QY 1165 GTTGTGAAGACAGACGCGACGCTGCAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1224
 DB 2800362 GCTGAGAGCGGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2800303
 QY 1225 CCAAGGTGCTGTGACGCTTCAAGTTGAGACCAATCTGTGTGTGTGTGTGTGTGTGTGTGT 1284
 DB 2800302 CTACGCGGCTCTCAATCAAGGTGAGACCACTGTGTGTGTGTGTGTGTGTGTGTGTGT 2800243
 QY 1285 CCTTCCCAAGTTGACACCGGCGCTGCGGACCTTGTGCAAGAGCAAGGCTCACTATTC 1344
 DB 2800242 CTTGCGGCGCGCGCGCTGAACTACCGGCTTACTGTGCGCGGCTGTGTGTGTGTGTGT 2800183
 QY 1345 TGCAGCCACATCTTGGG 1361
 DB 2800182 CGAGGTGCGGTTCTGGG 2800166

RESULT 12

US-09-924-035A-370/c
 ; Sequence 370, Application US/09924035A
 ; Patent No. US20020142319A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Glaxo, Jm
 ; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 ; FILE REFERENCE: 2011US
 ; CURRENT APPLICATION NUMBER: US/09/924,035A
 ; CURRENT FILING DATE: 2000-08-11
 ; PRIOR APPLICATION NUMBER: US 60/148,784
 ; PRIOR FILING DATE: 1999-08-13
 ; NUMBER OF SEQ ID NOS: 900
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 370
 ; LENGTH: 480
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-924-035A-370

Query Match 6.5%; Score 115.2; DB 10; Length 480;
 Best Local Similarity 61.0%; Pred. No. 2.8e-21;
 Matches 205; Conservative 0; Mismatches 128; Indels 3; Gaps 1;
 QY 1191 TGCATCTCTGTGCTCTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1250
 DB 478 TGCATCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419
 QY 1251 AGCACCATCTGTGTCCCGCTTACCTGCTGTCACCTTGTGCAAGGTTGACCGGCGTCC 1310
 DB 418 AGCATATTTGTTTCCCGCTTACCTGCTGTCACCTGCTGTCACCTGCTGTCACCTGCTGTCAC 359

QY 1311 GCGACCTTGGCAAGACGAGCTCACTATTCTGCAGCCACATTCTGGGGTCAATG 1370
 DB 358 AAGACCTTGGCAAGACGATATCTCCGTATAGAGATGCTGCTTTGAAGCAATG 299
 QY 1371 TGTCTACATGAGACACTGAGGCTGCTGCATTGCAGCCAGACCCCTCAAGTGGTG 1430
 DB 298 TGTTCACCATTTAACAATTGAGACAGAGCTTATCAAGCTAAGACGTGGCTAATCCG 239
 QY 1431 GTGCTCCGAGAAATTTGGATGGAGGCTGAGAACCCATGATTAATGGATGAAGAT 1490
 DB 238 TGGTT---AAGAACTTGGTTGGGAGCTTGAATATCTCATGCGCTAATGATTTAATCA 182
 QY 1491 ACGGGCTAATGCGCACTTCTGGTTTTCAGCTTGGTG 1526
 DB 181 AAACAAATATGCTTTTGTGGGTTAATTTGAATG 146

RESULT 13
 US-09-878-574-9255
 ; Sequence 9255, Application US/09878574
 ; Patent No. US20020110548A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Byrum, Joseph R.
 ; APPLICANT: Thompson, Michael D.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(15401)B
 ; CURRENT APPLICATION NUMBER: US/09/878,574
 ; PRIOR FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: 09/333,535
 ; NUMBER OF SEQ ID NOS: 15775
 ; SEQ ID NO 9255
 ; LENGTH: 263
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; OTHER INFORMATION: Clone ID: 701102270H1
 US-09-878-574-9255

Query Match 6.5%; Score 114; DB 10; Length 263;
 Best Local Similarity 68.1%; Pred. No. 4.6e-21;
 Matches 173; Conservative 0; Mismatches 80; Indels 1; Gaps 1;

QY 641 CTGACCGCGTGTGCTGAGTGTCTCTCGGAGACTGCTCAGCGCTCAGCATGCGCTG 700
 DB 11 CTGAGCGGCTCGAGCAATCTTTGTGGCAATTGATGATGATGATGATGATGATG 70
 QY 701 TGAAGGTATACACAAACAGCAGCATGCTGCAAGAGCTGAGCAATGACCCGAG 760
 DB 71 TGAAGGTGACTACAAATGCTCAACATCTCATGAAATGATGATGATGATGATGATG 129
 QY 761 CTCAGACATGCGCTCTTTGCGGTCTCCCAAGCTGTGGCAACATATGATGCTTAC 820
 DB 130 TTCAGACATGCTCTTTGCGGTCTCCCAAGCTGTGGCAACATATGATGCTTAC 189
 QY 821 TTTTACCAACGAGCCTTGGGTTGATGCGGCTCGAAATTTCTTCATGACTACGAC 880
 DB 190 TTTTATGGAAGAAATGGGTTCGATTTATATCAAGGTTCTCATGCTACGACGAC 249
 QY 881 TGAACCTTACGCC 894
 DB 250 TTCACATTTTACCC 263

RESULT 14
 US-09-967-477B-7
 ; Sequence 7, Application US/09967477B
 ; Patent No. US20020156254A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xiao Qiu
 ; APPLICANT: Haiping Hong

;; TITLE OF INVENTION: PAD4, PAD5, PAD5-2, AND PAD6, NOVEL
 ;; FILE REFERENCE: BNZ-001
 ;; CURRENT APPLICATION NUMBER: US/09/967,477B
 ;; PRIOR FILING DATE: 2002-04-16
 ;; PRIOR APPLICATION NUMBER: 60/236,303
 ;; PRIOR FILING DATE: 2000-09-28
 ;; PRIOR APPLICATION NUMBER: 60/297,562
 ;; NUMBER OF SEQ ID NOS: 8
 ;; SOFTWARE: FastSeq for Windows Version 4.0
 ;; SEQ ID NO 7
 ;; LENGTH: 1380
 ;; TYPE: DNA
 ;; ORGANISM: Thraustochytrium sp.
 ;; FEATURE:
 ;; NAME/KEY: CDS
 ;; LOCATION: (1)...(1380)
 US-09-967-477B-7

Query Match 6.3%; Score 112; DB 10; Length 1380;
 Best Local Similarity 47.0%; Pred. No. 3.3e-20;
 Matches 612; Conservative 0; Mismatches 600; Indels 90; Gaps 5;

QY 138 CCGGCGACGTGGGCAATGATCTCTCCAGAGACTCCGCGCTTCCGCGACGACC 197
 DB 17 CTGAGTGAAGCGCTGAGACTGGAAGAGATCCGAGACCGACCGCCGACCG 76
 QY 198 TCTGATCTCATCTCCGCGAGCTGTAGAGCTACGCGCCCTGGCTCCCGACCAACCG 257
 DB 77 CGTGATGTGATTTACCAACAAAGTCTAGACATCTCCAAAGTGGAGCTCGACCGGGTG 136
 QY 258 GCGGAGACCTCCCGCTTCTCAACCTGCGGCGGAGAGCCACCGACCTTTCGCGCT 317
 DB 137 GCTCCGT-----GATGCTCAAGCAGCGCGGAGAGAGCCACCGACCGCTTTCGCGCT 190
 QY 318 ACCACCGCGCTGCGGCGCGCGCGCTCCCGCGCTTCTTGTGGCGCGCTTCTGACT 377
 DB 191 TCCACCGCTCTCGCGCTCAAGCTGCTGAGAGCTTCAAGTCTGAGCGAGCGAGAA 250
 QY 378 ACGCG----- 383
 DB 251 CCTCAAGCGGAGATTCAGGGGGAGCGGAGAGAGAGAGCGCGCGCGCGAGC 310
 QY 384 ---TCTCCCGCGCTCCCGCACTACCGCGCTCTCTGCGACGTATCTTCGCGGCGC 440
 DB 311 GCATCAAGATTCATTCGCGCTTACCGCTCTGCGCTGCAAGGTCAAGGGCATGGGCG 370
 QY 441 TCTTGAACGAGTGGGCGCCCAACCCCAAGGTCAGCTGCTGTATGAGCGCTCTCTTCT 500
 DB 371 TCTAAGAGCGCAGCGCGCTTCTAAGCGGTGAGAGCTGTGAGCACTTTCGCGCATGCGCG 430
 QY 501 ACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
 DB 421 TGTCTGATGCGCATCTGCTTCTTCTTCAACATTTTGGCATATATGATGATGATGATG 490
 QY 561 GCTCATTTGCTTGTCTGATTCAGTTCGCGCTGATGAGGCGACGACTCGGCGACCAAC 620
 DB 491 TGAATTAAGGGCTTTTTCACAGCAAGTCGAGTGGCGGCGACGACTTCTTTCGACAAAC 550
 QY 621 GCATCACCGGCGCATCGGCTCTGACCGCGCTGCGAGGTCGCTGCTGCGGGAAGCGCTCA 680
 DB 551 AGTGTGAGAAACCGACGCTGGCAACTTATCGGCTGCTGCTGCGGAGAGCGCTGCG 610
 QY 681 CCGGCTCAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 740
 DB 611 AGGCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 667
 QY 741 GCTTGACCATGACCGGACCTCCAGACATGCGCGCTTTCGCGCTTCCCGCAAGCTGT 800
 DB 668 ACTTGACAGCGCGCAGAGAGAGGCTTTCATGCGCGACCGGACATGACATGATGCGCG 727
 QY 801 TCGCAACATATGATGCTTCTTCTTCAACAGGACCTGCGGCTTGCATGCGCGCTCGAAAT 860

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Db      728  TGCTGGCGTGGTCTTAAGAGATGGCGGCGAAGCGCTTGAGTCCGGCGACAGGCGCG---T 784
Qy      861  TCTTCATAGCTACCAAGCACTGGACCTTCTACCCGGTAATGTGATCGCCAGAGATAATC 920
Db      785  TCTTCATCCGGAACAGCGCGTTCATACCTTCCCGCTGCTGCTCCGCGCTCGACT 844
Qy      921  TTTCGCGCAGTCCGCGCCCTGTTCGTTTCAAGGAG-----AAGA 959
Db      845  GCGTCCGCGCACTGTTCTTCTAAGGTTTCAACGAACTTCTCGTGGCACTTTCGCAAGG 904
Qy      960  GGGTCCGCGCAGCGGTTGCTTAGATCGCGGGGTGCGCAATCTGGGCTTGGTACCCT 1019
Db      905  TCGAGTTGCAAGGCAACCGGAAGAGCGGGGTGTGATGTGCACTACATCTGGACGTCGGGA 964
Qy      1020  TGTCTGTGGCTTCCCTGCGCAATTGTGTGGAGAGGGTTCGCGTTGTGCTTTCAAGTTCA 1079
Db      965  TCCCGTACTTGTGCAACATGAGCCCTGTTTGAAGGGGTGGCACTACTCTCAATGGGCTCAG 1022
Qy      1080  CCATCTGGGGGATTGAGCAGCTCCAAATTCTGCTGAACACACTCTGTCGACGTTATG 1139
Db      1025  CGTCTGTGGGCTTGCTCTTGCGCGCTGTGTTCAGTATTTGGCCACAAGCGCATGTGGGT 1088
Qy      1140  TCGGGCCACCCAGGGCAATGACTGTGTTTGAAGAACAGACGCGACGCAAGCTCGACATCC 1199
Db      1085  ACGAGCGGAAACCAAGCCGGAAGCTTCTGGCAGCTGCAAGTGACCAAGACGGCAATCC 1144
Qy      1200  TGTGCTCTCTTGATGATTTGTTTCCACGCTGCTGCAAGTTCCAGATTGAGACCATC 1255
Db      1145  GCGCGTCCGTAATCATGAGCTGGTTCAACCGGCTGTTAATCATCAGATCGACATCC 1204
Qy      1260  TGTTCCTCCGCGCTACCTCGGTGGCCACTTTCGCAAGTTGCAACCGGCGCGGCACTTT 1319
Db      1205  TGTTCCTCCGCTGTGCGCGGCCACAACATTGCCAAAGTCAAGGTGCTCATCAAGTGTAT 1266
Qy      1320  GCAGAAAGCATGGGCTCACTTATTTCTGACGCCAATTTCTGGG 1361
Db      1265  GCAAGGAGTTGCACATCCCGTTCCACGAGACCGGCTTGGG 1306

RESULT 15
US-10-032-393-47/c
; Sequence 47, Application US/10033393
; Publication No. US2003027286A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Wall, Daniel
; APPLICANT: Gross, Mollie
; TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
; FILE REFERENCE: ELITRA.010A
; CURRENT APPLICATION NUMBER: US/10/032,393
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/255,434
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 09/948,993
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 12733
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vector pEPEFL4
; US-10-032-393-47

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[illegible]

Search completed: January 1, 2004, 05:19:13
Job time : 458.973 secs

Query Match	5.7%	Score 100.4	DB 15	Length 12733
Best Local Similarity	45.4%	Pred. No. 1.3e-16		
Matches 359	Conservative 0	Mismatches 431	Indels 0	Gaps 0

4 CGAGCTCCCTCTCTCTCCCAATCTCCCCGCTCCCCCTACCAATACAGCACCAACCA 63

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:54:32 / Search time 3928.96 Seconds
(without alignments)
14889.683 Million cell updates/sec

Title: US-09-857-524B-3
Perfect score: 1764
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 33363688 seqs, 1658189874 residues

Total number of hits satisfying chosen parameters: 66727376

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1764	100.0	1764	33	US-09-857-524B-3
2	1406.4	79.7	2067	55	US-10-612-783-1024
3	1349	76.5	1541	48	US-10-219-999-27869
4	1349	76.5	1541	52	US-10-425-114-14218

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5 1333.8 75.6 2054 1 PCT-US03-07858-288 Sequence 288, App
6 1333.8 75.6 2054 1 PCT-US03-07858-288 Sequence 288, App
7 1333.8 75.6 2054 1 PCT-US03-07858-288 Sequence 288, App
8 1333.8 75.6 2054 2 PCT-US03-07858-288 Sequence 288, App
9 1333.8 75.6 2054 51 US-10-389-566-288 Sequence 288, App
10 1333.8 75.6 2054 53 US-10-613-520-288 Sequence 288, App
11 1175 66.6 1448 30 US-09-654-617-265928 Sequence 265928,
12 1175 66.6 1448 38 US-09-684-016-265928 Sequence 265928,
13 1091.4 56.7 1944 53 US-09-857-524B-9 Sequence 9, Appl1
14 1000.6 56.7 1944 53 US-10-437-963-83761 Sequence 83761, A
15 973.6 55.2 14392 51 US-09-702-134-25614 Sequence 25614, A
16 973.6 55.2 14392 34 US-09-815-264-72548 Sequence 72548, A
17 973.6 55.2 14581 27 US-09-620-392-30987 Sequence 30987, A
18 891.4 50.5 1407 86 US-60-312-544-3168 Sequence 3168, Ap
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31 491.2 27.8 1702 30 US-09-685-775-26 Sequence 26, Appl
32 491.2 27.8 1702 44 US-10-029-756-26 Sequence 26, Appl
33 486.6 27.6 514 65 US-60-110-784-6 Sequence 6, Appl1
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36 486.2 27.6 1940 52 US-10-424-599-36789 Sequence 36789, A
37 486.2 27.6 1934 35 US-09-857-524B-7 Sequence 7, Appl1
38 479.8 26.3 615 36 US-09-865-419A-52475 Sequence 52475, A
39 453.8 25.7 110149 23 US-09-534-859-381 Sequence 381, App
40 453.8 25.7 110149 34 US-09-803-736-381 Sequence 381, App
41 452 25.6 1465 22 US-09-513-996A-34823 Sequence 34823, A
42 452 25.6 1465 31 US-09-708-427-1024 Sequence 1024, Ap
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44 452 25.6 1650 22 US-09-513-996A-68612 Sequence 68612, A

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ALIGNMENTS

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RESULT 1
US-09-857-524B-3
; Sequence 3, Application US/09857524B
; GENERAL INFORMATION:
; APPLICANT: Edgar B. Cahoon
; APPLICANT: Rebecca E. Cahoon
; APPLICANT: William D. Hitz
; APPLICANT: Anthony J. Kinney
; TITLE OF INVENTION: Membrane-Bound Desaturases
; FILE REFERENCE: B01264
; CURRENT APPLICATION NUMBER: US/09/857, 524B
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/110,784
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Zea mays
US-09-857-524B-3

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Query Match 100.0%; Score 1764; DB 35; Length 1764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2

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 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53373)A
 ; CURRENT APPLICATION NUMBER: US/10/612.783
 ; CURRENT FILING DATE: 2003-07-02
 ; NUMBER OF SEQ ID NOS: 7098
 ; SEQ ID NO 1024
 ; LENGTH: 2067
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4577_136542C.1
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Query Match 79.7%; Score 1406.4; DB 53; Length 2067;
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Db	1222	CCCAAGGGCAACGACTGGTTCGAGAAAGACAGACGAGCAGCAGCTTGACATCCTGTGCTCT	1281
Qy	1208	CCTTGATGATGATTTGGTTTCCACGATGCTCTGACATGCTTCAGATTGACACCATCTGTTCCC	1267
Db	1282	CCTTGATGATGATTTGGTTTCCACGATGCTCTGACATGCTTCAGATTGACACCATCTGTTCCC	1341
Qy	1268	CGCCTACCTCGGATGACCTTTCGACAGGTTGCAACGAGCGGCTGCGGACCTTTGCAAGAG	1327
Db	1342	CGCCTACCTCGGATGACCTTTCGACAGGTTGCAACGAGCGGCTGCGGACCTTTGCAAGAG	1401
Qy	1328	CATGGGCTCACTTATTTGACAGCCACATCTGGGGTGCAGAAATGCTTTACATGGAAGACA	1387
Db	1402	CATGGGCTCACTTATTTGACAGCCACATCTGGGGTGCAGAAATGCTTTACATGGAAGACA	1461
Qy	1388	CTCAGGGCTGCTGCATTTGACAGCCACGCTACA-----AGTGTGTGTCTCCGAG	1441
Db	1462	CTCAGGGCTGCTGCATTTGACAGCCACGCTACA-----AGTGTGTGTCTCCGAG	1521
Qy	1442	AATTTGGTATGGAGGCTGTGAACCCCATG---GATAATGGGATGAAGATACG---	1494
Db	1522	AATTTGGTATGGAGGCTGTGAACCCCATGATGATTAACGGGACGAGATATGGCTGA	1581
Qy	1495	GCTAATGGCACTTCTGTG- TTCACTTGGTGCCCATGTGATTTGTCTGATGC-----C	1548
Db	1582	GGGAGGCACTTCTGTGTTGCTTGTGCGCAGGATTTGTCTGATTTGTCTGATTTGTCT	1641
Qy	1549	TTTCACTTATTTAGA-GATATTTGATCATTTCAACTGCTGATGACAGTTGGAAATTTCTGT	1607
Db	1642	TCTCAGTTGTTAGATTGATTTGTCATTTGAACCCGCTCGAGTCGGGCTGGAATTTTGT	1701
Qy	1608	GTTGACAGTGGCTGTATTCACATTTGAGAGTTGATGCTTCAATAGCTGGTGTTCAC	1667
Db	1702	GTTGACAGTGGCTGTATTCACATTTGAGAGTTGATGCTTCAATAGCTGGTGTTCAC	1761
Qy	1668	GGGATGTTCTGTTCTCCCTATCAGCGTAACTATATGATGATGATCCTTGAATTCAT	1727
Db	1762	GGGATGTTCTGTTCTCCCTATCAGCGTAACTATATGATGATGATCCTTGAATTCAT	1821
Qy	1728	GAACTGTTGTTCAAGATTA	1747
Db	1822	GAACTGTTGTTCAAGATTA	1841

[illegible]

DB 961 GGGGTGCAATGCTGCTTACATGAGACACTGAGGCTGCTGATGACAGGACG 1020
QY 1419 CTACAGTGTGTGTGCTCCGAGAAATTTGTATGGAGCTGTGACACCCATGTATAA 1478
DB 1021 CTACAGTGTGTGTGCTCCGAGAAATTTGTATGGAGCTGTGACACCCATGTATAA 1080
QY 1479 TGGGATGAAGATACGGGCTAATGCAACTTCTGTGTGCTGCTGCTGCTGCTGCTG 1538
DB 1081 TGGGATGAAGATACGGGCTAATGCAACTTCTGTGTGCTGCTGCTGCTGCTGCTG 1140
QY 1539 TCTGATGCTTTCAGTTATTTAGAGATATGATCATTCACCTGCTGAGTGTG 1598
DB 1141 TCTGATGCTTTCAGTTATTTAGAGATATGATCATTCACCTGCTGAGTGTG 1200
QY 1599 AATTTTCGTGTGACAAAGGCTGTATATCCAGTTGAGAGTTCAATGCTTGTG 1658
DB 1201 AATTTTCGTGTGACAAAGGCTGTATATCCAGTTGAGAGTTCAATGCTTGTG 1260
QY 1659 GTTGTTCAGGGAGTGTCTGTCTCCCTATACAGGTATCATATATGATGATCTTGT 1718
DB 1261 GTTGTTCAGGGAGTGTCTGTCTCCCTATACAGGTATCATATATGATGATCTTGT 1320
QY 1719 TTAATTCATGAACACTGTTTCAAGATTA 1747
DB 1321 TTAATTCATGAACACTGTTTCAAGATTA 1349

RESULT 4
US-10-425-114-14218
; Sequence 14218, Application US/10425114
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 14218
; LENGTH: 1541
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB148-051-G4_FLI
US-10-425-114-14218

Query Match 76.5%; Score 1349; DB 52; Length 1541;
Best Local Similarity 100.0%; Pred. No. 1.5e-241;
Matches 1349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 399 CCGACTACCGCGCTCTCTGCGCAGCTATCTTCGCGGGCTCTTTCGAAACGCGTGGCC 458
DB 1 CCGACTACCGCGCTCTCTGCGCAGCTATCTTCGCGGGCTCTTTCGAAACGCGTGGCC 60
QY 459 CCAACCCCAAGGTCAGCTCTCTGAGTGGCGCTCTTCTTCAAGCGCGCTGTACTCG 518
DB 61 CCAACCCCAAGGTCAGCTCTCTGAGTGGCGCTCTTCTTCAAGCGCGCTGTACTCG 120
QY 519 TCTTCGATGCGCAGCGCTCTGCGCAGCTCTTCGCGGGGCTCTCATTTGCTGTCT 578
DB 121 TCTTCGATGCGCAGCGCTCTGCGCAGCTCTTCGCGGGGCTCTCATTTGCTGTCT 180
QY 579 GGATTCAGTCTGGCTGTGATGGCCAGACTCGGGCCACACCGCATACCGGCTATCCG 638
DB 181 GGATTCAGTCTGGCTGTGATGGCCAGACTCGGGCCACACCGCATACCGGCTATCCG 240
QY 639 TCTTCGATGCGCAGCTCTCTGAGTGGCGCTCTTCGCGGAACTGCTCACGGGCTCAGATGCT 698

DB 241 TCTTCGATGCGCAGCTCTCTGAGTGGCGCTCTTCGCGGAACTGCTCACGGGCTCAGATGCT 300
QY 699 GGATTCAGTCTGGCTGTGATGGCCAGACTCGGGCCACACCGCATACCGGCTATCCG 758
DB 301 GGATTCAGTCTGGCTGTGATGGCCAGACTCGGGCCACACCGCATACCGGCTATCCG 360
QY 759 ACCGTCAGACATATGCGCTCTTTCGCGCTCTTTCGCGGCTCTTTCGCGGCTCTTTCG 818
DB 361 ACCGTCAGACATATGCGCTCTTTCGCGCTCTTTCGCGGCTCTTTCGCGGCTCTTTCG 420
QY 819 ACTTCACCAACGAGACCTGCGGCTGTGATGCGGCTGTGAAATTTCTTCACTACCTACAC 878
DB 421 ACTTCACCAACGAGACCTGCGGCTGTGATGCGGCTGTGAAATTTCTTCACTACCTACAC 480
QY 879 ACTGACCTTCTTACCCCGTATATGATATGATATGATATGATATGATATGATATGATATG 938
DB 481 ACTGACCTTCTTACCCCGTATATGATATGATATGATATGATATGATATGATATGATATG 540
QY 939 TGTGCTTCTCAAGGAGAGAGGCTGCGCAGCGGCTGTGAGATCGCGGGGCTGCGCA 998
DB 541 TGTGCTTCTCAAGGAGAGAGGCTGCGCAGCGGCTGTGAGATCGCGGGGCTGCGCA 600
QY 999 CATTCGCGCTTGTATACCGCTGTGATGCTGTGCTTCCCTGCGAATTTGAGAGAGGCTG 1058
DB 601 CATTCGCGCTTGTATACCGCTGTGATGCTGTGCTTCCCTGCGAATTTGAGAGAGGCTG 660
QY 1059 CGTTGTGCTTTCAGCTTACCATCTGCGGATTCAGACGCTCCATTTCTGCTTAAC 1118
DB 661 CGTTGTGCTTTCAGCTTACCATCTGCGGATTCAGACGCTCCAAATTTCTGCTTAAC 720
QY 1119 ACTTCGCGCTGCGAGGATATGCGGGCCACCGAAGGCGCATGCTGTTGAGAGACAG 1178
DB 721 ACTTCGCGCTGCGAGGATATGCGGGCCACCGAAGGCGCATGCTGTTGAGAGACAG 780
QY 1179 CCGCAGGCAAGCTGCAACATCTGTGCTCTTTCGATGATGATGATGATGATGATGATG 1238
DB 781 CCGCAGGCAAGCTGCAACATCTGTGCTCTTTCGATGATGATGATGATGATGATGATG 840
QY 1239 AGTTCCAGATTAGACCACTGTTTCCCGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTG 1298
DB 841 AGTTCCAGATTAGACCACTGTTTCCCGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 1299 CACCGCGCTGCGCAGCTTTCGAGAGAGATGGGCTCATTTCTGAGCCACTTCT 1358
DB 901 CACCGCGCTGCGCAGCTTTCGAGAGAGATGGGCTCATTTCTGAGCCACTTCT 960
QY 1359 GGGGTGCAATGTGCTTACATGGAAGACACTGAGGCTGCTGCTGCTGCTGCTGCTGCTG 1418
DB 961 GGGGTGCAATGTGCTTACATGGAAGACACTGAGGCTGCTGCTGCTGCTGCTGCTGCTG 1020
QY 1419 CTACAGTGTGTGTGCTCCGAGAAATTTGTATGGAGCTGTGACACCCATGTATAA 1478
DB 1021 CTACAGTGTGTGTGCTCCGAGAAATTTGTATGGAGCTGTGACACCCATGTATAA 1080
QY 1479 TGGGATGAAGATACGGGCTAATGCAACTTCTGTGTGCTGCTGCTGCTGCTGCTG 1538
DB 1081 TGGGATGAAGATACGGGCTAATGCAACTTCTGTGTGCTGCTGCTGCTGCTGCTG 1140
QY 1539 TCTGATGCTTTCAGTTATTTAGAGATATGATCATTCACCTGCTGAGTGTG 1598
DB 1141 TCTGATGCTTTCAGTTATTTAGAGATATGATCATTCACCTGCTGAGTGTG 1200
QY 1599 AATTTTCGTGTGACAAAGGCTGTATATCCAGTTGAGAGTTCAATGCTTGTG 1658
DB 1201 AATTTTCGTGTGACAAAGGCTGTATATCCAGTTGAGAGTTCAATGCTTGTG 1260
QY 1659 GTTGTTCAGGGAGTGTCTGTCTCCCTATACAGGTATCATATATGATGATCTTGT 1718
DB 1261 GTTGTTCAGGGAGTGTCTGTCTCCCTATACAGGTATCATATATGATGATCTTGT 1320
QY 1719 TTAATTCATGAACACTGTTTCAAGATTA 1747

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Db      1321 TTAATTCATGAACACTGTGTTCAAGATTA 1349

RESULT 5
PCT-US03-07858-288
; Sequence 288, Application PC/TUS0307858
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: PCT/US03/07858
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 288
; LENGTH: 2054
; TYPE: DNA
; ORGANISM: Zea mays
PCT-US03-07858-288

Query Match      75.6%; Score 1333.8; DB 1; Length 2054;
Best Local Similarity 88.4%; Pred. No. 1,1e-238;
Matches 1558; Conservative 0; Mismatches 177; Indels 28; Gaps 9;

QY      4 CGAGCTCCCTCTCTCTCCCAATCCTCCGCGCTCCCTCAACCAATCAGACCAACCA 63
Db      78 CGATCTCCCTCTCTCTCCCAATCTCTCCGCGCTCCCTCCGACCTCCCAATCAGAC 137
QY      64 GGGCGATCCGAGCCACGCGCGCGCAATGCGCCCTCTGTGATGCAATGCGCGCCCG 123
Db      138 CACCCATAGGGGCGACGCGCGCGCAATGCGCCCTCTGTGCGCAATGCGCGCCCG 197
QY      124 CGAGCGCGCGCGCGCGCGCGCAATGCGCGATGATTTCTCTCAAGAGCTCGCGCTCA 183
Db      198 AGAGCGCGCGCGCGCGCGCGCAATGCGCGATGATTTCTCTCAAGAGCTCGCGCG 257
QY      184 TTCGCGCGAGGAGCTCTGATCTTCATCTCCGCGAGAGTGAAGAGCTCAAGCGCTG 243
Db      258 GTCCGCGCGCGAGCTCTGATCTTCATCTCCGCGAGAGTGAAGAGCTCAAGCGCT 317
QY      244 CCCCACCAACCGCGCGCGCGCACTCCGCTTCTCAACCTGCGCGCGAGAGAGCGCA 303
Db      318 TCCCGACCAACCGCGCGCGCGCACTCCGCTTCATCACTTGGCGGAGAGCGCA 377
QY      304 CGCTTTGCGCGCGCGCAACCGCGCGCTTGGCGCGCGCGCTCTCGCGCGCTTTCTT 363
Db      378 CGCTTTGCGCGCGCGCAACCGCGCGCTTGGCGCGCGCGCTCTCGCGCGCTTTCT 437
QY      364 CGCGCTCTGATGAGCGCGCTCTCCGCGGTCCGCGAGTCAACCGCGCGCTCTCG 423
Db      438 CGCGCTCTGATGAGCGCGCTCTCCGCGGTCCGCGAGTCAACCGCGCGCTCTCG 497
QY      424 GCTATCTTCGCGCGCGCTCTTTCGAACGCTTCGCGCGCGCAACCGCGCGAGTCA 483
Db      498 GCTCTCTTCGCGCGCGCTCTTTCGAACGCTTCGCGCGCGCAACCGCGCGAGTCA 557
QY      484 GATGCGCGCTCTCTTCTTCAAGCGCGCTTACCTTCTCTGCGATGCGCGCGCTG 543
Db      558 GATGCGCGCTCTCTTCTTCAAGCGCGCTTACCTTCTCTGCGATGCGCGCGCTG 617
QY      544 GCACCTCTGCGCGCGGCTCATTTGCTTGTGATTCAGTCCGCGCTGAGTGGGCA 603
Db      618 GCACATCTGCTGCGCGGCTCATTCGCTTGTGATTCAGTCCGCGCTGAGTGGGCA 677
QY      604 CGACTCGGCGCACCGCGCATCAACCGCGCATCCGCTCTGACCGCGCTGCTGAGTGT 663

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Db      678 CGACTCGGCGCACCGCGCATCAACCGCGCATCCGCTCTGAGCCGCGCTGAGGTGT 727
QY      664 CTCGCGGAACCTGCTCAACCGCGCTCTGAGCATTCGCTGTGGAAGTGAACCAACACG 723
Db      738 CTCGGAACCTGCTCAACCGCGCTCTGAGCATTCGCTGTGGAAGTGAACCAACACG 797
QY      724 CCACATGCGCTGCAACAGCTGAGACCATGACCCGAGCTTCAGACATGCGCTCTTTC 783
Db      798 CCACATGCTGCAACAGCTGAGACCATGACCCGAGCTTCAGACATGCGCTCTTTC 857
QY      784 CGTCTCCCCAGCTGTTGGCAACATATGCTCTTCACTTCAACCAACGACCTTGGCT 843
Db      858 TGTCTCCCCAGCTGTTGGCAACATATGCTCTTCACTTCAACCAACGACCTTGGCT 917
QY      844 CATGCGCGCTGCAACATTTCTTCACTGAGTCAACGACCTGAGACCTTCAACCGGTAT 903
Db      918 CGAGCGCGCTGCAACATTTCTTCACTGAGTCAACGACCTGAGACCTTCAACCGGTAT 977
QY      904 CATGCGCGATTAATCTTCTGCGGAGTCCGCGCTGTTCTGCTCAAGGAAAGAGGT 963
Db      978 CATGCGCGATTAATCTTCTGCGGAGTCCGCGCTGTTCTGCTCAAGGAAAGAGGT 1037
QY      964 GCGGAGCGGTTGCTTGAATGCGGCGGCTGCGCAATTCGCGCTTGTGTAACCGTGT 1023
Db      1038 GCGGAGCGGTTGCTTGAATGCGGCGGCTGCGCAATTCGCGCTTGTGTAACCGTGT 1097
QY      1024 GGTGCTCCCTGCGCAATTTGTGGAAGAGGCTGCGGCTTGTGCTTCAAGCTTCAAC 1083
Db      1098 GGTGCTCCCTGCGCAATTTGTGGAAGAGGCTGCGGCTTGTGCTTCAAGCTTCAAC 1157
QY      1084 CTCGCGGATTCAGACAGTCCCAATTTGCTGTAACCACTTCTGCGGAGCTGATGCTG 1143
Db      1158 CTCGCGGATTCAGACAGTCCCAATTTGCTGTAACCACTTCTGCGGAGCTGATGCTG 1217
QY      1144 GCCACCAAGGCAATGATGCTGTTAGAAAGCAGCGAGGAGCACTTCAATCCTGTG 1203
Db      1218 GCCACCAAGGCAATGATGCTGTTAGAAAGCAGCGAGGAGCACTTCAATCCTGTG 1277
QY      1204 CTCCTCTGATGATGTTGTTCCAGGCTGCGCTGAGTTCCAGATTGACACATCTGTT 1263
Db      1278 CTCCTCTGATGATGTTGTTCCAGGCTGCGCTGAGTTCCAGATTGACACATCTGTT 1337
QY      1264 TCCCGCGCTACCTCGGTGCAACCTTGCAGAGTTGACCGGCGCTGCGACCTTTGCA 1323
Db      1338 CCCCCTGCTGCTCGGTGCAACCTTGCAGAGTTGACCGGCGCTGCGACCTTTGCA 1397
QY      1324 GAAGCATGCGCTCACTTATTTCTGACGCAACATTTGCGGCTGCAATGTGCTTAC 1383
Db      1398 GAAGCATGCGCTCACTTATTTCTGACGCAACATTTGCGGCTGCAATGTGCTTAC 1457
QY      1384 GACACTCAGGCTGCTGCAATGAGGCGCAGAACCGCTACA---AGTGTGTGCTCGAA 1440
Db      1458 GACACTCAGGCTGCTGCAATGAGGCGCAGAACCGCTACA---AGTGTGTGCTCGAA 1517
QY      1441 GAATTTGATGAGGAGCTGTGAACCAATG---GATAAATGAGTGAAGATACG--- 1494
Db      1518 GAATTTGATGAGGAGCTGTGAACCAATG---GATAAATGAGTGAAGATACG--- 1577
QY      1495 -GCTAATGCACTTGTGTG---TTCAGCTTGTGTGCTCATATGATGTCTGATGTC--- 1547
Db      1578 AGGGAAGGCACTTGTGTGTGCTTGTGCTTGTGCGAGCTGATGTCTGTGCTTCTA 1637
QY      1548 CTTTCAATTTATTAAG---GATATGATCATTTCAACCTGCTGAGTCAAGTTGAAATTT 1606
Db      1638 ATCTCAATTTATTAAG---GATATGATCATTTCAACCTGCTGAGTCAAGTTGAAATTT 1697
QY      1607 TGTGCAAGTGTGCTGTATCAAGTTGAGAGATTCATGCTCAATAGTCT---GTTGTTTC 1665
Db      1698 TGTGCAAGTGTGCTGTATCAAGTTGAGAGATTCATGCTCAATAGTCT---GTTGTTTC 1757
QY      1666 ACAGGATGTTCTGTCT---CCCTATCAGCGGTAATATATGATGATCTTGTCT 1718
Db      1758 GTCGGCTGTTCTATTTCTGTTCCCTATATATCATGTAAGAT---ATCGATGATCTTGTCT 1814

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QY 1719 TTAATTCATGAACACTGTTTCA 1741
 DB 1815 CTAAATCATGACACTCTGTTTCA 1837

RESULT 6

PCT-US03-07858A-288
 ; Sequence 288, Application PC/TUS0307858A
 ; GENERAL INFORMATION:
 ; APPLICANT: Monsanto Technology, LLC
 ; APPLICANT: Laurie, Cathy C
 ; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
 ; FILE REFERENCE: 38-77(52900)D
 ; CURRENT APPLICATION NUMBER: PCT/US03/07858A
 ; CURRENT FILING DATE: 2003-05-09
 ; PRIOR APPLICATION NUMBER: US 60/365,301
 ; PRIOR FILING DATE: 2002-03-15
 ; PRIOR APPLICATION NUMBER: US 60/391,786
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/392,018
 ; PRIOR FILING DATE: 2002-06-26
 ; NUMBER OF SEQ ID NOS: 2459
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 288
 ; LENGTH: 2054
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; PCT-US03-07858A-288

Query Match 75.6%; Score 1333.8; DB 1; Length 2054;

Best Local Similarity 88.4%; Pred. No. 1,1e-238;
 Matches 1558; Conservative 0; Mismatches 177; Indels 28; Gaps 9;

QY 4 CGAGCTCCCTCTCTCTCCCAATCTCTCCGCTCTCCCTCCCAATCAGACACCACCA 63
 DB 78 CGATCTCCCTCTCTCTCCCAATCTCTCCGCTCTCCCTCCCAATCAGACACCAC 137
 QY 64 GGGGCAATCCGAGCAGCGCGCGCAATGCGCGCTCTCTGATGCAATGCGCGCGCG 123
 DB 138 CACCCATAGGGGCGAGCGCGCGCAATGCGCGCTCTCTGCGAGCAATGCGCGCG 197
 QY 124 CGAGCGCGCGCGCGCGCGAGCTGCGCATGATCTCTCCAGAGAGCTCGCGCTGACG 183
 DB 198 AAGCGCGCGCGCGCGCGAGCTGCGCATGATCTCTCCAGAGAGCTCGCGAGACGC 257
 QY 184 TTCGCGCGAGCACTCTGATCTCATCTTCGCGGAGAGTGTAGAGCTGACGCGCTG 243
 DB 258 GTCGCGCGCGAGCTCTGATCTCATCTTCGCGGAGAGTGTAGAGCTGACGCGCTG 317
 QY 244 CCCCCACACCGCGCGCGCGAGCTCTCCGCTCTTCACTTGGCGGGGAGAGCGCCACGA 303
 DB 318 TCCCAACACCGCGCGCGCGAGCTCTCCGCTCTTCACTTGGCGGGGAGAGCGCCACGA 377
 QY 304 CGGCTTGGCGCGCTTACACCGCGCTCTGCGGCGCGCGCTCTCCGCGCTTCTGTTGG 363
 DB 378 CGGCTTGGCGCGCTTACACCGCGCTCTGCGGCGCGCGCTCTCCGCGCTTCTGTTGG 437
 QY 364 CGGCTTCTGATGAGCGCGCTCTCCGCGCGCTGCGGAGTACCGCGCGCTCTCTCGCGA 423
 DB 438 CGGCTTCTGATGAGCGCGCTCTCCGCGCGCTGCGGAGTACCGCGCGCTCTCTCGCGA 497
 QY 424 GCTATCTCTGCGCGCGCTCTTGAAGCGTGGCGCGCGAGCCCAAGTTCAGTCTGCT 483
 DB 498 GCTCTCTCTGCGCGCGCTCTTGAAGCGTGGCGCGCGAGCCCAAGTTCAGTCTGCT 557
 QY 484 GATGCGCGCTCTCTTCAAGCGCGCTGATGATCTGCTGCGAGTGGCGAGCGCGTGGG 543
 DB 558 GATGCGCGCTCTCTTCAAGCGCGCTGATGATCTGCTGCGAGTGGCGAGCGCGTGGG 617
 QY 544 GCACTCTCTGCGCGCGGCTCTCATTTGCTTGTCTGATCAGTCCGCGCTGATGGAGCA 603
 DB 618 GCACTCTCTGCGCGCGGCTCTCATTTGCTTGTCTGATCAGTCCGCGCTGATGGAGCA 677

QY 604 CGACTCGGGCCACACCGCATCACCGGCCATCCGGTCTCTGACCGCGCTGTGAGGTGCT 663
 DB 678 CGACTCGGGCCACACCGCATCACCGGCCATCCGGTCTCTGACCGCGCTGTGAGGTGCT 737
 QY 664 CTCGCGGAACTGCTTACCGGCTTACGATCGCTGTGTGGAAGTGTATACCAACACGA 723
 DB 738 CTCGCGGAACTGCTTACCGGCTTACGATCGCTGTGTGGAAGTGTATACCAACACGA 797
 QY 724 CCAATCTGCTTCAACAGCTGAGCATGACCGGACCTTCGAGCATCCGCTCTTTC 783
 DB 798 CCAATCTGCTTCAACAGCTGAGCATGACCGGACCTTCGAGCATCCGCTCTTTC 857
 QY 784 CCTTCCCGCAAGCTGTTGGCAACATATGCTTCTTACTTCAACAGGACCTTGGCTT 843
 DB 858 TGTCTCCCGCAAGCTGTTGGCAACATATGCTTCTTACTTCAACAGGACCTTGGCTT 917
 QY 844 CGATGCGCGCTTGAATTTCTTATCATGCTACAGCACTGAGCTTCTTACCGGTAAATGTG 903
 DB 918 CCAACGCGCTTGAATTTCTTATCATGCTACAGCACTGAGCTTCTTACCGGTAAATGTG 977
 QY 904 CATGCGCAAGATTAATCTTCTGCGGAGTCCGCTCTGTTCTTCTACCGAGAAAGGCT 963
 DB 978 CATGCGCAAGATTAATCTTCTGCGGAGTCCGCTCTGTTCTTCTACCGAGAAAGGCT 1037
 QY 964 GCGGAGCGGCTTGTAGATGCGCGGAGTCCGCACTTCTGAGCTTGGTACCGGTGCT 1023
 DB 1038 GCGGAGCGGCTTGTAGATGCGCGGAGTCCGCACTTCTGAGCTTGGTACCGGTGCT 1097
 QY 1024 GGTGCTTCTCTGCGAATTTGTGAGAGAGGTCGCTTGTGCTTTTCACTTCACT 1083
 DB 1098 GGTGCTTCTCTGCGAATTTGTGAGAGAGGTCGCTTGTGCTTTTCACTTCACT 1157
 QY 1084 CTGCGGATTCAGACAGTTCATTTCTGCTGAACCACTTCTGCTCGAGCTGTATGCTCG 1143
 DB 1158 CTGCGGATTCAGACAGTTCATTTCTGCTGAACCACTTCTGCTCGAGCTGTATGCTCG 1217
 QY 1144 GCGACCCAGAGGCAATGATGCTTTGAGAGAGAGAGGAGGAGCGCTGACATCTGCTG 1203
 DB 1218 GCGACCCAGAGGCAATGATGCTTTGAGAGAGAGAGGAGGAGGAGCGCTGACATCTGCTG 1277
 QY 1204 CTCTCTTGTGATGATTTGTTTCAAGTGTGCTGCACTTCTGAGTTCAGATTTAGCACCATCTGTT 1263
 DB 1278 CCTCTCTTGTGATGATTTGTTTCAAGTGTGCTGCACTTCTGAGTTCAGATTTAGCACCATCTGTT 1337
 QY 1264 TCCCGGCTTACTCGGTGCACTTTCGCAAGTTGCACTGCGCTGCGGACCTTTGCA 1323
 DB 1338 CCGCGGCTTACTCGGTGCACTTTCGCAAGTTGCACTGCGGCTGCGGACCTTTGCA 1397
 QY 1324 GAAGCATGGGCTCACTTATTTGCAAGCCCATTTGCGGCTGCAATGTCTTACATGAA 1383
 DB 1398 GAAGCATGGGCTCACTTATTTGCAAGCCCATTTGCGGCTGCAATGTCTTACATGAA 1457
 QY 1384 GACACTCAGGGCTGCTGATTCAGAGCCAGAGCCGCTACA---AGTGTGTGCTCCGA 1440
 DB 1458 GACACTCAGGGCTGCTGATTCAGAGCCAGAGCCGCTACA---AGTGTGTGCTCCGA 1517
 QY 1441 GAATTTGTGATGAGAGCTGTGAACACCCATG---GATTAATGGAATGAATACG--- 1494
 DB 1518 GAATTTGTGATGAGAGCTGTGAACACCCATGATGAATGAATGAGATGAGCTG 1577
 QY 1495 -GCTAATGCACTTCTGTG---TTCACTTGTGTGCTTGTATGTCTGTGATG--- 1547
 DB 1578 AGGGAGAGCACTTGTGTGTTTCACTTGTGTGCTTGTGTGTTGTTGTTCTA 1637
 QY 1548 CTTTCAATTTTGAAG---GATATGATCATTTCAACCTGCTGAGTCAAGTTTGAATTTTGA 1606
 DB 1638 ATCTCAATTTTGAAGTTTGTATTTGCTGATTTGAACCCGCTCGAGTGGGCTGGAATTTTGA 1697
 QY 1607 TGTGACAAATGAGCTGTCTATCAAGTTGAGAGTTTCAATGATCT---GGTTGTTT 1665
 DB 1698 TGTGACAAATGAGCTGTCTATCAAGTTGAGAGTTTCAATGATCT---GGTTGTTT 1757

QY 1666 ACCGATGTTCTGTTCT-----CCCTATACGGTAATATATGATGATGATCTTGGT 1718
 Db 1758 GTGGGCTGTTCTATGTTCTGTTCTCTCTATATCATATGTAACGAT---ATCGTATCTTGGT 1814
 QY 1719 TTAATTATGAACTGTTTCA 1741
 Db 1815 CTAAGTCATGACCTCTGTTTCA 1837

RESULT 7

PCT-US03-07858-288
 ; Sequence 288, Application PC/TUS0307858
 ; GENERAL INFORMATION:
 ; APPLICANT: Monsanto Technology, LLC
 ; APPLICANT: Laurie, Cathy C
 ; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
 ; FILE REFERENCE: 38-77(52800)D
 ; CURRENT APPLICATION NUMBER: PCT/US03/07858
 ; PRIOR FILING DATE: 2003-03-14
 ; PRIOR APPLICATION NUMBER: US 60/365,301
 ; PRIOR FILING DATE: 2002-03-15
 ; PRIOR APPLICATION NUMBER: US 60/391,786
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/392,018
 ; NUMBER OF SEQ ID NOS: 2459
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 288
 ; LENGTH: 2054
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 PCT-US03-07858-288

Query Match 75.6%; Score 1333.8; DB 2; Length 2054;
 Best Local Similarity 88.4%; Pred. No. 1,1e-238;
 Matches 1558; Conservative 0; Mismatches 177; Indels 28; Gaps 9;

QY 4 CGAGCTCCCTCTCTCCCAATCTCCGCGCTCCCTCCCAATCAGACCAACCCAA 63
 Db 78 CGATCTCCCTCTCTCCCAATCTCCGCGCTCCCTCCCAATCAGACCAACCCAA 137
 QY 64 GCGCATCCGAGCCAGCGCGCGCAATGCGGCTCTGTGATGCAATGCGCGCGCG 123
 Db 138 CACCCATAGGAGGCGCAGCGCGCGCAATGCGGCTCTGTGATGCAATGCGCGCG 197
 QY 124 CGAGCG 183
 Db 198 AGAGCG 257
 QY 184 TTCGCGCGAGCACTCTGATCTCATCTCCGCGCGCGCGCGCGCGCGCGCGCG 243
 Db 258 GTCCG 317
 QY 244 CCGCCACCAACCG 303
 Db 318 TCCCGACCAACCG 377
 QY 304 CGCGCTTCCG 363
 Db 378 CGCGCTTCCG 437
 QY 364 CGCGCTTCCG 423
 Db 438 CGCGCTTCCG 497
 QY 424 GCTATCTCCG 483
 Db 498 GCTATCTCCG 557
 QY 484 GATGCG 543
 Db 558 GATGCG 617

QY 544 GCACCTCTCCG 603
 Db 618 GCACCTCTCCG 677
 QY 604 CGACTGGGCG 663
 Db 678 CGACTGGGCG 737
 QY 664 CTCGCGGAACTGCTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 723
 Db 738 CTCGCGGAACTGCTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 797
 QY 724 CCAATCGCTCGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 783
 Db 798 CCAATCGCTCGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 857
 QY 784 CGTCTCCCCAGAGCTGTTGGCAACATATGCTCTCTTCAACCAACCGCGCG 843
 Db 858 TGTCTCCCCAGAGCTGTTGGCAACATATGCTCTCTTCAACCAACCGCGCG 917
 QY 844 CGATGCG 903
 Db 918 CGATGCG 977
 QY 904 CATCGCGAGATTAATCTTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 963
 Db 978 CATCGCGAGATTAATCTTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1037
 QY 964 GCGCGAGCGGCTGTTGAGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1023
 Db 1038 GCGCGAGCGGCTGTTGAGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1097
 QY 1024 GGTGGCTCCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1083
 Db 1098 GGTGGCTCCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1157
 QY 1084 CTCGCGGAACTGCTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1143
 Db 1158 CTCGCGGAACTGCTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1217
 QY 1144 GCCACCAACCG 1203
 Db 1218 GCCACCAACCG 1277
 QY 1204 CTCCTCTGATGATGTTGGTTCCAGCGCGCGCGCGCGCGCGCGCGCGCG 1263
 Db 1278 CTCCTCTGATGATGTTGGTTCCAGCGCGCGCGCGCGCGCGCGCGCGCG 1337
 QY 1264 TCCCGCGCTAATCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1323
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 QY 1324 GAAGCATGCGCTCAATTAATCTCGAGCGCGCGCGCGCGCGCGCGCGCGCG 1383
 Db 1398 GAAGCATGCGCTCAATTAATCTCGAGCGCGCGCGCGCGCGCGCGCGCGCG 1457
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 QY 1441 GAATTTGATGAGGAGGCTGTAACCAATG---GATTAATGAGATGAATACG 1494
 Db 1518 GAATTTGATGAGGAGGCTGTAACCAATG---GATTAATGAGATGAATACG 1577
 QY 1495 -GCTAATGCAATCTTGCTG-TTCACTTGTGCGCATATGATGCTTGATGCG 1547
 Db 1578 AGGGAAGGCAATCTTGCTG-TTCACTTGTGCGCATATGATGCTTGATGCG 1637
 QY 1548 CTTTCAATTAATGAG-GATATGATCAATCACTGCGCGCGCGCGCGCGCGCG 1606
 Db 1638 ATCTCAATTAATGAG-GATATGATCAATCACTGCGCGCGCGCGCGCGCGCG 1697
 QY 1607 TGTGCAAGTGGCTGCTATCACTGATGAGATGATGATGATGATGATGATGAT 1665

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Db      1698 TGTGCAAGTACCGCTATCCAGTTGAGAGTTCATGCTCAATGCTGGGTTGTC 1757
Qy      1666 ACGGAGTGTTCGTCTCT-----CCCTACAGGTAATATATGATGATGATCTTGGT 1718
Db      1758 GTCCGCTGTCTATCTCTGCTCTCTATATCATGTAACAT--ATCGATCTTGTCT 1814
Qy      1719 TTAATCATGAACACTTGTTC 1741
Db      1815 CTAACTCATGAGACTCTGTTTTA 1837

RESULT 8
PCT-US03-07858A-288
; Sequence 288, Application PC/TUS0307858A
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: PCT/US03/07858A
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 288
; LENGTH: 2054
; TYPE: DNA
; ORGANISM: Zea mays
PCT-US03-07858A-288

Query Match      75.6%; Score 1333.8; DB 2; Length 2054;
Best Local Similarity 88.4%; Pred. No. 1,1e-238;
Matches 1558; Conservative 0; Mismatches 177; Indels 28; Gaps 9;

Qy      4 CGAGCTCCCTCTCTCTCCCAATCTCCCGCCTCCCTACCAATACAGACACCACCA 63
Db      78 CGATCTCCCTCTCTCTCCCAATCTCCCGCCTCCCTACCAATACAGACACCAC 137
Qy      64 GGGGATCCGAGCAGCGCGCGCGCATGCGCGCTCTGTGATGCAATGCGCGCGCGCG 123
Db      138 CACCCATAGGGGCGACGCGCGCGCAATGCGCGCTCTGTGCGAGCAATGCGCGCGCG 197
Qy      124 CGACGCGCGGGGCGCGCGCGCATGCGCATGCTCTCCAGAGCTCCGCGCTCACGC 183
Db      198 AGACGCGCGGGCGCGCGCGCATGCGCTGATCTCTCCAGAGCTCCGCGCGCGCG 257
Qy      184 TTCGCGCGAGCATCTGTGATCTCAATCTCCGCGCGAGTGTAGAGTCAAGCTCTG 243
Db      258 GTCCGCGCGCGCATCTGTGATCTCAATCTCCGCGCGAGTGTAGAGTCAAGCTCTG 317
Qy      244 CCCCCACACCGCGCGCGCGCATCTCCGCTTCTCAACCTTGGCGGGGAGAGCGCCACGA 303
Db      318 TCCCCACACCGCGCGCGCGCATCTCCGCTTCTCAACCTTGGCGGGGAGAGCGCCACGA 377
Qy      304 CGCCTTCCGCGCGCTACACCGCGCTCCGCGCGCGCGCTCTCCGCGCTCTTCTGTTGG 353
Db      378 CGCCTTCCGCGCGCTACACCGCGCTCCGCGCGCGCGCTCTCCGCGCTCTTCTGTTGG 437
Qy      364 CCGCCTCTCTGATAGCGCTCTCCCGCGCGTCCGCGCATACCGCGCGCTCTCTGCGCA 423
Db      438 CGCCTCTCTGATAGCGCTCTCCCGCGCGTCCGCGCATACCGCGCGCTCTCTGCGCA 497
Qy      424 GCTATCTCTCGCGCGCTCTTTCAGAGCGGTGCGCGCGCGCGCGCGCGCGCGCTCTCT 483
Db      498 GCTCTCTCTCGCGCGCGCTCTTTCAGAGCGGTGCGCGCGCGCGCGCGCGCGCGCTCT 557
Qy      484 GATGCGCGCTCTCTTTCAGAGCGCGGTGATCTCTGCTGCGATGGCGCGCGCTGCGG 543

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Db      558 GATGCGCGCTCTCTTTCAGAGCGCGGTGATCTCTGCTGCGCGCGCGCGCTCTGCG 617
Qy      544 GCACCTCTCTCGCGCGCGGTCTATTTGGCTTCTGTGATTCAGTCCGGCTGATAGGCGCA 603
Db      618 GCACATGCTCTCGCGCGCGGTCTATTTGGCTTCTGTGATTCAGTCCGGCTGATAGGCGCA 677
Qy      604 CGACTCGCGCGCACACCGCATCACCGGCTCCGCTCTGAGACCGGCTGCGAGGCT 663
Db      678 CGACTCGCGCGCACACCGCATCACCGGCTCCGCTCTGAGACCGGCTGCGAGGCT 737
Qy      664 CTCGCGGAACTGCTCTACCGGCTCTAGCATCGCTGCTGAGAGTGAACCAACACGCA 723
Db      738 CTCGCGGAACTGCTCTACCGGCTCTAGCATCGCTGCTGAGAGTGAACCAACACGCA 797
Qy      724 CCACATGCTCTGAAAGCTGGAACCATGACCGGACCTTCAGACATGCGCTCTTTCG 783
Db      798 CCACATGCTCTGAAAGCTGGAACCATGACCGGACCTTCAGACATGCGCTCTTTCG 857
Qy      784 CGTCTCCCGCAAGCTGTTGGGCAACATATGCTCTCTTACCAACGAGCCCTGCGCT 843
Db      858 TGTCTCCCGCAAGCTGTTGGGCAACATATGCTCTCTTACCAACGAGCCCTGCGCT 917
Qy      844 CGATGCGCGCTCGAAATCTTTCATGACTACAGCATGGAACCTTCTACCCGGTAATGTG 903
Db      918 CGACGCGCGCTCGAAATCTTTCATGACTACAGCATGGAACCTTCTACCCGGTAATGTG 977
Qy      904 CATGCGCAGATTAATCTTCTGCGCGAGTCCGCTGTTCTGCTACGAGAGAGGCT 963
Db      978 CATGCGCAGATTAATCTTCTGCGCGAGTCCGCTGTTCTGCTACGAGAGAGGCT 1037
Qy      964 GCGCGAGCGGCTGTTGATGATGCGCGGCTGCGCAATCTGGGCTTGTGAACCGTGTCT 1023
Db      1038 GCGCGAGCGGCTGTTGATGATGCGCGGCTGCGCAATCTGGGCTTGTGAACCGTGTCT 1097
Qy      1024 GGTGCTTCTCTGCGCGCAATTTGTTGAGAGAGGCTGCGGTTGTTGCTTTCAGTTACCAT 1083
Db      1098 GGTGCTTCTCTGCGCGCAATTTGTTGAGAGAGGCTGCGGTTGTTGCTTTCAGTTACCAT 1157
Qy      1084 CTGCGGATTCAGACGTCGCAATCTGCTGAAACAATCTCTGCTGCGACGCTGATGTGG 1143
Db      1158 CTGCGGATTCAGACGTCGCAATCTGCTGAAACAATCTCTGCTGCGACGCTGATGTGG 1217
Qy      1144 GCGACCAAGAGGCAATGATCTGTTTGAAGAGAGAGGCAAGGCACTGCAATCTCTGTG 1203
Db      1218 GCGACCAAGAGGCAATGATCTGTTTGAAGAGAGAGGCAAGGCACTGCAATCTCTGTG 1277
Qy      1204 CTCTCTTGAATGATTTGTTCCACGCTGAGCTGAGTTCCAGATTTGAGACCATCTGTT 1263
Db      1278 CCTCTCTTGAATGATTTGTTCCACGCTGAGCTGAGTTCCAGATTTGAGACCATCTGTT 1337
Qy      1264 TCCCGCCTTACCTCGGTGCACTTGTGCAAGGTTGCAACCGCGCTGCGACCTTTGCA 1323
Db      1338 CCGCGCCTTACCTCGGTGCACTTGTGCAAGGTTGCAACCGCGCTGCGACCTTTGCA 1397
Qy      1324 GAAGCATGGGCTCACTTATTTCTGACGCAATTTCTGGGTTGCAAAATGTGTTACATGAA 1383
Db      1398 GAAGCATGGGCTCACTTATTTCTGACGCAATTTCTGGGTTGCAAAATGTGTTACATGAA 1457
Qy      1384 GACACTCAGAGGCTGCTGATTTGACAGGCAAGACCGGTACA--AGTGTGTGCTCCGAA 1440
Db      1458 GACACTCAGAGGCTGCTGATTTGACAGGCAAGACCGGTACAAGTGTGTGCTCCGAA 1517
Qy      1441 GAATTTGATAGGAGGCTGTGAACAACCATG--GATTAATGGATGAAGATACGG-- 1494
Db      1518 GAATTTGATAGGAGGCTGTGAACAACCATGATGAAGAGGAGGAGATATGGCTG 1577
Qy      1495 -GCTAATGGCAATTTGCTG--TTACGTTTGTGCTTGAATGTTGCTGATGCT-- 1547
Db      1578 AGGAGGAAGCACTTCTGTTGTTTCAAGCTTGTGCGAGGCAATTTCTGTTGCTTCTA 1637
Qy      1548 CTTTGAATTAATTAAG--GATATTAATCATTCACCTGCTGAGTCAAGTTGAAATTTTGG 1606

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Db 1638 ATCTCAGTTGTTAGATTGATGTCATTAAGAACCCCTCCGAGTCGGGCTGAATTTTG 1697
 Qy 1607 TGTGACAGTGTGCTGCTATTCATGAGAGTTGATGCTCAATATGCTT-GGTGTTC 1665
 Db 1698 TGTGACAGTGTGCTGCTATTCATGAGAGTTGATGCTCAATATGCTT-GGTGTTC 1757
 Qy 1666 ACCGAGTGTGCTGCTTCTT-----CCCTATCAGGTTAATATGATGATGATGCTTGT 1718
 Db 1758 GTGGGCTGTTCTATTCGTTGCTTCCCTATATCATGTAAGAT---ATCGATGCTTGTCT 1814
 Qy 1719 TTAATTCATGACATGTTTCA 1741
 Db 1815 CTAAGTATGAGACCTCTGTTTCA 1837

RESULT 9

US-10-389-566-288
 ; Sequence 288, Application US/10389566
 ; GENERAL INFORMATION:
 ; APPLICANT: Monsanto Technology, LLC
 ; APPLICANT: Laurie, Cathy C
 ; TITLE OR INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
 ; FILE REFERENCE: 38-77(52900) D
 ; CURRENT APPLICATION NUMBER: US/10/389,566
 ; PRIOR FILING DATE: 2003-03-31
 ; PRIOR APPLICATION NUMBER: US 60/365,301
 ; PRIOR FILING DATE: 2002-03-15
 ; PRIOR APPLICATION NUMBER: US 60/391,786
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/392,018
 ; PRIOR FILING DATE: 2002-06-26
 ; NUMBER OF SEQ ID NOS: 2459
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 288
 ; LENGTH: 2054
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 US-10-389-566-288

Query Match 75.6%; Score 1333.8; DB 51; Length 2054;

Best Local Similarity 88.4%; Pred. No. 1,1e-238;

Matches 1558; Conservative 0; Mismatches 177; Indels 28; Gaps 9;

Qy 4 CGAGCTCCCTCTCTCCCAATCTCCCGCCCTCCCAACCAATACAGCACCCCA 63
 Db 78 CGATCTCCCTCTCTCCCAATCTCCCGCCCTCCCAACCAATACAGCAC 137
 Qy 64 GCGCATCCGAGCCAGCCGCGCAATGCGCCCTCTGTCGATGCAATGCGGCGCCG 123
 Db 138 CACCCATAGGGGCGAGCGCGCGCAATGCGCCCTCTGCGCAATGCGGCGCCG 197
 Qy 124 CGAGCGCGCGCGCGCGCGCGAGCTGGCATGATCTCTCCAGAGCTCCGCGCTACGC 183
 Db 198 AGACGCGCGGTGGCGCGCGAGCTGGCATGATCTCTCCAGAGCTCCGCGAGAGC 257
 Qy 184 TTCGCGCGAGCATCTGATCTCAATCTCCGCGAGCTGAGAGCTACGCGCTGAGCT 243
 Db 258 GTCCGCGCGAGCATCTGATCTCAATCTCCGCGAGCTGAGAGCTACGCGCTGAGCT 317
 Qy 244 CCCCCACACCCCGGCGCGAGCTCCGCTTCTACCTTGGCGGCGAGAGCCACCGA 303
 Db 318 TCCCAACACCCCGGCGGAGACTCCGCTCATCACTTGGCGGAGAGAGCCACCGA 377
 Qy 304 CGCTTGGCGCGCTTACCACTCCGCTTGGCGGCGCGCTCTCCGCGCTTCTTCTGTG 363
 Db 378 CGCTTGGCGCGCTTACCACTCCGCTTGGCGGCGCGCTCTCCGCGCTTCTTCTGTG 437
 Qy 364 CGGCTCTGATGATGAGCGCTTCCCGCGGTCCGCGAGTACCGCGCTCTCTGCGCA 423
 Db 438 CGGCTCTGATGATGAGCGCTTCCCGCGGTCCGCGAGTACCGCGCTCTCTGCGCA 497
 Qy 424 GCTATCTCCGCGGCGCTCTTGAAGCGGTGCGGCGCCACCCCAAGGTCAGCTGCT 483

Db 498 GCTCTCCCGCGGCGCTCTTTCAGGCGCGTCGCGGCCACCCCAAGGTCAGCTCGCCT 557
 Qy 484 GATGCGCGCTCTCTTCTACGCGCGGCTGTAACCTGCTCCGCAATGCGCCAGCGCTGGC 543
 Db 558 GATGCGCGCTCTCTTCTACGCGCGGCTGTAACCTGCTCCGCAATGCGCCAGCGCTGGC 617
 Qy 544 GCACTCTCTGCGGCGGCTCTCAATGAGCTTCTGTCGATGATGATGCGGCTGATGAGCA 603
 Db 618 GCACTGCTCTGCGGCGGCTCTCAATGAGCTTCTGTCGATGATGATGCGGCTGATGAGCA 677
 Qy 604 GACTGCGGCGCAACCGCATCAACCGGCTCTGACCGGCTCTGAGTGTCT 663
 Db 678 GCACTGCGGCGCAACCGCATCAACCGGCTCTGACCGGCTCTGAGTGTCT 737
 Qy 664 CTCGCGGAATGCTCTACCGGCTCTGACGATGCGCTGTAAGTGAACCAACACGCA 723
 Db 738 CTCGGAATGCTCTACCGGCTCTGACGATGCGCTGTAAGTGAACCAACACGCA 797
 Qy 724 CCAATGCGCTGCAAGAGCTGAGACATGACCCGACCTTCACACATGCGCTTTCG 783
 Db 798 CCAATGCGCTGCAAGAGCTGAGACATGACCCGACCTTCACACATGCGCTTTCG 857
 Qy 784 GCTCTCCCGCAAGCTGTTGGCAATATGCTCTTCTTACCAACGACCTGCGCTT 843
 Db 858 GCTCTCCCGCAAGCTGTTGGCAATATGCTCTTCTTACCAACGACCTGCGCTT 917
 Qy 844 CGATGCGGCTGCAATCTCTCATGATGACGACCTGACCTTACCCGCTTATG 903
 Db 918 CGAGCGGCTGCAATCTCTCATGATGACGACCTGACCTTACCCGCTTATG 977
 Qy 904 CATGCGGATTAATCTTCTCGCGAGTCCGCTGTTCTCTACGAGAGAGGT 963
 Db 978 CATGCGGATTAATCTTCTCGCGAGTCCGCTGTTCTCTACGAGAGAGGT 1037
 Qy 964 GCGGAGCGGCTGTTGAGATGCGGCGGCTGCGCAATCTGCGCTTGTGCT 1023
 Db 1038 GCGGAGCGGCTGTTGAGATGCGGCGGCTGCGCAATCTGCGCTTGTGCT 1097
 Qy 1024 GGTGCTTCCCGCAATGTTGAGAGAGGCTGCTTGTGCTTTCAGCTTACCAT 1083
 Db 1098 GGTGCTTCCCGCAATGTTGAGAGAGGCTGCTTGTGCTTTCAGCTTACCAT 1157
 Qy 1084 CTGCGGATTAATCTTCTCGCGAGTCCGCTGTTCTCTACGAGAGAGGT 1143
 Db 1158 CTGCGGATTAATCTTCTCGCGAGTCCGCTGTTCTCTACGAGAGAGGT 1217
 Qy 1144 GCGGAGCGGCTGTTGAGATGCGGCGGCTGCGCAATCTGCGCTTGTGCT 1203
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 Db 1338 CCGCGCTGCTGCTGTCACCTTCCGCAAGTTGACCGGCTGCGCACTTTGCA 1397
 Qy 1324 GAGGATGAGGCTCAATTTCTGACCACTTCTGAGGCTGCAATGCTTACATGAA 1383
 Db 1398 GAGGATGAGGCTCAATTTCTGACCACTTCTGAGGCTGCAATGCTTACATGAA 1457
 Qy 1384 GAGGATGAGGCTGCTGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1440
 Db 1458 GAGGATGAGGCTGCTGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1517
 Qy 1441 GATTTGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1494
 Db 1518 GATTTGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1577
 Qy 1495 -GCTATGCACTTCTGAGG-TTGAGCTTGTGCTGCTGATGCTGATGCTGATGCTG 1547
 Db 1578 AGGGAAGGCACTTGTGATGCTTGTGCTGCTGATGCTGATGCTGATGCTGATGCTG 1637

QY 1548 CTTGAGTATTAGG-GATATGATCATTAACCTGCGAGTCAAGTTGGAATTTTG 1606
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 QY 1607 TGTGACAGAGGCTGTCTATCCAGTTGAGAGTTGATCTTCAATAGTCT-GGTTGTTG 1665
 Db 1698 TGTGACAGAGTCAAGTCTATCCAGTTGAGAGTTGATTCATTGAATTTGCTGGGTTGTTG 1757
 QY 1666 ACGGAGTGTCTGTTT-----CCCTATCAGGTAATCATATGATGATGATCTTGGCT 1718
 Db 1758 GTGCGGTGTCTATCTGTTCTCTCATATCATATGTAACGAT--ATCGTGAATCTTGGCT 1814
 QY 1719 TTAATCATGAACACTGTTTCA 1741
 Db 1815 CTAGTCATGACCTCTGTTTAA 1837
 RESULT 10
 US-10-613-520-288
 ; Sequence 288, Application US/10613520
 ; GENERAL INFORMATION:
 ; APPLICANT: Monsanto Technology, LLC
 ; APPLICANT: Laurie, Cathy C
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Maolong, Lu
 ; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
 ; FILE REFERENCE: 38-77(52900)E
 ; CURRENT APPLICATION NUMBER: US/10/613,520
 ; PRIOR FILING DATE: 2003-07-02
 ; PRIOR APPLICATION NUMBER: US 60/365,301
 ; PRIOR FILING DATE: 2002-03-15
 ; PRIOR APPLICATION NUMBER: US 10/389,566
 ; PRIOR FILING DATE: 2003-03-14
 ; PRIOR APPLICATION NUMBER: US 60/391,786
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/392,018
 ; PRIOR FILING DATE: 2002-06-26
 ; NUMBER OF SEQ ID NOS: 2578
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 288
 ; LENGTH: 2054
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 US-10-613-520-288
 Query Match 75.6%; Score 1333.8; DB 53; Length 2054;
 Best Local Similarity 88.4%; Pred. No. 1,1e-238;
 Matches 1558; Conservative 0; Mismatches 177; Indels 28; Gaps 9;

QY 364 CGGCTCTCTGACTAGGCGGCTCTCCCGCGCTCCGCGACTACCGCGGCTCTCGCGCA 423
 Db 438 CGGCTCTCTGACTAGGCGGCTCTCCCGCGCTCCGCGACTACCGCGGCTCTCGCGCA 497
 QY 424 GCTATCTCTCGGCGGCTCTTGAAGCGGTGGGCCCAACCCCGAAGTTCAGCTGCTCT 483
 Db 498 GCTCTCTCTCGGCGGCTCTTGAAGCGGTGGGCCCAACCCCGAAGTTCAGCTGCTCT 557
 QY 484 GATGCGGCT 543
 Db 558 GATGCGGCT 617
 QY 544 GCACT 603
 Db 618 GCACT 677
 QY 604 GCACT 663
 Db 678 GCACT 737
 QY 664 CTCCGGAACCTGCT 723
 Db 728 CTCCGGAACCTGCT 797
 QY 724 CCACATCT 783
 Db 798 CCACATCT 857
 QY 784 GCT 843
 Db 858 GCT 917
 QY 844 GATGCGGCT 903
 Db 918 GATGCGGCT 977
 QY 904 CATGCGGCT 963
 Db 978 CATGCGGCT 1037
 QY 964 GCGGAGCGGCT 1023
 Db 1038 GCGGAGCGGCT 1097
 QY 1024 GGTGCT 1083
 Db 1098 GGTGCT 1157
 QY 1084 CTGCGGAGTTCAGCACT 1143
 Db 1158 CTGCGGAGTTCAGCACT 1217
 QY 1144 GCCACCAAGGCAATGATGCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1203
 Db 1218 GCCACCAAGGCAATGATGCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1277
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 Db 1278 CT 1337
 QY 1264 TCCCGGCT 1323
 Db 1338 TCCCGGCT 1397
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 Db 1458 GACACTAGGGGTCTGATGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1517

QY 1441 GAATTTGATGAGGCTGTGAACCCATG---GATAATGAGATGAATACGG--- 1494
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 QY 1495 -GCTAATGCACTTCTGTG-TTCACTTGTGCTCCATGATGATGCTGATGCTG 1547
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 QY 1548 CTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1606
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 QY 1607 TGTGCAAGTGTGCTGTATGATGATGATGATGATGATGATGATGATGATGATG 1665
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RESULT 11

US-09-654-265928
 ; Sequence 265928, Application US/09654617
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Liu, Jindong
 ; TITLE OF INVENTION: Annotated Plant Genes
 ; FILE REFERENCE: 38-21(15097)D
 ; CURRENT APPLICATION NUMBER: US/09/654,617
 ; CURRENT FILING DATE: 2000-09-05
 ; NUMBER OF SEQ ID NOS: 463173
 ; SEQ ID NO 265928
 ; LENGTH: 1448
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 US-09-654-617-265928

Query Match 66.6%; Score 1175; DB 28; Length 1448;
 Best Local Similarity 98.3%; Pred. No. 4,5e-209;
 Matches 1187; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 541 GAGCGCACTCTGCGGGGGGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 DB 38 GAGCGCACTCTGCGGGGGGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 97
 QY 601 CCAAGCACTGCGGGGCAACCGGCACTGCGGGGCACTGCGGGGCACTGCGGGGCACTG 660
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 QY 721 GCAACCACTGCTGCAACCGGCTCAACCGGCTCAACCGGCTCAACCGGCTCAACCG 780
 DB 218 GCAACCACTGCTGCAACCGGCTCAACCGGCTCAACCGGCTCAACCGGCTCAACCG 277
 QY 781 TGCGGCTCTGCGGCAAGTGTGCGGCAAGTGTGCGGCAAGTGTGCGGCAAGTGTGCG 840
 DB 278 TGCGGCTCTGCGGCAAGTGTGCGGCAAGTGTGCGGCAAGTGTGCGGCAAGTGTGCG 337
 QY 841 GTTCGATGCGGCTCGAATTTCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 DB 338 GTTCGATGCGGCTCGAATTTCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 357
 QY 901 GTTCGATGCGGATTAATTTCTTCGCGGAGTCTGCGGAGTCTGCTGCTGCTGCTGCTG 960
 DB 398 GTTCGATGCGGATTAATTTCTTCGCGGAGTCTGCGGAGTCTGCTGCTGCTGCTGCTG 457

QY 961 GGTGCGCAAGCGGCTTGAAGTGTGCGGGGGTGTGCGCACTTCTGCGGCTTGTACCGGT 1020
 DB 458 GGTGCGCAAGCGGCTTGAAGTGTGCGGGGGTGTGCGCACTTCTGCGGCTTGTACCGGT 517
 QY 1021 GCTGTGAGTCTGCTGCGCAATTTGTGAGGAGAGGAGTGTGCTTGTGCTTGTGCTTGC 1080
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 QY 1261 GTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
 DB 758 GTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 817
 QY 1321 CAGAAGCACTGCGGCTCACTTATTCGAGCACTTCTGAGGAGAGAGAGAGAGAGAGAG 1380
 DB 818 CAGAAGCACTGCGGCTCACTTATTCGAGCACTTCTGAGGAGAGAGAGAGAGAGAGAG 877
 QY 1381 GAAGCACTGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
 DB 878 GAAGCACTGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 937
 QY 1441 GAATTTGATGAGGAGCTGTGAACCCATGATGAATGAGATGAATGAGATGAGATG 1500
 DB 938 GAATTTGATGAGGAGCTGTGAACCCATGATGAATGAGATGAATGAGATGAGATG 997
 QY 1501 GCGCACTTCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
 DB 998 GCGCACTTCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1057
 QY 1561 AGAGATATTGATTCATTCACCTGCTGAGTCAAGTGTGAATTTCTGTTGACAGTGGC 1620
 DB 1058 AGAGATATTGATTCATTCACCTGCTGAGTCAAGTGTGAATTTCTGTTGACAGTGGC 1117
 QY 1621 TGTCTATCCAGTGTGAGAGTTCATGCTTCAATGCTGCTGCTGCTGCTGCTGCTG 1680
 DB 1118 TGTCTATCCAGTGTGAGAGTTCATGCTTCAATGCTGCTGCTGCTGCTGCTGCTG 1177
 QY 1681 CTCCTATCAGGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
 DB 1178 CTCCTATCAGGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1237
 QY 1741 AAGATTA 1747
 DB 1238 AAGATTA 1244

RESULT 12

US-09-684-016-265928
 ; Sequence 265928, Application US/09684016
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Liu, Jindong
 ; TITLE OF INVENTION: Annotated Plant Genes
 ; FILE REFERENCE: 38-21(15097)D
 ; CURRENT APPLICATION NUMBER: US/09/684,016
 ; CURRENT FILING DATE: 2000-10-10
 ; PRIOR APPLICATION NUMBER: US 09/654,617
 ; NUMBER OF SEQ ID NOS: 463173
 ; SEQ ID NO 265928
 ; LENGTH: 1448

TYPE: DNA
ORGANISM: Zea mays
US-09-857-524b-3

Query Match 66.6%; Score 1175; DB 30; Length 1448;
Best Local Similarity 98.3%; Pred. No. 4.5e-209;
Matches 1187; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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QY 541 GGGGACCTCTCGCGGGGGGCTCATATGAGTGTGCTGATCCAGTCCGGCTGATGG 600
Db 38 GGGGACATGCTCGCGGGGGGCTCATATGAGTGTGCTGATCCAGTCCGGCTGATGG 97
QY 601 CCAGATCTGGGGCCACACCGCATACCGGCTCCGCTCTGACCGGCTGTGAGGT 660
Db 98 CCAAGATCTGGGGCCACACCGCATACCGGCTCCGCTCTGACCGGCTGTGAGGT 157
QY 661 GCTCTCGGGGAACTGCTCAACCGGCTCAGATGCGCTGGGGAAGTAAACCAACAC 720
Db 158 GCTCTCGGGGAACTGCTCAACCGGCTCAGATGCGCTGGGGAAGTAAACCAACAC 217
QY 721 GCACCATCTGCTGCAACAGCTGACATGACCCGAGCTCCAGACATGCGCTCTT 780
Db 218 GCACCATCTGCTGCAACAGCTGACATGACCCGAGCTCCAGACATGCGCTCTT 217
QY 781 TGCGGTCTCCCGCAAGCTGTTCGCAACATATGCTCTTCTTCAACACGACCTTGC 840
Db 278 CGGTGTCTCCCGCAAGCTGTTCGCAACATATGCTCTTCTTCAACACGACCTTGC 337
QY 841 GTTCGATCGCGCTCGAAATTTCTCATACGTAACAGACTGACCTTCAACCGGTAT 900
Db 338 GTTCGATCGCGCTCGAAATTTCTCATACGTAACAGACTGACCTTCAACCGGTAT 397
QY 901 GTTCGATCGCGCTCGAAATTTCTCATACGTAACAGACTGACCTTCAACCGGTAT 960
Db 398 GTTCGATCGCGCTCGAAATTTCTCATACGTAACAGACTGACCTTCAACCGGTAT 457
QY 961 GTTCGATCGCGCTCGAAATTTCTCATACGTAACAGACTGACCTTCAACCGGTAT 1020
Db 458 GTTCGATCGCGCTCGAAATTTCTCATACGTAACAGACTGACCTTCAACCGGTAT 517
QY 1021 GCTGTGAGTCTCTCGCAATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
Db 518 GCTGTGAGTCTCTCGCAATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 577
QY 1081 CATCTGCGGATTCAGACGCTTCATCTCTGCAACCACTTCTGCTGACGCTGATGT 1140
Db 578 CATCTGCGGATTCAGACGCTTCATCTCTGCAACCACTTCTGCTGACGCTGATGT 637
QY 1141 CGGGCCACCCCAAGGCAATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
Db 638 CGGGCCACCCCAAGGCAATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 697
QY 1201 GTCTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
Db 698 GTCTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 757
QY 1261 GTTTCCTCGGCTTCTCTGATGATGATGATGATGATGATGATGATGATGATG 1320
Db 758 GTTTCCTCGGCTTCTCTGATGATGATGATGATGATGATGATGATGATGATG 817
QY 1321 CAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Db 818 CAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 877
QY 1381 GAAGACATCAGGAGCTGATGATGATGATGATGATGATGATGATGATGATG 1440
Db 878 GAAGACATCAGGAGCTGATGATGATGATGATGATGATGATGATGATGATG 937
QY 1441 GAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
Db 938 GAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 997
QY 1501 GGCAACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560

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Db 998 GGCAACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1057
QY 1561 AGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
Db 1058 AGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1117
QY 1621 TGTCTATCAGGATGATGATGATGATGATGATGATGATGATGATGATG 1680
Db 1118 TGTCTATCAGGATGATGATGATGATGATGATGATGATGATGATGATG 1177
QY 1681 CTCCTATCAGGATGATGATGATGATGATGATGATGATGATGATGATG 1740
Db 1178 CTCCTATCAGGATGATGATGATGATGATGATGATGATGATGATGATG 1237
QY 1741 AAGATTA 1747
Db 1238 AAGATTA 1244

```

RESULT 13

US-09-857-524B-9

Sequence 9, Application US/09857524B

GENERAL INFORMATION:

APPLICANT: Edgar B. Caboon

APPLICANT: Rebecca E. Caboon

APPLICANT: William D. Hitz

APPLICANT: Anthony J. Kinney

TITLE OF INVENTION: Membrane-Bound Desaturases

FILE REFERENCE: B1264

CURRENT APPLICATION NUMBER: US/09/857,524B

CURRENT FILING DATE: 2001-06-04

PRIOR APPLICATION NUMBER: 60/110,784

PRIOR FILING DATE: 1998-12-03

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Microsoft Office 97

SEQ ID NO 9

LENGTH: 1972

TYPE: DNA

ORGANISM: Trifolium aestivum

US-09-857-524B-9

Query Match 61.9%; Score 1091.4; DB 35; Length 1972;
Best Local Similarity 79.0%; Pred. No. 1.9e-193;
Matches 1355; Conservative 0; Mismatches 341; Indels 19; Gaps 4;

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QY 27 CCTCCCGCTCTCCCTTACCAATGACACACCAAGGCGATCCGACGCGCG 86
Db 89 CCTCCCTCTCGCTCAGCTAATCCAGCCACCGATGCGCGACGCGGAGC 148
QY 87 CAATCCCGCTCTCTGATGATGATGATGATGATGATGATGATGATGATG 146
Db 149 CAACGCGCGGAGACCGCAATGCGGCGCGCAAGAA-----GAGCGCGCGAG 202
QY 147 TCGCATGATCTCTCAAGAGCTCCGCGCTCAGCTTCCGCGAGCACTTGATCT 206
Db 203 TCGCATGATCTCTCAAGAGCTCCGCGCTCAGCTTCCGCGAGCACTTGATCT 262
QY 207 CCATCTCCGCGAGCTGATGATGATGATGATGATGATGATGATGATGATG 266
Db 263 CCATCTCCGCGAGCTGATGATGATGATGATGATGATGATGATGATGATG 322
QY 267 TCCGCTCTCAACCTTCCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 326
Db 323 TCCGCTCTCAACCTTCCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 382
QY 327 CCTCGCGCGCGCTCTCTCGCGCTTCTGATGATGATGATGATGATGATGATG 386
Db 383 CCTCGTGCGCGCGCTCTCTCGCGCTTCTGATGATGATGATGATGATGATG 442
QY 387 CCGCGCGCTCGCGAGCTACCGCGCTCTCTCGCGAGCTATCTCTCGCGGCGCTT 446
Db 443 CCGCGCGCTCGCGAGCTACCGCGCTCTCTCGCGAGCTATCTCTCGCGGCGCTT 502

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Db 425 CTCGAGACTACAGGCTCTCCGCGCGTCCGCGACTTCCGCGCGCTCTCCGCGAGCTC 484
Qy 428 TCTCCGCGGCGCTCTTTCGAGACCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 487
Db 485 TCTCCGCGGCGGCTTTCGAGACCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 544
Qy 488 GCGGCTCTCTTTCGAGACCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 547
Db 545 CTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 604
Qy 548 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 607
Db 605 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 664
Qy 608 TCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 667
Db 665 TCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 724
Qy 668 GGGAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 727
Db 725 GCGAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 784
Qy 728 ATGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 787
Db 785 ATGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 844
Qy 788 TCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
Db 845 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 901
Qy 848 GCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 907
Db 902 GCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 961
Qy 908 GCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 967
Db 962 GCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1021
Qy 968 GCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1027
Db 1022 GCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1081
Qy 1028 GCTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1087
Db 1082 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1141
Qy 1088 GCGATTCAGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1147
Db 1142 GCGATTCAGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1201
Qy 1148 CCCAAGGCGAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1207
Db 1202 CCAGAGGCGAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1261
Qy 1208 CTTTGATGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1267
Db 1262 CCATGATGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1321
Qy 1268 CCGCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1327
Db 1322 CCGCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1381
Qy 1328 CATGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1387
Db 1382 CATGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1441
Qy 1388 CTCAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1447
Db 1442 TTGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1501
Qy 1448 GTATGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1507
Db 1502 GTTGGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1550

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Qy 1508 TCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1567
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Qy 1568 TTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1620
Db 1599 TTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1658
Qy 1621 TGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1676
Db 1659 TGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1718
Qy 1677 TGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1689
Db 1719 GATGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1731

RESULT 15
US-09-702-134-25614/c
; Sequence 25614, Application US/09702134
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIntosh, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-21(51237)F
; CURRENT APPLICATION NUMBER: US/09/702,134
; CURRENT FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 52202
; SEQ ID NO 25614
; LENGTH: 14392
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-702-134-25614

Query Match 55.2%; Score 973.6; DB 31; Length 14392;
Best Local Similarity 76.6%; Pred. No. 2.6e-171;
Matches 1297; Conservative 0; Mismatches 359; Indels 38; Gaps 7;

Qy 8 CTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 67
Db 8263 CTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8204
Qy 68 CATCGAGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 127
Db 8203 CCGACGATGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8144
Qy 128 GCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 187
Db 8143 AGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 8084
Qy 188 GCGGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 247
Db 8083 AGGAGCGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8024
Qy 248 CACGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 307
Db 8023 CACGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 7964
Qy 308 TTGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 367
Db 7963 TTCTGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 7904
Qy 368 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 427
Db 7903 CTAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 7844
Qy 428 TCTCTCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 486

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Db 7843 TCCTCGGGGGGCTGTTCAGACGGGAGGAGCCACCCCGAGATGACAGGTGCGCCGGGAT 7784
QY 487 GGCCTCTCTTCTTCAAGCCGCGCTGPACTGTCTTCGATGAGCCAGCGCTGGGGCA 546
Db 7783 GCTGCTCTCTTCTTATGCGCGCGCTATACCTGCTCTGCGCGAGCGAGCGGAGGCA 7724
QY 547 CTTCTTCGCGGGGGGCTCAATGAGCTTCATCTGATCAGTCCGCTGATGAGGCGCA 606
Db 7723 CTTCTTCGCGGGGGCTCAATGAGCTTCATCTGATCAGTCCGCGGAGATGAGGCGCA 7664
QY 607 CTGCGGCGCACACCGCATACCGGCGCATCGGCTCTTCAGCGGTGAGGTGCTTC 666
Db 7663 CTGCGGCGCACACCGCATACCGGCGCATCGGCTCTTCAGCGGTGAGGTGCTTC 7604
QY 667 CGGGAATGCTCTACCGGCTTCAGCATTCGCTGTGAGATGTTACACAAACCGACCA 726
Db 7603 CGGGAATGCTCTACCGGCTTCAGCATTCGCTGTGAGATGTTACACAAACCGACCA 7544
QY 727 CATGCGCTTCAGACGCTTCGATGACACCGGACCTTCAGACATGCGCTTTGCGCT 786
Db 7543 CATGCGCTTCAGACGCTTCGATGACACCGGACCTTCAGACATGCGCTTTGCGCT 7484
QY 787 CTGCGGCGCACGCTTCGATGACACCGGACCTTCAGACATGCGCTTTGCGCT 846
Db 7483 CTGCGGCGCACGCTTCGATGACACCGGACCTTCAGACATGCGCTTTGCGCT 7427
QY 847 TCGCGCTTCGAAATTCCTTCAGCTACAGCATGAGCATGAGCTTCACCGGTAATGAGAT 906
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QY 907 CGGCAAGATTAATCTTCTCGCGGAGTCCGCTGTCTGCTCAGAGAGAGAGGAGG 966
Db 7366 CGGCAAGATTAATCTTCTCGCGGAGTCCGCTGTCTGCTCAGAGAGAGAGGAGG 7307
QY 967 GCAAGCGCTTCGATGAGTCCGCGGAGTCCGCAATTCGAGCTTCGAGCTTCGCTG 1026
Db 7306 GCAAGCGCTTCGATGAGTCCGCGGAGTCCGCAATTCGAGCTTCGAGCTTCGCTG 7247
QY 1027 GCGCTTCGCGGATTCGAGTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1086
Db 7246 GCGCTTCGCGGATTCGAGTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7187
QY 1087 CGGATTCAGACAGTCCCAATTCGCTGACCACTTCGCTCAGAGCTTCGAGGAGG 1146
Db 7186 CGGATTCAGACAGTTCGAGTTCGCTGACCACTTCGCTCAGAGGAGTTCGAGGAG 7127
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Db 7126 ACCCAAGGCGATGAGTTCGAGTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7067
QY 1207 TCGTTGAGATTCGAGTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1266
Db 7066 TCGTTGAGATTCGAGTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7007
QY 1267 CGGCTTCAGCTTCGAGTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1326
Db 7006 TCGCTTCGCGGAGTTCGAGTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6947
QY 1327 GATGAGGCTTCATTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1386
Db 6946 GATGAGGCTTCATTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6887
QY 1387 ACTGAGGCTTCGAGTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1446
Db 6886 ACTGAGGCTTCGAGTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6827
QY 1447 GATGAGGAGGCTTCGAGTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1506
Db 6826 GATGAGGAGGCTTCGAGTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6778
QY 1507 TTTGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGAT 1566
Db 6777 TTTGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGAT 6730

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QY 1567 ATGATCATTCACCT-----GCTGAGTCAAGTTCGATTCGATTCAGAGTGGC 1620
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QY 1621 -TGTCTATCCAGTTGAGA-----GTTCAATGCTTCGATTCGATTCAGAGTGGC 1675
Db 6669 TGTCTATCCAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGAT 6610
QY 1676 CTGTTCTCCCTATC 1689
Db 6609 AGATTCGAGTTC 6596

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Search completed: January 1, 2004, 04:20:52
 Job time : 3937.96 sec

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 16:17:02 / Search time 445.364 Seconds
(without alignments)
9535.036 Million cell updates/sec

Title: US-09-857-524B-3
Perfect score: 1764
Sequence: 1 gcacgagcctccctccctc.....ttaaaaaaaaaaaaaa 1764

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4483691 seqs, 1203673480 residues

Total number of hits satisfying chosen parameters: 8967382

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Pending Patents NA New:*
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2: /cgn2_6/prodata/1/pna/US06_NEW_COMB.seq:*
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4: /cgn2_6/prodata/1/pna/US08_NEW_COMB.seq:*
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6: /cgn2_6/prodata/1/pna/US10_NEW_COMB.seq:*
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8: /cgn2_6/prodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1349	76.5	1541	7	US-10-425-114A-14218 Sequence 14218, A
2	891.4	50.5	1408	7	US-10-425-114A-17460 Sequence 17460, A
3	609.6	34.6	1967	7	US-10-425-114A-14991 Sequence 14991, A
4	602	34.1	1207	7	US-10-425-114A-28231 Sequence 28231, A
5	491.2	27.8	1702	7	US-10-702-777-26 Sequence 26, Appl
6	486.2	27.6	1828	7	US-10-425-114A-14869 Sequence 14869, A
7	459	26.0	1953	8	US-60-496-751-1 Sequence 1, Appl1
8	453.8	25.7	1389	8	US-60-496-751-1 Sequence 2, Appl1
9	452.2	25.6	1341	8	US-60-496-751-2 Sequence 3, Appl1
10	439.2	24.9	1244	7	US-10-425-114A-15122 Sequence 15122, A
11	385.2	21.8	1719	7	US-10-425-114A-10327 Sequence 10327, A
12	365.4	20.7	1685	7	US-10-702-777-4 Sequence 2, Appl1
13	337.6	19.1	966	7	US-10-425-114A-6172 Sequence 6172, Ap
14	273.8	15.5	1071	7	US-10-425-114A-10518 Sequence 10518, A
15	213.6	12.1	663	7	US-10-425-114A-14800 Sequence 14800, A
16	194	11.0	626	7	US-10-425-114A-10881 Sequence 10881, A
17	103	5.8	262	7	US-10-680-765-14762 Sequence 14762, A
18	100.4	5.7	340	7	US-10-680-765-11214 Sequence 11214, A
19	89	5.0	1455	5	US-10-425-114A-5694 Sequence 5694, Ap
20	83.6	4.7	1215	5	US-09-897-516A-4197 Sequence 4197, Ap
21	80.2	4.5	85632	1	PCT-US03-18787-1 Sequence 1, Appl1
22	80.2	4.5	85632	1	PCT-US03-19069-1 Sequence 1, Appl1
23	79.4	4.5	616	7	US-10-425-114A-5327 Sequence 5327, Ap
24	76.8	4.4	1380	7	US-10-417-700A-138 Sequence 138, App
25	76.4	4.3	560	7	US-10-425-114A-13841 Sequence 13841, A

26	76.4	4.3	630	7	US-10-425-114A-28252 Sequence 28252, A
27	76.4	4.3	1574	7	US-10-324-316-11 Sequence 11, Appl
28	76.4	4.3	1574	7	US-10-324-316-11 Sequence 11, Appl
29	75.6	4.3	2253	8	US-60-494-568-34 Sequence 34, Appl
30	75.6	4.3	164051	8	US-60-494-568-16 Sequence 16, Appl
31	75	4.3	86941	1	PCT-US03-18787-2 Sequence 2, Appl1
32	75	4.3	86941	1	PCT-US03-19069-2 Sequence 2, Appl1
33	74.4	4.2	37307	8	US-60-500-315-11904 Sequence 11904, A
34	72.8	4.1	2151	7	US-10-389-647-123 Sequence 123, App
35	72.6	4.1	1848	7	US-10-425-114A-23176 Sequence 23176, A
36	72	4.1	986	7	US-10-425-114A-17564 Sequence 17564, A
37	72	4.1	1041	7	US-10-425-114A-16902 Sequence 16902, A
38	71.8	4.1	1450	7	US-10-425-114A-15517 Sequence 15517, A
39	70	4.0	1705	1	PCT-US03-27523-523 Sequence 523, App
40	70	4.0	1772	7	US-10-296-115-562 Sequence 562, App
41	69.8	4.0	2200	7	US-10-425-114A-35258 Sequence 35258, A
42	69.6	3.9	2336	7	US-10-679-063-119 Sequence 119, App
43	69.6	3.9	2336	7	US-10-679-063-119 Sequence 119, App
44	68.6	3.9	8705	1	PCT-US03-3131-16 Sequence 16, Appl
45	68.6	3.9	10330	7	US-10-656-269-24 Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-10-425-114A-14218
Sequence 14218, Application US/10425114A
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425, 114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 14218
LENGTH: 1541
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB148-051-G4_F11
US-10-425-114A-14218

Query Match	76.5%	Score 1349	DB 7	Length 1541
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1349	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0
QY	399	CCGATACCGCGCGCTCTCGGCGAGCTATCTCGCGGCGCTTTCGACCGTTCGGCC	458	
DB	1	CCGATACCGCGCGCTCTCGGCGAGCTATCTCGCGGCGCTTTCGACCGTTCGGCC	60	
QY	459	CCACCCCAAGTTCAGCTCTCTGATGAGCCGCTCTTTCAGCCGCGTGAACCTTG	518	
DB	61	CCACCCCAAGTTCAGCTCTCTGATGAGCCGCTCTTTCAGCCGCGGCTGAACCTTG	120	
QY	519	TCTTGATGCGCGCGCTCTCGGCGAGCTATCTCGCGGCGCTTTCGATGAGCTTCGT	578	
DB	121	TCTTGATGCGCGCGCTCTCGGCGAGCTATCTCGCGGCGCTTTCGATGAGCTTCGT	180	
QY	579	GGATCCAGTCCGCGCTCTGATGAGCGAGCTCGGCGAGCTCGGCGAGCTCGGCG	638	
DB	181	GGATCCAGTCCGCGCTCTGATGAGCGAGCTCGGCGAGCTCGGCGAGCTCGGCG	240	
QY	639	TCTTGATGCGCGCTCTGATGAGCTCTCTCGGCGAGCTCGGCGAGCTCGGCG	698	
DB	241	TCTTGATGCGCGCTCTGATGAGCTCTCTCGGCGAGCTCGGCGAGCTCGGCG	300	

QY 699 GGTGAGAGTGAACACACACGACACATCCGCTGCAACAGCTGAGACATGACCCG 758
 DB 301 GGTGAGAGTGAACACACACGACACATCCGCTGCAACAGCTGAGACATGACCCG 360
 QY 759 ACCTCCAGCAGATGCGCTCTTTGCGCTGCTCCCAAGCTGTTGGCAATATGCTCT 818
 DB 361 ACCTCCAGCAGATGCGCTCTTTGCGCTGCTCCCAAGCTGTTGGCAATATGCTCT 420
 QY 819 ACTTCAACAGAGGAGCTGCGCTGAGTGCCTGCAAAATCTTATCAGCTACCGAGC 878
 DB 421 ACTTCAACAGAGGAGCTGCGCTGAGTGCCTGCAAAATCTTATCAGCTACCGAGC 480
 QY 879 ACTGACCTTCTACCCGCTGATGATGATCCGACAGATAAATCTTCTGCGCAGTCCGCC 938
 DB 481 ACTGACCTTCTACCCGCTGATGATGATCCGACAGATAAATCTTCTGCGCAGTCCGCC 540
 QY 939 TGTTCCTTCTACGAGAGAGAGGATGCGCAGACCGCTTCTTGAAGATGCGCGGCTGCCA 998
 DB 541 TGTTCCTTCTACGAGAGAGAGGATGCGCAGACCGCTTCTTGAAGATGCGCGGCTGCCA 600
 QY 999 CATTTGGGCTGCTGATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1058
 DB 601 CATTTGGGCTGCTGATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 QY 1059 CGTTTGTCTTTTCAAGCTTCAACATCTGCGGATTCAGACATCTTCAATCTTCTGCTGAACC 1118
 DB 661 CGTTTGTCTTTTCAAGCTTCAACATCTGCGGATTCAGACATCTTCAATCTTCTGCTGAACC 720
 QY 1119 ACTTCTGCTGCAAGCTGATGATGCGGCTCAACCCCAAGGCAATGATGCTTTGAGAGAGA 1178
 DB 721 ACTTCTGCTGCAAGCTGATGATGCGGCTCAACCCCAAGGCAATGATGCTTTGAGAGAGA 780
 QY 1179 CGGAGGAGCAGCTGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1238
 DB 781 CGGAGGAGCAGCTGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 QY 1239 AGTTCAGATTGAGACACATCTGTTTCCCGCTTACCTCGGTGCACTTTCGCAAGGTTG 1298
 DB 841 AGTTCAGATTGAGACACATCTGTTTCCCGCTTACCTCGGTGCACTTTCGCAAGGTTG 900
 QY 1299 CACCGGCTGCTGCGGACCTTTCGCAAGAGAGATGAGGCTCACTTATTCGCAAGCATTTT 1358
 DB 901 CACCGGCTGCTGCGGACCTTTCGCAAGAGAGATGAGGCTCACTTATTCGCAAGCATTTT 960
 QY 1359 GGGGTGCAATGCTTCAATGAGAGACATCTGAGGCTGCTGCAATTCGCAAGGACGACG 1418
 DB 961 GGGGTGCAATGCTTCAATGAGAGACATCTGAGGCTGCTGCAATTCGCAAGGACGACG 1020
 QY 1419 CTACAAGTGTGCTGCTGCAAGAGATTTGATGAGGCTGAGTGAACCCATGATGATAA 1478
 DB 1021 CTACAAGTGTGCTGCTGCAAGAGATTTGATGAGGCTGAGTGAACCCATGATGATAA 1080
 QY 1479 TGGGATGAGATGAGGCTTATGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTG 1538
 DB 1081 TGGGATGAGATGAGGCTTATGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTG 1140
 QY 1539 TCTGAGATGCTTCAATGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTG 1598
 DB 1141 TCTGAGATGCTTCAATGATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGATTTG 1200
 QY 1599 AATTTTCTGTTGAGATGAGTCTGCTATCAGATTTGAGATTTGAGATTTGAGATTTG 1658
 DB 1201 AATTTTCTGTTGAGATGAGTCTGCTATCAGATTTGAGATTTGAGATTTGAGATTTG 1260
 QY 1659 GTTGTTCAGGAGATGCTGCTGCTGCTATCAGATTTGAGATTTGAGATTTGAGATTTG 1718
 DB 1261 GTTGTTCAGGAGATGCTGCTGCTGCTATCAGATTTGAGATTTGAGATTTGAGATTTG 1320
 QY 1719 TTAATTCATGAACCTGTTTCAAGATTA 1747
 DB 1321 TTAATTCATGAACCTGTTTCAAGATTA 1349

RESULT 2
 US-10-425-114A-17460
 ; Sequence 17460, Application US/10425114A
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaka, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(5313) B
 ; CURRENT APPLICATION NUMBER: US/10/425,114A
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 17460
 ; LENGTH: 1408
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3069-031-B5_FLI
 ; US-10-425-114A-17460
 Query Match 50.5%; Score 891.4; DB 7; Length 1408;
 Best Local Similarity 88.0%; Pred. No. 2,1e-225;
 Matches 1082; Conservative 0; Mismatches 116; Indels 31; Gaps 9;
 QY 541 GGGGCACTCTCTGCGGGGGGCTCAATGAGCTTCTGCTGATCAGTCCGCTGATGGG 600
 DB 3 GGGGCACTCTCTGCGGGGGGCTCAATGAGCTTCTGCTGATCAGTCCGCTGATGGG 62
 QY 601 CCAAGACTGGGGGCAACACCGCATCAACCGGCTGCTGAGCTGCTGAGCTGAGG 660
 DB 63 CCAAGACTGGGGGCAACACCGCATCAACCGGCTGCTGAGCTGCTGAGCTGAGG 122
 QY 661 GCTCTCGGGAATCTGCTTCAACCGGCTTCAAGATGCTGCTGAGTGAATGACACAAAC 720
 DB 123 GCTCTCGGGAATCTGCTTCAACCGGCTTCAAGATGCTGCTGAGTGAATGACACAAAC 182
 QY 721 GCAACATGCTGCTGCAACAGCTGAGCAATGACCTGCAACCTTCAACATGCTGCTT 780
 DB 183 GCAACATGCTGCTGCAACAGCTGAGCAATGACCTGCAACCTTCAACATGCTGCTT 242
 QY 781 TGGCGTCTCCCAAGCTGCTGCGCAATGAGTCTTCTTACCAAGGACCTTGGC 840
 DB 243 TGGCGTCTCCCAAGCTGCTGCGCAATGAGTCTTCTTACCAAGGACCTTGGC 302
 QY 841 GTTCGATGCTGCTGCAATCTTCAATGAGTCAACGACTGAGCTTCAACCGGTAAT 900
 DB 303 GTTCGATGCTGCTGCAATCTTCAATGAGTCAACGACTGAGCTTCAACCGGTAAT 362
 QY 901 GTTCGATGCTGCTGCAATCTTCAATGAGTCAACGACTGAGCTTCAACCGGTAAT 960
 DB 363 GTTCGATGCTGCTGCAATCTTCAATGAGTCAACGACTGAGCTTCAACCGGTAAT 422
 QY 961 GGTGCGGAGCGGCTTCTGAGATGCGGGGGGCTGCAATCTGAGCTTGGATCCGTT 1020
 DB 423 GGTGCGGAGCGGCTTCTGAGATGCGGGGGGCTGCAATCTGAGCTTGGATCCGTT 482
 QY 1021 GCTGTGAGCTTCTGCTGCAATGAGTGGAGAGAGGCTGCGTTGCTTTCAGCTTCAAC 1080
 DB 483 GCTGTGAGCTTCTGCTGCAATGAGTGGAGAGAGGCTGCGTTGCTTTCAGCTTCAAC 542
 QY 1081 CATCTCGGAGATTCAGACAGTCAATTTCTGCTGAAACATTTCTGCTGAGCTGATGT 1140
 DB 543 CATCTCGGAGATTCAGACAGTCAATTTCTGCTGAAACATTTCTGCTGAGCTGATGT 602
 QY 1141 CGGGCCACCAAGAGGCAATGATGCTGTTTGAAGAGAGAGGAGGAGGAGGAGGAGGAGG 1200
 DB 603 CGGGCCACCAAGAGGCAATGATGCTGTTTGAAGAGAGAGGAGGAGGAGGAGGAGGAGG 662
 QY 1201 GTGCTCTCTTGGATGATGATTTGTTTCAAGGCTGCAAGTTCAGATTTGAGACCATCT 1260

Db 1219 AGAAGATTCGGCTTTGGTTAAGATCTTTCAGAGAAATAGTCTTCTTAATATGT 1278
Qy 1349 GCCACATTCCTGGGGTGAAGATGCTTACATGAGAGACACTGAGGGCTGCTGATTCAG 1408
Db 1279 GTGTCTGTTCTGGAAGGCAATGCTCAATTCAGACTTGAAGAAATGCTGCTTTCAG 1338
Qy 1409 GCCAGACCGCTCAAGTGTGTGCTCCAGAAATTTGATGAGAGGCTGTGACACC 1468
Db 1339 GCCAGAGACGGTTTCCA---ATCCGGTTCCAAAGATTTGTTGGAGGCTGTTAACACT 1395
Qy 1469 CATGATTAATGGG 1482
Db 1396 CATGATTAATGGG 1409

RESULT 4
US-10-425-114A-28231
; Sequence 28231, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yinhua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 28231
; LENGTH: 1207
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4748-018-D3_FLI
US-10-425-114A-28231

Query Match 34.1%; Score 602; DB 7; Length 1207;
Best Local Similarity 89.6%; Pred. No. 7.9e-149;
Matches 658; Conservative 0; Mismatches 75; Indels 1; Gaps 1;
Qy 4 CGAGCTCTCTCTCTCTCCCAATCTCTCCGCGCTCCCTCCCAACCA-AATCAGACACACCA 62
Db 13 CGAATTTCCCACTTCCCAATTTCTCCGCGCTCCCTCCCAACCAACCA 72
Qy 63 AGGCGCATCCGAGCGAGCGCGCGCAATGCGCGCTCTGTGATGCAATGCGCGCGCG 122
Db 73 CACCCATAGGGGCGAGCGCGCGCAATGCGCGCTCTGTGCGAAGCAATGCGCGCGCG 132
Qy 123 GCGAGCGCGCGCGCGCGCGCGAGCTGTGCGATGATCTCTCCAGAGAGCTCCGCGCTAG 182
Db 133 GAGAGCGCGCGGTGTGCGCGCGAGCTGTGCGATGATCTCTCCAGAGAGCTCCGCGAGCG 192
Qy 183 CTTCGCGCGAGAGCTGTGATCTCATCTCCGCGAGAGTGAAGAGTACGCGCGCG 242
Db 193 GCTTCGCGCGAGAGCTGTGATCTCATCTCCGCGAGAGTGAAGAGTACGCGCGCG 252
Qy 243 TCCCGCACACCGCGCGCGCGAGCTCCCGCTTCTCACTTGTGCGCGCGAGAGCGCACCG 302
Db 253 TTCCCGCACACCGCGCGCGCGAGCTCCCGCTTCTCACTTGTGCGCGCGAGAGCGCACCG 312
Qy 303 ACGGCTTGTGCGCGCTTACACACCGCGCTTGTGCGCGCGCGCTTCTTCTTGTG 362
Db 313 ACGGCTTGTGCGCGCTTACACACCGCGCTTGTGCGCGCGCGCTTCTTCTTGTG 372
Qy 363 GCGGCTTGTGAGTACAGCGGTCTCCCGCGGTGCGCGAGTACCGCGCGCTCTCTGCGG 422
Db 373 GCGGCTTGTGAGTACAGCGGTCTCCCGCGGTGCGCGAGTACCGCGCGCTCTCTGCGG 432
Qy 423 AGCTATCTCTGCGCGCGCTTCTTCAAGCGGTGCGCGCGCGCGCGCGCGCGCGCG 482

Db 433 AGCTCTCTCCGCGCGCTCTTTCAGAGCGGCTGCGGCCACCCCGAGGTAACAGCTGCCC 492
Qy 483 TGATGCGCGGCTCTCTTCTTACGCGCGCTGACTGCTGCTGCTGCTGCTGCTGCTGCTG 542
Db 493 TGATGCGCGGCTCTCTTCTTACGCGCGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTG 552
Qy 543 CGGAGCTCTCTGCGCGCGGCTCTTATGCTTGTGCTGATTCAGTCCGCTGATGAGGCG 602
Db 553 CGGAGATGCTGCTGCGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 612
Qy 603 ACGACTGCGCGCACACCGCATACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 662
Db 613 ACGACTGCGCGCACACCGCATACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 672
Qy 663 TCTCGGGAAGTCTCTACCGCGCTGAGATGCTGAGTGAAGTGAACACACACGCG 722
Db 673 TCTCGGGAAGTCTCTACCGCGCTGAGATGCTGAGTGAAGTGAACACACACGCG 732
Qy 723 ACCACATCGCTGCG 736
Db 733 TCGACATCTGCTGCG 746

RESULT 5
US-10-702-777-26
; Sequence 26, Application US/10702777
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/702,777
; FILING DATE: 06-Nov-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,254
; FILING DATE: 19-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 83832YXWVU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 48..1406
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: 48..1406
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-702-777-26

Query Match 27.8%; Score 491.2; DB 7; Length 1702;
 Best Local Similarity 62.0%; Pred. No. 2e-119;
 Matches 832; Conservative 0; Mismatches 498; Indels 12; Gaps 3;

155 ATCTCTCCAGAGAGTCCGCGCTCAAGCTCCGCGAGAGCTGTGATCTTCATCTCC 214
 DB ATTCACGCGCGAGAGCTCCGCGCGCGCAACAGTCCGCGATCTGTGATCTTCATCTCCAG 131
 215 GCGAGGTGTAGAGTCAAGCTCCGCGCTCCCGCACACCCCGGCGCGAGCTCCGCGCTT 274
 DB GCGAAGGTGTAGAGTCAAGCTCCGCGCTCCCGCACACCCCGGCGCGAGCTCCGCGCTT 191
 132 GCGAAGGTGTAGAGTCAAGCTCCGCGCTCCCGCACACCCCGGCGCGAGCTCCGCGCTT 191
 275 CTCACCTCTGCGCGCGAGAGCGCGACCGCGAGCTTCGCGCGCTTCAGCGCGCG 334
 DB CTCACCTCTGCGCGCGAGAGCGCGACCGCGAGCTTCGCGCGCTTCAGCGCGCG 251
 192 CTCACCTCTGCGCGCGAGAGCGCGACCGCGAGCTTCGCGCGCTTCAGCGCGCG 251
 335 GCGCGCGCTCTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCG 388
 DB TGGCGCGCTCTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCG 311
 252 TGGCGCGCTCTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCG 311
 389 CCGCGCTCTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCG 448
 DB CCGCGCTCTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCG 371
 312 GAGATCTCCAGAGCTCAAGAGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGAG 371
 449 CCGCGCTCTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCG 508
 DB AAGAGAGGCTCAAGAGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCG 431
 372 AAGAGAGGCTCAAGAGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCG 431
 509 CTGTACTCTGCTCTCGCATGCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCG 568
 DB GTCTACGCGGTGCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCG 491
 432 GTCTACGCGGTGCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCG 491
 569 GCGTCTGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 628
 DB GCGTCTGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 551
 492 GCGTCTGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 551
 629 GCGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 688
 DB CCAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 611
 552 CCAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 611
 689 AGCATCTGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 748
 DB AGCATCTGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 671
 612 AGCATCTGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 671
 749 CATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 808
 DB TACGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 731
 672 TACGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 731
 809 ATATGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 868
 DB ATATGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 791
 732 ATATGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 791
 869 AGCTACGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 928
 DB AGCTACGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 851
 792 AGCTACGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 851
 929 CAGTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 988
 DB CAGTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 911
 852 CAGTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 911
 989 GGGGTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1048
 DB GGGGTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 971
 912 GGGGTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 971
 1049 GAGAGGTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1108
 DB GAGAGGTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1031
 972 GAGAGGTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1031
 1109 TGGTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1168
 DB TGGTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1091
 1032 TGGTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1091

1169 GAGAGCAGACCGCAGCAGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1228
 DB GAGAGCAGACCGCAGCAGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1151
 1092 GAGAGCAGACCGCAGCAGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1151
 1229 GGTGCGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1288
 DB GGTGCGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1211
 1152 GGTGCGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1211
 1289 CCGAAGTGTGACCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 1348
 DB CCGAAGTGTGACCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 1271
 1212 CCGAAGTGTGACCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 1271
 1349 CCGAAGTGTGACCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 1405
 DB CCGAAGTGTGACCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 1331
 1272 CCGAAGTGTGACCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTG 1331
 1406 CAGCGCGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1462
 DB CAGCGCGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1391
 1332 CAGCGCGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1391
 1463 AACACCATGATGATTAATGGAT 1484
 DB AACACCATGATGATTAATGGAT 1413

RESULT 6
 US-10-425-114A-14869
 ; Sequence 14869, Application US/10425114A
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaka, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425, 114A
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 14869
 ; LENGTH: 1828
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3030-005-A3_FLI
 ; US-10-425-114A-14869

Query Match 27.6%; Score 486.2; DB 7; Length 1828;
 Best Local Similarity 61.2%; Pred. No. 4.5e-118;
 Matches 820; Conservative 0; Mismatches 513; Indels 6; Gaps 2;

155 ATCTCTCCAGAGAGTCCGCGCTCAAGCTCCGCGAGAGCTGTGATCTTCATCTCC 214
 DB ATCTCTCCAGAGAGTCCGCGCTCAAGCTCCGCGAGAGCTGTGATCTTCATCTCC 211
 172 ATCTCTCCAGAGAGTCCGCGCTCAAGCTCCGCGAGAGCTGTGATCTTCATCTCC 211
 215 GCGAGGTGTAGAGTCAAGCTCCGCGCTCCCGCACACCCCGGCGCGAGCTCCGCGCTT 274
 DB GCGAGGTGTAGAGTCAAGCTCCGCGCTCCCGCACACCCCGGCGCGAGCTCCGCGCTT 291
 232 GCGAGGTGTAGAGTCAAGCTCCGCGCTCCCGCACACCCCGGCGCGAGCTCCGCGCTT 291
 275 CTCACCTCTGCGCGCGAGAGCGCGACCGCGAGCTTCGCGCGCTTCAGCGCGCG 334
 DB CTCACCTCTGCGCGCGAGAGCGCGACCGCGAGCTTCGCGCGCTTCAGCGCGCG 351
 292 CTCACCTCTGCGCGCGAGAGCGCGACCGCGAGCTTCGCGCGCTTCAGCGCGCG 351
 335 CCGCGCTCTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCG 391
 DB CCGCGCTCTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCG 411
 352 TGGTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 451
 392 TGGTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 451
 412 TGGTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 471

QY 452 GTCCGCCCCAAGGCTGAGCTGCTGATGAGCGCTCTTCTAAGCGCGCTG 511
 DB 472 AAGGCGCATGCTCTTCTGACCTTGTGATCTGTTGCTGTATGTTCCATTTGATG 531
 QY 512 TACCTGCTCTGCGATGCGCAGCGCTGGGCGACCTCTCCGCGGGGGTCTCATTTGC 571
 DB 532 TATGCTGTGAGGCTGACTAGTGTGCGCTCATTTGGGGCTCAGGATGATTAAGG 591
 QY 572 TTGCTGTGATGAGTCCGCGCTGATGAGGCGACAGCTCGGCGCAACCGCATCACCGG 631
 DB 592 TTGCTGTGATGAGTCCGCTGTATGAGGCTGATGATTTGCGGCACTATGTTAGACA 651
 QY 632 CATCCGCTCTGAGCGCGCTGCTGAGGCTCTCCGCGGAACTGCTCAACCGGCTGAG 691
 DB 652 AGCAATGTTTCAACAAGTTGACAGATCTCTCTGAGAACTGCTTGAATGGATTAAG 711
 QY 692 ATGCGCTGTGAGTGTATCAACAACGACACCACTGCTGCAACAGCTTGAACAT 751
 DB 712 ATTTGCTGTGAGTGTGAGTCAACAATGCTCACCACTGCTGCAACAGCTTGAATCAT 771
 QY 752 GACCCGAGCTCTGAGACATGCGGCTTGTGCGGCTCTCCCGCAAGCTGTTGGCAATTA 811
 DB 772 GACCTGTGATGAGACATGCGGCTTGTGCGGCTCTCCGCTGCTTCAATTCGATA 831
 QY 812 TGGTCTGCTTCTACCAAGGAACTGCGCTGATGCGGCTGCAAAATCTTCATCAGC 871
 DB 832 ACTTCTCATTTCTATGAGGAGAGTTGAGATTTGATTTCAATGCAAGTTCTTGAATCTG 891
 QY 872 TACAGCACTGACCTTCTTACCCGCTGATGCTGATGCGGAGTAAATCTTTCGCGCAG 931
 DB 892 TACAGCACTTCACTTTTACCCGCTGATGCTGATGCGGAGTAAATCTTTCGCGCAG 951
 QY 932 TCCGCGCTGCTGCTGCTGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 991
 DB 952 ACCATTTCTGATTTGTTTGAAGCGTAAAGTCAAGATTAAGCTTGAACATTAATGAGG 1011
 QY 992 GTCCGACATTTCTGAGCTTGTATCCGCTGCTGAGCTTCTCCGCGAAATGTTGAGGAG 1051
 DB 1012 ATCTGTTGTTTGTGAGCTTGTGCTCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTG 1071
 QY 1052 AAGGCTGCTGTTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 1111
 DB 1072 AAGGCTGCTGTTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 1131
 QY 1112 CTGAACCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1171
 DB 1132 TTGAATCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1191
 QY 1172 AAGCAGACGCGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1231
 DB 1192 AAGCAGACGAGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1251
 QY 1232 GGCCTGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1291
 DB 1252 GGCCTGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1311
 QY 1292 AAGGCTGACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1351
 DB 1312 AACATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1371
 QY 1352 ACATTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1411
 DB 1372 TCAATTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1431
 QY 1412 AAGCAGCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1471
 DB 1432 AAGGAGCTTGAACA--ACCTGCGCTGAAGATTTGTTGAGGAGGAGGAGGAGGAGGAGG 1488
 QY 1472 GGATTAATGGATGAAGAT 1490
 DB 1489 GGCTGAGGATTTGGAGTT 1507

RESULT 7
 US-60-496-751-1
 ; Sequence 1 Application US/60496751
 ; GENERAL INFORMATION:
 ; APPLICANT: Ursin, Virginia
 ; APPLICANT: Roman, Byron
 ; APPLICANT: Gonzalez, Jennifer
 ; TITLE OF INVENTION: Fatty Acid Desaturases from *Primula*
 ; FILE REFERENCE: MONS:044USP1
 ; CURRENT APPLICATION NUMBER: US/60/496, 751
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 1953
 ; TYPE: DNA
 ; ORGANISM: *Primula juliae*
 ; US-60-496-751-1

Query Match 26.0%; Score 459; DB 8; Length 1953;
 Best Local Similarity 60.3%; Pred. No. 7.4e-111;
 Matches 794; Conservative 1; Mismatches 516; Indels 6; Gaps 2;

QY 189 CCGAGCAGCTTGGATCTTCATCTCCGCGGAGCTGTAGAGCTACAGCCCTGCTCCCC 248
 DB 187 CAGTACCTATGATATATCAATTCAGGTCAGATTACAGCGTTTCTCTCGGGCTGGC 246
 QY 249 ACCACCGGCGGCGGACCTCCGCTTCTACCTCTGGCGGGGAGAGCCGACGAGCCT 308
 DB 247 TTCACCGGCGGCGGACCTCCGCTTCTCGGCTTCCAGAGACATGATGAGCAGGCTT 306
 QY 309 TCGCGGCTTACACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 368
 DB 307 TCTCGCTTACACATCCCTTCCAGCTCCGCGCTTCTCTCTCTCTCTCTCTCTCTCT 366
 QY 369 TCTCTG---ACTAGCGGCTCTCCCGCGGCTGCGGAGCTACAGCCGCTCTTCCGCGAGC 425
 DB 367 TTTCTAATAAACAATTCGATGCGAGACCTTTCGATATGCAAACTTCTAGACAGCT 426
 QY 426 TATCTCCGCGGCGCTTCTGAAAGCGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 485
 DB 427 TTTATAGATGAGGATGTTGCTGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 486
 QY 486 TGGCGGCTCTCTTACGCGCGGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 545
 DB 487 TGAATTAATGTTGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
 QY 546 ACTTCTCGCGGCGGCTCTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 605
 DB 547 ATTGCTTTGAGAGGCGGAGATGGGTTTGGCTGATTCAGATGCGATGATGATGATG 606
 QY 606 ACTGCGGCGGAGCGGAGCTGACCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 665
 DB 607 ATTCCGAGATTAACCGGATTAATGATGACAGGAAATGAAACCGGTTTCTGATCTGA 666
 QY 666 CCGGGAATGCTCTACCGGCTGAGATGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 725
 DB 667 GCTCAATGCTCTCAAGGATTAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 726
 QY 726 ACATGCTGCGCAACAGCTGAGACATGACCGGAGCTTCCAGGACATGCGCTTGTGCGG 785
 DB 727 ACATGCTGCGCAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 786
 QY 786 TCTTCCCGCAAGCTTGTGCGCAACATGATGCTTCTTCTTCAACAGGAGCTTGGCTTG 845
 DB 787 TGTCCCGCAAGCTTCTTCACTCCCTCACTTCTGTTTCAACAGGAGGAGGAGGAGGAGG 846
 QY 846 ATGCGGCTGGAATTTCTTCACTGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 905
 DB 847 ACGGCTGCTGAGGTTTGTGTTCAATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 906
 QY 906 TCGCCAGATTAATCTTCTGCGAGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 965

Db 907 TTGTAGGCTGAACATGCTTGGCAGTCTGTATTAATCTGCTTTTTCAGAGAGGAGTGG 966
 Qy 966 CGCAGGGTGTGTTGATGATCGGGGGGTGCGCAATTCGGGCTGTGTAACCGGTGTGG 1025
 Db 967 CGAAGGGGTGAGGAGATTTCTTGAATGACGGGTTTGTGGCTTGTTCGGCTCTGC 1026
 Qy 1026 TGGCTTCCCTGCGAATTTGTGTGAGAGGGTGGCGCTTGTGCTTTTCACTTACCATCT 1085
 Db 1027 TTTCTTGGCTTCTATATTTGGGGTGAAGAAATATGTTTTGTCTCGGAGACTCTCCGTTA 1086
 Qy 1086 GGGGATTCAGACGCTCCATTTCTGCTTAACCACTTCTGTCCGAGCTGTATGTGCGC 1145
 Db 1087 CGGGATTAACAACGTCGAGTTTCAAGCTTCAACCATTTCTCATCTGACGTTTACGTGGCC 1146
 Qy 1146 CACCAAGGCAATGATCGTGTGGAAGCAGACGCGACGCGTCCGATCTGTGTGT 1205
 Db 1147 CACCGTAGGTAACGATTTGGTTTAAAGAAACAGCTGACGAGACACTCAACATATGCTGCC 1206
 Qy 1206 CTCTTGTGATGATTTGTTTCAACGCTGCGCTGCAAGTTGAGACCACTTCTTTTC 1265
 Db 1207 CGGCGTGAATGATTTGTTTCCAGGTGATGCAAGTTTGAAGTTCAGACCACTTGTTC 1266
 Qy 1266 CCGGCTTACTTGTGTCACCTTTCGACAGTTGACCGGCGCTGCGCACTTTGCAAGA 1325
 Db 1267 CGCGATGCTTGAAGGGTCAAGTTTCGGAGATTTCTCTTTGTGAGGAGATTTGTGTAAGA 1326
 Qy 1326 AACATGGGCTCATTTATTTGACAGCAATTCGGGGTCCAAATGTGCTTAATAGAGAA 1385
 Db 1327 AACACAATTTGACTTAACAATATTTGCTTTTAATAACCAATGTGTGACGCTTGAGA 1386
 Qy 1386 CACTCAGGCTCTGCTGATTTGACAGGACGAGACGCTCAAGTGTGTGCTCGAAGATT 1445
 Db 1387 CCTGAGAAACACAGCATTTGAGGCTCGGAGCTCTC---TAATCCGATCCCAAGAAATA 1443
 Qy 1446 TGGTATGGAGCGCTGTGAACACCCATGATTAATGAGATGAAGATACGGGCTAATGG 1502
 Db 1444 TGGTGTGGAGGCTGTAAATATGTCGGGTGAATGATGATGTTGTTGCTAATGG 1500

RESULT 8

US-60-496-751-3
 ; Sequence 3, Application US/60496751
 ; GENERAL INFORMATION:
 ; APPLICANT: Urelin, Virginia
 ; APPLICANT: Froman, Byron
 ; APPLICANT: Gonzalez, Jennifer
 ; TITLE OF INVENTION: Fatty Acid Desaturases from *Primula*
 ; FILE REFERENCE: MONS:044USP1
 ; CURRENT APPLICATION NUMBER: US/60-496,751
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 1389
 ; TYPE: DNA
 ; ORGANISM: *Primula juliae*
 US-60-496-751-3

Query Match 25.7%; Score 453.8; DB 8; Length 1389;
 Best Local Similarity 60.7%; Pred. No. 1.5e-109;
 Matches 778; Conservative 0; Mismatches 497; Indels 6; Gaps 2;

Qy 189 CCGAGAGCTCTGATCTCATCTCCGCGAGGTGTAAGACGTACAGCCCTGGCTCCCC 248
 Db 101 CAGGTGACCTATGATATCAATTCACGTCAGATTACACAGTTCTCTCGGCTGCGC 160
 Qy 249 ACCACCGGGGCGGCACTCCGCTTCTACCCCTGGCGGGGAGAGCGCACCGAGCT 308
 Db 161 TTCACCCGGGGGAGATCGCTCCCTCTCTGCTTTCAGAGACATGATGTGACCGAGCTT 220
 Qy 309 TGGCGGCTTACGACCGGCTCGGCGCGCGCTCTCTCGCGCTTCTTGTGGCGGC 368
 Db 221 TCCTGCTTACCATCCCTTCCACCTCCGCGCTCTCTCCCTTCTCCACCAACCTATC 280

Qy 369 TCTGTG---ACTACCGGCTCTCCCGGCTCGCGGCACTACCGCGGCTCTCGCGAC 425
 Db 281 TTTTGAAAAAATTCCTGCTGTCGAGACTCTTCCGACTATGCAAACTTCTAGACAGCT 340
 Qy 426 TATCTCCGGGCTCTTTCGACCGGTGCGGCCACCCCAAGGTCCAGCTGTCTGA 485
 Db 341 TTTATTAAGATGGGCAATGTTGTGTCAGAGGCACTGCTGCTTACCGACCTTTGTATTA 400
 Qy 486 TGGCGGCTCTCTTACCGCGGCTGTACCTGTCTGCGATGCGCCAGCGCTGGGCGC 545
 Db 401 TGATATTAATGTGTGTTCTCTGTGACTGGGCTCTTTCAGTAAATTCGTGGGTGC 460
 Qy 546 ACTCTCTCGGGGGGCTCATTTGCTTCTGTGATCCAGTCCGAGTATGGGACAG 605
 Db 461 ATTTGCTTTGTGAGCGGCAATGGGTTTGTCTGATTCAGTCCGATGATGATGATG 520
 Qy 606 ACTCGGGCCACCAACCGCATCAACCGGCATCCGCTCTGACCGCGCTGTGAGGTCT 665
 Db 521 ATTCGGAATATACCGGATTAATGACTAGAGAAATGGAACCGGTTCCGTGATCTGA 580
 Qy 666 CCGGAACTGCTTCAACCGGCTCAGCATGCTGTGTGAAGTGAACCAACACGACAC 725
 Db 581 GCTCAAACTGCTCCAGGGGATTAACATCGGTGTGGAAGTGAACCAACACGCGCAC 640
 Qy 726 ACATGGCTGCAACAGCCCTGACATGACCGGACCTCGACAGACATGCGGCTCTTGCCG 785
 Db 641 ACATGGCTGCAATGCTTGAAGTACAGCCGACCTCGAGTACATTCCTTGTGTGG 700
 Qy 786 TCTCCCAAGCTGTTCGCAACATATGCTCTTCTTACCAACGCAACCTGTGGCTTCG 845
 Db 701 TGTCCCGAAGTCTTAAATCTCCCTCACTTCTGTTTCTAGACAAAGACTGAATCTTG 760
 Qy 846 ATGCGGCTCGAATTTCTTATCAGCTACAGCACTGACCTTCTTACCCGGTATGTGA 905
 Db 761 ACGGTGTGCGAGTTTGTGTTCAATACAGCACGTGCTGTTTATCCGATCATGTGG 820
 Qy 906 TCGCAGATTAATCTTCGCGGCGAGTCCGCTGTGCTGTCTCAGGAGAGAGGTGC 965
 Db 821 TTGTAGGCTGAACATGCTGTGCGCAGTGTGTATACGCTTTTTCAGAGAGAGGTGC 880
 Qy 966 CGCAGCGTGTGTTGATTCGCGGGGTGCGCACATTCGTGGCTTGTATCCCGTGTG 1025
 Db 881 CGAAGGGGTGAGAGAAATTTCTGSACTAGCGGTTTTTGTGCTTGTTCGGCTCTGC 940
 Qy 1026 TGGTTCCTTGCAGATTTGTGAGAGAGGTCGCTTGTGCTTTTCACTTACCATCT 1085
 Db 941 TTTCTTGCCTTCTAATTTGGGGTGAAGAAATATGTTTTGTCTCGGAGCTACTCGTTA 1000
 Qy 1086 GGGGATTCAGACGTCATTCGCTGGAACCACTTCTGCTCGACAGTATGTGCGGC 1145
 Db 1001 CGGGATTAACAACGTCGACGTTGACCTTGAACATTTCTCATCTTACGTTTACGTGGCC 1060
 Qy 1146 CACCAAGGCAATGATGTTTGAAGACAGACGCGACGCTCGACATCTGTGTCT 1205
 Db 1061 CACCGTAGTACGATGTTGTTTGAAGAAACAGACTGCGAGACATCAACATATGTGTC 1120
 Qy 1206 CTCTTGTGATGATTTGTTTCAACGCTGCGCTGACGTTCCAGATTGAGACCATCTGTTTC 1265
 Db 1121 CGGCTGATGATGATTTGTTTCAATGCGGGTGTGCAATTTCAAGTCCAGACCACTGTTCC 1180
 Qy 1266 CCGGCTTACTTGTGTCACCTTTCGCAAGTTGACACCGGCGCTCGGCACTTTGCAAGA 1325
 Db 1181 CGCGATGCTTAAGGGGTAGTTTGGAAATTTCTCTTTGTGTGAGGAATTTGTGTAAAGA 1240
 Qy 1326 AGCATGGGCTCACTAATTTCTGAGCAATTTCTGGGGTGAAGTATGTGCTTACATGAAGA 1385
 Db 1241 AACACAATTTGACTTAACAATATGTGCTTTTACTTAAAGCAAAATGTGTGACGCTTGA 1300
 Qy 1386 CACTCAGGCTGTGCTATTTGACGCGCAGACCGCTTACAAAGTGTGTCTCGAAGATT 1445
 Db 1301 CCTGAGAAACACAGCCATTTAGGCTCGGAGCTCTC---TAATCCGATCCCAAGAAATA 1357

QY 1446 TGGATGAGAGGCTGTGAACA 1466
 Db 1358 TGGTGTGGAGGCTGTAAAAA 1378

RESULT 9

US-60-496-751-2
 ; Sequence 2, Application US/60496751
 ; GENERAL INFORMATION:
 ; APPLICANT: Froman, Virginia
 ; APPLICANT: Froman, Byron
 ; APPLICANT: Gonzalez, Jennifer
 ; TITLE OF INVENTION: Fatty Acid Desaturases from Primula
 ; FILE REFERENCE: MONS:04USPI
 ; CURRENT APPLICATION NUMBER: US/60/496,751
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 1341
 ; TYPE: DNA
 ; ORGANISM: Primula juliae
 ; US-60-496-751-2

Query Match 25.6%; Score 452.2; DB 8; Length 1341;
 Best Local Similarity 60.7%; Pred. No. 3,8e-109;
 Matches 777; Conservative 0; Mismatches 498; Indels 6; Gaps 2;

QY 189 CCGAGCAGCTCTGGATCTCCATCTCCGGCAGCTGTACAGAGTACAGCCCTGCTCCCC 248
 Db 53 CAGGTACCTATGATATCAATTCACGGTCAAGTTTACGAGTTCCTCTGGGCTGCG 112
 QY 249 AACACCCGGGGCGGACCTCCCGCTTCTACCTCTGGGGGGGAGAGCCACCGAGCCCT 308
 Db 113 TTCAACCCGGGGGAGTCTCCCTCTCTGCTTGGAGAGATGATGACCGAGCTT 172
 QY 309 TCGCCGCTTACACACCGCCCTCGGCGCGCCGCTCTCTGCTCTTCTTGTGGCGCC 368
 Db 173 TCTCTGCTTACATCCCTCTTCCACCTCCGCTCTCTCTCTCTCTCTCTCTCTCT 232
 QY 369 TCTCTG--ACTAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 425
 Db 233 TTCTAGAAAAAATCT 292
 QY 426 TATCTCTCCGCGGCT 485
 Db 293 TTCAATAGATGGGATGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 352
 QY 486 TGGCCGCT 545
 Db 353 TGAATCTTATGTTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 412
 QY 546 ACCT 605
 Db 413 ATTGTTTGTGGAGCGGCAATGGGGTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 472
 QY 606 ACTCGGGCCACACCGGATACCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 665
 Db 473 ATTCGGAATTAACCGGATTAATGATGACGAGAAATGAAACCGGTTCTCTCTCT 532
 QY 666 CCGGGAATGCT 725
 Db 533 GCTCAAAATGCT 592
 QY 726 ACATGCT 785
 Db 593 ACATGCT 652
 QY 786 TCT 845
 Db 653 TGTCT 712
 QY 846 ATGCGCGCT 905

Db 713 AGGTTGTCTGAGGTTTTTGTTCATATACAGACTGTGCTTTATCCGGTATGTGTG 772
 QY 906 TCGCCAGATTAATCT 965
 Db 773 TTGCTAGGCTGAAACATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 832
 QY 966 CCGAGCGTTGTCTGATCTGCGGGGGTGGCCCATTTCTGGGCTTGGTACCCGTTG 1025
 Db 833 CGAACGGGTGCAAGGATTTCTGACTAGCGGTTTTTGTGGCTTTCCGCTCTCT 892
 QY 1026 TGGCTTCCCTGCGAATGATGAGAGGCTGCGGTTTGTCTTTTCACTTCCATCT 1085
 Db 893 TTTCTTCCCTCTCTATATGAGGAGATATATGTTTGTCTGCGAGCTACTCCGTT 952
 QY 1086 GCGGATTTAGACAGCTCTCAATTTCTGCTGTAACCACTTCTCTCTCTCTCTCT 1145
 Db 953 CCGGATTTAGACAGCTCTCAATTTCTGCTGTAACCACTTCTCTCTCTCTCTCT 1012
 QY 1146 CACCCAGGCAATGACTGTTTGAAGAGAGAGCGGACGCTCGACATCTGTGCT 1205
 Db 1013 CACCGTAGATGATGATGTTGTTTAAAGAAAGAGCTGAGGACATCAATATCTG 1072
 QY 1206 CTCTCTGATGATGATGTTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1265
 Db 1073 CCGCGTATGATGATGTTTCAATGCGGGTTGAGTTTCAAGTTCAGGTCAGACCA 1132
 QY 1266 CCGGCTTACTCTGCTGCTCACTTCTGCAAGTTGACCGGCTCTGCGACCTTT 1325
 Db 1133 CCGGATGCTCTGAGGCTGAGTTCTGCAAGATTTCTCTTTTGTAGAGGATTT 1192
 QY 1326 AGCATGGGCTCACTTATTTGACAGCCCATTTCTGGGGTCAATGCTTATATGA 1385
 Db 1193 AACCAATTTGATTAATTAATTTGCTTTTACTAAGCAATGTTGACCTTGA 1252
 QY 1386 CACTCAGGCTGCTGATTTGACAGCCAGGACGCTTCAAGTGTGCTCTCTCTCT 1445
 Db 1253 CCTTGAGAAACAGGATTTGAGGCTCGGGACCTCTC--TATCGATCTCCAAAT 1309
 QY 1446 TGGTATGGAAGCTGTGAACA 1466
 Db 1310 TGGTGTGGAGGCTGTAAAAA 1330

RESULT 10

US-10-425-114A-15122
 ; Sequence 15122, Application US/10425114A
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114A
 ; NUMBER OF SEQ ID NOS: 28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 15122
 ; LENGTH: 2144
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3051-045-B9_F11
 ; US-10-425-114A-15122

Query Match 24.9%; Score 439.2; DB 7; Length 2144;
 Best Local Similarity 59.0%; Pred. No. 1.4e-105;
 Matches 791; Conservative 0; Mismatches 543; Indels 6; Gaps 2;

QY 155 ATCTCTCAAGAGCTCGCGCTCAAGCTTCCGCGGAGAGACTCTGATCTCATCTCC 214

Db 100 ATCACATCTGAGAGCTGAAGGAGCACAATAAGCCAGGGATTGTGGATTCAATCCAA 159
 Qy 215 GGGAGAGTATGACATCAAGCCCTGGCTCCCAACACCCGGGCGGCACTCCGGCTT 274
 Db 160 GGAAGATTATCAATTTTCAATTTGGGCAAGAACACCCCTGGAGAGATTTCCCTTG 219
 Qy 275 CTCACCTGGCGGGGAGAGACGCCACGACGCTTGGCGGCTTACCAACCGGCTCGGCG 334
 Db 220 TTGAACCTTGGAGCCAGATGTGACTGATGCTTGTAGCATACATCAAGCTCAGCA 279
 Qy 335 CGCCGCTCTCCGCGGCTTCTTGTGG---CGGCTCTGTGATCAACGCGCTTCCGCC 391
 Db 280 TGAAGATATCTGATCCCTTCTTCAAGGGTACCACTTAAGATTTCAAAGGCTCAGAG 339
 Qy 392 GGTCCGCGGACATACCGCGGCTCTCCGAGCATATCTCCGCGGCGCTTTCAGACGC 451
 Db 340 GTGTCAAAAGATTACGAAGAGCTGTGTGATGATTGTCAAAATGGGCTCTTTTGAAG 399
 Qy 452 GTGCGCCCAACCCCAAGGTCAGCTGTCTGTATGAGCGGCTCTTCAACGCGGCGCTG 511
 Db 400 AAGAGCATGTACTCTTTACACACTGTCTCTGTGTCTGTATGTTTCAATTTGTTT 459
 Qy 512 TACCTGTCTGATGATGCGCAGCGGCTGGCGCACCTCTCGCGGGGCTCTCATTTGCG 571
 Db 460 TATGATGATAGGGGTGAGTGTGTGGGCTCATCTTGTGTGCTCCCTTTTGTGTGGC 519
 Qy 572 TTGCTGTGATCCAGTCCGCGCTGATGAGGCGACAGATCTCGGCGCACCAACCGCATACCGGC 631
 Db 520 TTGCTTTGATGAGAAAGCACTTACGTTGATGATGATCTGGCGCATATAGGTTATGTCT 579
 Qy 632 CATCCGCTCTGACCGCGCTGAGGTCTCTCGGGAACGCTCAACCGGCGCTCAGC 691
 Db 580 AGCCCTGGCTACAAATTTGGACAAATCTTTTGGCAATTTGCAATGATGAGATTAAC 639
 Qy 692 ATCCGCTGTGAGATGTAAACAACAACGACACCATGCGCTGCAACAGCTTGACAT 751
 Db 640 ATTGATGATGAGATGTAAACAACAATGCTCAACCATGATGATGATGATGATGAT 699
 Qy 752 GACCGGAGCTCAGACATGCGGCTTTTGGCGCTCTCCCGCAAGCTTTGGCAACATA 811
 Db 700 GATCTGATCTCAGACATACCTGTCTTGGCGCTGACACGCTTCTTCAATTCATTC 759
 Qy 812 TGGTCTACTCTTACCAAGGACCCGCGGCTGATGAGCGGCTCGAAATTTCTACATCAGC 871
 Db 760 AATCTTGTCTTATGAGAAATTTGATTTGATTTATCAAGTTTCTCATCACAC 819
 Qy 872 TACAGACATGACCTTTACCGGATATGTGATGCGCAGAGATTAATCTTCTCGCGAG 931
 Db 820 TACAGACATGACATTTACCAAGTTTGTGCTTTGCAAGGTCATTTGATCTCCAG 879
 Qy 932 TCGCGCTTGTGTTTCAAGAGAGAGGTCGCGACGCTTGTAGATCGCGGG 991
 Db 880 ACTTTGTCTGTGTCTTCTAGAGAAAGGTCAGATAGAGCTTTAACTAATAGGG 939
 Qy 992 GTCCGACATTTCTGGGCTGTACCGGCTGTGCTGTGCTTCCCTGCGAAATTTGGGAG 1051
 Db 940 ATCTTGT 999
 Qy 1052 AAGGTGCGCTTGT 1111
 Db 1000 AAGGTGATGT 1059
 Qy 1112 CTGAACCTTCTGT 1171
 Db 1060 TTGAACATTTCTCAGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1119
 Qy 1172 AAGCAAGGCAAGGCAAGCTTCAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1231
 Db 1120 AAGCAAACTGT 1179
 Qy 1232 GGCCTGACCTTCCAGATGAGACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1291

Db 1180 GCGTTGCAATTCAGCTTGTGAGCACCATTGTGCCAAGGCTTCCAAGGCAATTTAGG 1239
 Qy 1292 AAGTTGACCGCGCGCTCCGACCTTTGCAAGAGCATGAGGCTCAATATCTGAGGC 1351
 Db 1240 AAAATCTCACCTTTGT 1299
 Qy 1352 ACATTTGCGGGGTGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1411
 Db 1300 ACATTTGTTGAGGCCAATCTTTGAGACTCTTAAGACCTTCAGAGCTGTCTTCAAGCC 1359
 Qy 1412 AGAACCGCTCAAGT 1471
 Db 1360 AGGA---ATCTGATTAACCTTCTTCCAGAAATTTGTGTGTGTGTGTGTGTGTGT 1416
 Qy 1472 GGATTAATGGATGAAGATA 1491
 Db 1417 GGATGATTTTGTGAAGAA 1436

RESULT 11
 US-10-425-114A-10327
 ; Sequence 10327, Application US/10425114A
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 10327
 ; LENGTH: 1719
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700904851_FLI
 US-10-425-114A-10327

Query Match 21.8%; Score 385.2; DB 7; Length 1719;
 Best Local Similarity 62.1%; Pred. No. 2,4e-91;
 Matches 625; Conservative 0; Mismatches 378; Indels 3; Gaps 1;

Qy 486 TGGCGCTCTCTTACACCGCGCTGTACCTGTCTGATGCGCAGCGCTGGGCGC 545
 Db 9 TTGCTGTATGTTTTCAATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 68
 Qy 546 ACCTCTCGCGGGGGTCTCATTTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 605
 Db 69 ATCTTGT 128
 Qy 606 ACTGGGCGACCAACCGCATACCGGCTATCGGCTCTGACCGGCTGTGAGGTGTCT 665
 Db 129 ACTTGGCGACATGAGGTATGTCTACCGCTGTGACCAACAAATTTGACCAAAATCTTT 188
 Qy 666 CCGGAACTGCTCAACCGGCTCAGATGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 725
 Db 189 GTGGCAATGCTATGCTGT 248
 Qy 726 ACATGCTGCAACAGCTGTGACCAATGACCGGCTCAGACATGCGCTCTTTGCGC 785
 Db 249 ACATCTGATGCAATGCTGT 308
 Qy 786 TCTCCCAAGCTGT 845
 Db 309 TGTTCACAGCTTCTTCAATTCATCAATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 368
 Qy 846 ATGCGGCTCGAAATTTCTTCACTGATGCTACGACATGAGCTTCAACCGGTAATGTGA 905

Db 848 TCTCTCATATGTTGTTGACCAAGAAATGTCCTATGAGCTCAGGAACTCTTGGGA 907
 Qy 992 GTCCGACCAATCTGGGCTGTGTACCGCTGTGTGGGCTTCCCTGCGAATGTGGAG 1051
 Db 908 TGCCTAGTGTCTTCGATTTGGTACCCGTTGTTTCTTGTGCTTAATGGGGTGA 967
 Qy 1052 AAGGTCGCTTGTGCTTTCACCTTCACATCTGGGGAATTCAGACGCTCCAAATCTGC 1111
 Db 968 AGAATATATGTTGTATGATGCAAGTTATCATGTGACGTGAATGCAACAAGTTCACTTCC 1027
 Qy 1112 CTGAACCACTTCTCGTCCAGCTGTATGTGGGCAACCCAGGCAATGACTGTTGAG 1171
 Db 1028 TTGAACCACTTCTCTCAAGTGTATGTGGAAACCTTAAGGGAAATATGTTGAG 1087
 Qy 1172 AAGCAGAGGCAAGGCAAGCTCGATCTGTCTCTGTAATGATGTTCCACGGT 1231
 Db 1088 AACAACAGATGGGACACTGATCTTCTGCTCTGATGATGGATTGGTTTCAGGT 1147
 Qy 1232 GGCCTGAGTTCCAGATTGAGCAACATCTGTTCCCGGCTACCTGCTGCCACTTCCG 1291
 Db 1148 GGAATTCATTTCCAAATTTAGCATCTTGTTCCTCCAAAGTGTGATGCAACCTTAG 1207
 Qy 1292 AAGTTGCAACCGGCGCTCCGCACTTTGCAAGAGCATGGGCTCACTTATCTGAGCC 1351
 Db 1208 AAAATCTCCGCTCAGTGTGATGATGCAAGAAACATTAATTTGCTTACAATATGCA 1267
 Qy 1352 ACATTCGTGGGTCGAATGTGCTTATCATGAGAGCACTCAGGGCTGCTGATGAGGCC 1411
 Db 1268 TCTTCTCCAGGCAATGAATGAACCTCAGAACTTGAAGAACACACATTTGACGGCT 1327
 Qy 1412 AGGACCGCTACAAAGTGTGTGCTCCGAAATTTGGTATGGAGGCTGTGAACCCAT 1471
 Db 1328 AGG---GATATACCAAGCGCGCTCCGAAATTTGGTATGGAGGCTTCCACACTCAT 1384
 Qy 1472 GGATAAA 1478
 Db 1385 GGTTAAA 1391

RESULT 13
 US-10-425-114A-6172
 ; Sequence 6172, Application US/10425114A
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114A
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 6172
 ; LENGTH: 966
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700556019_FLI
 US-10-425-114A-6172

Query Match 19.1%; Score 337.6; DB 7; Length 966;
 Best Local Similarity 66.2%; Pred. No. 6.9e-79;
 Matches 503; Conservative 0; Mismatches 254; Indels 3; Gaps 1;
 Qy 731 GCCTGAAGAGCTGTGACCATGACCCGAGCTTCACACATGCGCTCTTGGCGCTCC 790
 Db 2 GCCTGAAGAGCTGTGACCATGACCCGAGCTTCACACATGCGCTCTTGGCGCTCC 61
 Qy 791 CCAGAGCTGTGGCAACATATGCTCTTACCAAGGAGCCCTGGCGTTGATGCC 850

Db 62 TCGCGTCTTCAATTCATTAATCTTCTATTTGAGAGAGAGTTGATTTG 121
 Qy 851 GCTCGAATTCCTTATGACATGACGACCTGACCTTCTACCGGTATGTCATGCC 910
 Db 122 ATTGCAAGGTTCTTATCTGCTACGACCTTCTACCTTCTTACCGGTATGTCATGCC 181
 Qy 911 AGAATAAATCTTCTGCGCAGTCCGCTGTTCTTCTACGAGAGAGGCTGCGCAG 970
 Db 182 AGGTCACCTGTATCTGACGACATCTTCTATTTGTTGAGGCGTAAATGACAGAT 241
 Qy 971 CGGTTGCTGAGATCGCGGGGTGCCACATTTGGGGTGTGTACCGCTGTGCTG 1030
 Db 242 AGAGCTTGAACATATATGAGGATCTTGTGTTGAGTGTGCTCTTCTTGTGCTCT 301
 Qy 1031 TCCCTCGGAATTTGAGGAGAGGCTGCGTTGCTTTGAGTTACATCACTGCGGG 1090
 Db 302 TTCTCGCAAAATTTGCTGAGAGGTTATGTTGTGCTGCTAGCTTGTGCTGTTTCC 361
 Qy 1091 ATTGACAGCTTCAATTTGCTGCAACCACTTCTGCTCGAGCTGTATGTCGGGCAACC 1150
 Db 362 ATCCAGCATTCACTTCTGCTGATCATCTTGTGCAAAATGTATGTTGGCTACCG 421
 Qy 1151 AAGGCAATGACTGTGTTGAGAGAGAGAGGAGGAGCTGCAATCTGTGCTCTCT 1210
 Db 422 AGTGGAAATGACTGTGTTGAAAGAGAGAGGAGGAGATGATATCTCTTCTCTCT 481
 Qy 1211 TGGATGATGTTGTTCCAGGCTGCTGAGTTCAGATTGAGACATCTGTTCCCGC 1270
 Db 482 TCGATGATGTTGTTCTTGGTGTGTTGCAATTTGAGTTCATTTGTTCCAGG 541
 Qy 1271 CTACCTGCTGACCTTTCGCAAGGTTGCAACCGGCTGCTGCGGCACTTTGCAAGAGAT 1330
 Db 542 CTACCTGCTGCAATTTGAGAGACATTTGCTTGTGTGAGGACCTTTGCAAGAGAT 601
 Qy 1331 GGGCTCACTTATTTGCAAGCAGCTTGTGGGTGCAATGTGCTTACATGAGAGACTC 1390
 Db 602 AATTGCTTATGAGAGCTGTGCTATTTGGAGGCGCAATGAGTGAACAATTTGAGACCTTC 661
 Qy 1391 AGGCTGCTGATTTGAGGCGGAGACCGCTACAAATGTGTGCTTCCAAAGATTTGTA 1450
 Db 662 AGGACTGCTGCTTACAGGCTTACAGGCTTACAGGCTTACAGGCTTACAGGCTTAC 718
 Qy 1451 TGGAGGCTGTGAACACCATGATTAATGGATGAAGAT 1490
 Db 719 TGGAACTGTTAATCCCATGCTGAGGTATTTGGAGTT 758

RESULT 14
 US-10-425-114A-10518
 ; Sequence 10518, Application US/10425114A
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114A
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 10518
 ; LENGTH: 1071
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700942135_FLI
 US-10-425-114A-10518

Query Match 15.5%; Score 273.8; DB 7; Length 1071;
 Best Local Similarity 68.6%; Pred. No. 5.6e-62;
 Qy 731 GCCTGAAGAGCTGTGACCATGACCCGAGCTTCACACATGCGCTCTTGGCGCTCC 790
 Db 2 GCCTGAAGAGCTGTGACCATGACCCGAGCTTCACACATGCGCTCTTGGCGCTCC 61

Matches 393; Conservative 0; Mismatches 177; Indels 3; Gaps 1;

QY 912 GGATTAATCTTCTCGCGCACTCCGCCCTGTTCTGTTCTCAGGAGAGAGGAGTCCGAGC 971
 Db 1 GGAATTAATCTTCTCGCGCACTCTTTTCTTCTGTTATGTTTAAAGAGAGAGTGAAGACA 60
 QY 972 GGTGCTTGAGATCGCGGGGTCGCCAATTCCTGGGCTTGTAACCCGTTGCTGGTCTT 1031
 Db 61 GATGAGATGAGCTTTTGGGGCTGCTGCGTTCGGGTTGTAACCCGTTGTTGTTCTT 120
 QY 1032 CCTTCCGAATTTGTTGAGAGAGGTCGCCGTTTGTCTTTCAGTTTCAACATCTGCGGA 1091
 Db 121 TCTTGGCCAAATGTTGAGAGAGGTTTGTGTTTGTGAGCTTTTCTGTTACGGGTA 180
 QY 1092 TTGAGCAGCGCAATCTGCTGACCACTTCCTGTCGAGGTAAGTGGGCCACCCCA 1151
 Db 181 TTGAGCAGCGCAATCTGCTGACCACTTCCTGTCGAGGTAAGTGGGCCACCCCA 240
 QY 1152 AGGCGCAATGACTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1211
 Db 241 GCGGGCGCAATGTTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 QY 1212 GGATGATGTTGTTCAAGGTCGCTGCAATTCAGATTGAGACCAATCTGTTCCCGCC 1271
 Db 301 GGATGATGTTGTTCAAGGTCGCTGCAATTCAGATTGAGACCAATCTGTTCCCGCC 360
 QY 1272 TACTCGGTCGCACTTTCGCAAGGTTGCAAGGTCGCAAGGTCGCAAGGTCGCAAGG 1331
 Db 361 TGCACAGGTCGCACTTTCGCAAGGTTGCAAGGTCGCAAGGTCGCAAGGTCGCAAGG 420
 QY 1332 GGTCTCAATTTATTCGAGCCCAATTCGAGGTCGCAAGGTCGCAAGGTCGCAAGG 1391
 Db 421 ATCTTCTTATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 480
 QY 1392 GGGCTGCTGATTCGAGGTCGCAAGGTCGCAAGGTCGCAAGGTCGCAAGGTCGCA 1451
 Db 481 GGAATGCTGTTTTCGAGGTCGCAAGGTCGCAAGGTCGCAAGGTCGCAAGGTCGCA 537
 QY 1452 GGGAGGCTGTAACACCACTGATTAATGGGAT 1484
 Db 538 GGGAGGCTGTAACACCACTGATTAATGGGAT 570

RESULT 15

US-10-425-114A-14800
 ; Sequence 14800, Application US/10425114A
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114A
 ; NUMBER OF SEQ ID NOS: 2003-04-28
 ; SEQ ID NO 14800
 ; LENGTH: 663
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3028-013-H6_FLI
 ; US-10-425-114A-14800

Query Match 12.1%; Score 213.6; DB 7; Length 663;

Best Local Similarity 66.5%; Pred. No. 3.7e-46;

Matches 322; Conservative 0; Mismatches 159; Indels 3; Gaps 1;
 QY 1001 TTCTGGGCTTGTACCGGTGCTGCTGCTTCCCTCGAATTCGAGAGAGAGGTCGCG 1060

Db 2 TTTTGATTTGTTCCCTCTATGATCTCATCCCTGCCAAATTGGGAGAGAGAGGTCATG 61
 QY 1061 TTGTCCTTTTACGTTCAACATTCGCGGAGATTCAGACGTCATTCCTGTAACAC 1120
 Db 62 TTGTTTGGCCAGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 121
 QY 1121 TTCTCGTCGAGCTGTATGTCGCGCCACCAAGGCAATGACTGTTTGAAGACAGC 1180
 Db 122 TTGCGAGAGATGTATAGAGGCGCCACCAATGCAATGACTGTTTGAAGACAACT 181
 QY 1181 GCAAGCAGCTGCACTCTGCTGCTCTCTGATGATGATGTTGCCAGGTGCTGAG 1240
 Db 182 GGTGCAATGAGACATCTCTGCTCTACATGATGATGTTGTTGCGGCTTGCA 241
 QY 1241 TTCCAGATTGAGACATCTGTTCCCGCTTACCTCGGTCACCTTGGCAAGTTGA 1300
 Db 242 TTCCAGATTGAGACATCTGTTCCCGCTTACCTCGGTCACCTTGGCAAGTTGA 301
 QY 1301 CCGGCGCTCCGCACTTTCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1360
 Db 302 CTTTGTGATGACCTTTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 361
 QY 1361 GGTGCAATGTCCTTATGATGAGAGACATCAAGGCTGCTGCAATTCGAGAGAGAG 1420
 Db 362 GAGGCCAATCTTTCGACTCTTAAAGACCTTAAAGACTGCTCTCCAGGCGCAGGA 418
 QY 1421 ACAAGTGTGTGCTCCGAAGATTGTTATGAGAGAGCTGTGAACCCATGATGAATG 1480
 Db 419 CTCAGTAACCTTCTTCCAGAAATTTGTGTGAGAGCTTTTAACTCATAGTGAATTT 478
 QY 1481 GGAT 1484
 Db 479 GGAT 482

Search completed: January 1, 2004, 04:50:00
 Job time : 449.364 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 42.535 Seconds
(without alignments)
1724.030 Million cell updates/sec

Title: US-09-857-524B-4
Perfect score: 2521
Sequence: 1 MPESTDAMPAPGDAAAGADV.....TATSGAPKLVWEAVNTHG 462

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A.Geneseq.19Jun03.*
2: /SIDSI/gcgdata/geneeq/geneeqp-emb1/AA1980.DAT.*
3: /SIDSI/gcgdata/geneeq/geneeqp-emb1/AA1981.DAT.*
4: /SIDSI/gcgdata/geneeq/geneeqp-emb1/AA1982.DAT.*
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9: /SIDSI/gcgdata/geneeq/geneeqp-emb1/AA1987.DAT.*
10: /SIDSI/gcgdata/geneeq/geneeqp-emb1/AA1988.DAT.*
11: /SIDSI/gcgdata/geneeq/geneeqp-emb1/AA1990.DAT.*
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22: /SIDSI/gcgdata/geneeq/geneeqp-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneeq/geneeqp-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneeq/geneeqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2521	100.0	462	21	AAV71552
2	2064	81.9	469	21	AAV71555
3	1484	58.9	450	21	AAV71554
4	1466	58.2	449	21	AAV71553
5	1429	56.7	449	21	AAV71552
6	1427.5	55.6	448	21	AAV71548
7	1393	55.3	448	19	AAV71545
8	1393	55.3	448	19	AAV71541
9	1393	55.3	448	20	AAV71530

10	1391	55.2	448	21	AAV51349
11	1387	55.0	448	23	AAV79830
12	1387	55.0	448	24	ABG73095
13	1387	55.0	449	21	AAV53861
14	1387	55.0	449	21	AAV51334
15	1382	54.8	449	21	AAV70392
16	1382	54.8	517	21	AAV70391
17	1379	54.7	452	23	AAV79851
18	1379	54.7	452	24	ABG73416
19	1376	54.6	448	24	ABG73417
20	1370	54.3	446	20	AAV81522
21	1358	53.9	450	24	ABG73418
22	1295.5	51.4	448	21	AAV71551
23	1200.5	47.6	326	21	AAV29291
24	1168	46.3	353	21	AAV53862
25	1163	46.1	353	21	AAV70393
26	1133.5	45.0	326	21	AAV53863
27	992	39.3	284	21	AAV51351
28	881	34.9	252	19	AAV84141
29	795	31.5	224	21	AAV51350
30	771	30.6	222	21	AAV51352
31	688.5	27.3	253	21	AAV71553
32	612	24.3	459	23	AAV22063
33	597	23.7	178	22	AAV46439
34	571	22.6	453	24	AAV31900
35	564.5	22.4	483	22	AAV46435
36	564.5	22.4	483	22	AAV46436
37	552	21.9	520	22	AAV46440
38	535	21.2	477	23	ABG73600
39	535	21.2	477	23	ABV98275
40	523	20.7	457	19	AAV84137
41	523	20.7	457	20	AAV95504
42	523	20.7	457	21	AAV92599
43	523	20.7	457	21	AAV56045
44	523	20.7	457	22	AAV31684
45	523	20.7	458	23	ABV94693

ALIGNMENTS

RESULT 1	AAV71552	standard; Protein; 462 AA.
ID	AAV71552;	
AC	AAV71552;	
XX		
XX		
DT	12-OCT-2000	(first entry)
XX		
DE	Corn sphingolipid desaturase.	
XX		
KW	Corn, sphingolipid desaturase; membrane-bound desaturase;	
KW	transgenic plant; fatty acid.	
XX		
OS	Zea mays.	
XX		
EN	WO200032790-A2.	
XX		
PD	08-JUN-2000.	
XX		
PF	02-DEC-1999;	99WO-US28589.
XX		
PR	03-DEC-1998;	98US-0110784.
XX		
PA	(DUPO) DU PONT DE NEMOURS & CO E I.	
XX		
PI	Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;	
XX		
XX	WPI, 2000-412336/35.	
DR	N-PSDB; AAD01350.	
XX		
PT	Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is	

Sunflower HADES pr
Borage officinalis
Borage delta-6-des
Arabidopsis thaliana
A. thaliana sldi p
Arabidopsis thaliana
Arabidopsis thaliana
Evening primrose d
Evening primrose d
Borage delta-6-des
A delta-6 desatura
Evening primrose d
Florida bicetubus
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Protein b51do with
Desaturase enzyme
Protein d51pu with
Soybean sphingolip
Pythium irregulare
C. purpureus delta
Saprolegnia diclin
C. purpureus delta
C. purpureus delta
C. purpureus delta
P. tricornutum D6
Phaeodactylum trit
A delta-6 desatura
Mortierella alpina
M. alpina delta-6
Fungal delta-6-dea
Amino acid sequenc
Human delta5-deaat

PT useful for screening cDNA expression libraries -
 XX
 PS Claim 10; Page 42-43; 57pp; English.

XX The present sequence is a sphingolipid desaturase
 CC from clone cdelc.pk001.08.115 isolated from corn developing
 CC embryo cDNA library, cdelc. The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is also useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.

XX Sequence 462 AA;

Query Match 100.0%; Score 2521; DB 21; Length 462;
 Best Local Similarity 100.0%; Pred. No. 1.4e-251;
 Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPVDMPAPGDAAGDVYRMISSEKELRAHASADDLWISGVDYDTPMLPHHGGDL 60
 DB 1 MPSPVDMPAPGDAAGDVYRMISSEKELRAHASADDLWISGVDYDTPMLPHHGGDL 60
 QY 61 PLITLACQDATDAFAAYHPPSARPLRRFVGRSLDYAVSPASADYRRLAQLSSAGLFE 120
 DB 61 PLITLACQDATDAFAAYHPPSARPLRRFVGRSLDYAVSPASADYRRLAQLSSAGLFE 120
 QY 121 RVGPTRPVQVLMAVLYFAALYLVLACASAMHLLAGLIGFWITQSGMGGHSGHRRIT 180
 DB 121 RVGPTRPVQVLMAVLYFAALYLVLACASAMHLLAGLIGFWITQSGMGGHSGHRRIT 180
 QY 181 GHPLVDVVOVLSGNCITGSLIAWKCNNHTNTHACNSLDHDPDLQHMPLFAVSPKLFEN 240
 DB 181 GHPLVDVVOVLSGNCITGSLIAWKCNNHTNTHACNSLDHDPDLQHMPLFAVSPKLFEN 240
 QY 241 IWSFYQRTLAFDAASKFISYQHTFYPVWCJARINLLAQSALFVLEKRVQRLLEIA 300
 DB 241 IWSFYQRTLAFDAASKFISYQHTFYPVWCJARINLLAQSALFVLEKRVQRLLEIA 300
 QY 301 GVATFMAVYPLVLAASLPMWMEVAVFLFSTICIGIQVQCLNHFSSDYVGPCKGDMF 360
 DB 301 GVATFMAVYPLVLAASLPMWMEVAVFLFSTICIGIQVQCLNHFSSDYVGPCKGDMF 360
 QY 361 EKQTAGTLDILCSFPMWDFHGGLOFOLEHLLFRLPRCHLRKVAFAVADLCKKGLTYS 420
 DB 361 EKQTAGTLDILCSFPMWDFHGGLOFOLEHLLFRLPRCHLRKVAFAVADLCKKGLTYS 420
 QY 421 ATFWGANVLTWKTLLRAAALQARTATSGAPKNLVMEAVNTHG 462
 DB 421 ATFWGANVLTWKTLLRAAALQARTATSGAPKNLVMEAVNTHG 462

RESULT 2

AAAY71555
 ID AAY71555 standard; Protein; 469 AA.

AC AAY71555;

DT 12-OCT-2000 (first entry)

DE wheat sphingolipid desaturase #1.

XX wheat; sphingolipid desaturase; membrane-bound desaturase;

KM transgenic plant; fatty acid.

XX Triticum aestivum.

OS W0200032790-A2.

PN 08-JUN-2000.

PF 02-DEC-1999; 99WO-US28589.

XX

PR 03-DEC-1998; 98US-0110784.

XX (DUPO) DU PONT DE NEMOURS & CO E. I.

XX Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;

XX WPI; 2000-412336/35.

XX N-PSDB; AAD01353.

XX Polynucleotide encoding delta-6 desaturase enzyme useful for producing

PT transgenic plants and for producing antibodies specific to which is

PT useful for screening cDNA expression libraries -

XX Example 4; Page 49-50; 57pp; English.

XX The present sequence is a sphingolipid desaturase

CC from clone wrel.pk004.c7.115 isolated from wheat etiolated

CC seedling root cDNA library, wrel.

CC The present sequence is useful for producing

CC transgenic plants having altered levels of sphingolipid desaturase which

CC in turn would alter the fatty acid composition. The enzyme is also useful

CC for producing polyclonal or monoclonal antibodies. The polynucleotide

CC is useful as primer or probe for screening cDNA libraries to

CC isolate desired full-length cDNA clones.

XX Sequence 469 AA;

Query Match 81.9%; Score 2064; DB 21; Length 469;
 Best Local Similarity 80.9%; Pred. No. 2.6e-204;
 Matches 372; Conservative 35; Mismatches 51; Indels 2; Gaps 1;

QY 3 PSVDAMPAPGDAAGDVYRMISSEKELRAHASADDLWISGVDYDTPMLPHHGGDLPL 62
 DB 12 PEADAMPAA--SKDAADVDMISTKELQARAADDLWISGVDYDTPMLPHHGGSEVL 69
 QY 63 LTLACQDATDAFAAYHPPSARPLRRFVGRSLDYAVSPASADYRRLAQLSSAGLFEV 122
 DB 70 ITLACQDATDAFAAYHPPSARPLRRFVGRSLDYAVSPASADYRRLAQLSSAGLFEV 129
 QY 123 GTPPKQLVLAVALYFAALYLVLACASAMHLLAGLIGFWITQSGMGGHSGHRRITGH 182
 DB 130 GHPKFLVLAAMSVLFCIALYCVLACSSGAHMFAGGLIFIMTQSGMGGHSGHRRITGH 189
 QY 183 PVLDRVVOVLSGNCITGSLIAWKCNNHTNTHACNSLDHDPDLQHMPLFAVSPKLFEN 242
 DB 190 PALNRLQVYSSGNCITGSLIAWKCNNHTNTHACNSLDHDPDLQHMPLFAVSPKLFEN 249
 QY 243 SYFYQRTLAFDAASKFISYQHTFYPVWCJARINLLAQSALFVLEKRVQRLLEIAGV 302
 DB 250 SYCYERTLAFDAASKFISYQHTFYPVWCJARINLLAQSALFVLEKRVQRLLEIAGV 309
 QY 303 ATFWANVYPLVLAASLPMWMEVAVFLFSTICIGIQVQCLNHFSSDYVGPCKGDMF 362
 DB 310 AAFWVYPLVLAASLPMWMEVAVFLFSTICIGIQVQCLNHFSSDYVGPCKGDMF 369
 QY 363 QTAGTLDILCSFPMWDFHGGLOFOLEHLLFRLPRCHLRKVAFAVADLCKKGLTYSAT 422
 DB 370 QTAGTLDILCSFPMWDFHGGLOFOLEHLLFRLPRCHLRKVAFAVADLCKKGLTYSAT 429
 QY 423 FVGANVLTWKTLLRAAALQARTATSGAPKNLVMEAVNTHG 462
 DB 430 FVEANVLTWKTLLRAAALQARTATSGAPKNLVMEAVNTHG 469

RESULT 3

AAAY71554
 ID AAY71554 standard; Protein; 450 AA.

AC AAY71554;

DT 12-OCT-2000 (first entry)

DE soybean sphingolipid desaturase #2.

XX Soybean; sphingolipid desaturase; membrane-bound desaturase;
 KW transgenic plant; fatty acid.
 XX Glycine max.
 OS WO200032790-A2.
 PN 08-JUN-2000.
 PD 02-DEC-1999; 99MO-US28589.
 PF 03-DEC-1998; 98US-0110784.
 PR (DUPO) DU FONT DE NEMOURS & CO E I.
 PA Cahocon EB, Cahocon RE, Hiltz WD, Kinney AJ;
 PI MPI; 2000-412336/35.
 DR N-PSDB; AAD01352.
 XX Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries
 PS Claim 10; Page 47-48; 57pp; English.
 CC The present sequence is a sphingolipid desaturase
 CC from clone sbl.pK0017.b4.f15 isolated from soybean seedling cDNA
 CC library, sbl. The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is also useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
 SQ Sequence 450 AA;
 Query Match 58.9%; Score 1484; DB 21; Length 450;
 Best Local Similarity 60.0%; P-adj. No. 2.3e-144;
 Matches 266; Conservative 62; Mismatches 113; Indels 2; Gaps 2;
 QY 21 RMISSEKELPAHSAADLWISISGVDYDTPWLPHPHFGDLPPLTLGADATDAFAAYHP 80
 DB 9 KYTSEELKGNHNEGDLMSIOGKYNVNSVKNHFGDVPISNLGQVTDPAFIYHFG 68
 QY 81 SARPLRRFFVG-RISDYAVSPASADYRRLAQLSSAGLEFRVGPPTPKVQLVMAVLFYA 139
 DB 69 TAWSHLEKEFTGYHLSDFKVSEVSKDYKRLASBFSKLGPDRTGHTVTSCTLASVAVMFLI 128
 QY 140 ALYLVLAASAMHLLAGLIGVWIOSGMGHDGSHRITGHPVLDRVVQVLSGCLTG 199
 DB 129 VLVGVLRCTSVMAHLSGMLGLLWQSAVGHDSGHVYVMTNGFNKVAQIISGCLTG 188
 QY 200 LSTAMKCNHNTTHIACNSLDHDPDLOHMPLPAVSPKLFEGNIMSYFPORTLAFAASKPF 259
 DB 189 ISTAMKMTNHAHICNSLDHDPDLOHMPVAVSSRFNSISHTYGRLEDFIARL 248
 QY 260 ISYQHTFFPVMCIARINLLAQSALFVLTEKRVPOBLLEIAGVATFWAMYPLIVASIPW 319
 DB 249 ICYQHTFFPVMCVARVNLVLTQITLLFSSRKVQDBALNIMGLVMTWTFPLVSLPFW 308
 QY 320 WERVAVLSFTTCGLOHVOFLNHFSSDYVGPPEKNDMEFEQITGTDILCSPMWDMF 379
 DB 309 PERVMFVLASFACSIQIIOFLCNHFAANYVGPPEGNMFEKQISGTIDISGASMDWF 368
 QY 380 HGGLOQIEHNLPPRPPCHLRKAVAPVRLCKKHGITYSAATFWGANVLTWKTBAAL 439
 DB 369 FGGLOQLEHNLPPRPPCHLRKAVAPVRLCKKHGITYSAATFWGANVLTWKTBAAL 428
 QY 440 QARTATSGAPKULWEAVNTHG 462
 DB 429 QARDLTN-PAPKULWEAVNTHG 450

RESULT 4
 ID AAG29290
 AC AAG29290; standard; Protein; 449 AA.
 AC AAG29290;
 DT 17-OCT-2000 (first entry)
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 34824.
 DE Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridization assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 OS Arabidopsis thaliana.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 XX 25-FEB-2000; 2000EP-0301439.
 PF 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 01-APR-1999; 99US-0126785.
 PR 06-APR-1999; 99US-0127462.
 PR 08-APR-1999; 99US-0128234.
 PR 16-APR-1999; 99US-0128714.
 PR 19-APR-1999; 99US-0128845.
 PR 21-APR-1999; 99US-0130077.
 PR 23-APR-1999; 99US-0130449.
 PR 23-APR-1999; 99US-0130510.
 PR 23-APR-1999; 99US-0130891.
 PR 28-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132048.
 PR 30-APR-1999; 99US-0132407.
 PR 04-MAY-1999; 99US-0132484.
 PR 05-MAY-1999; 99US-0132485.
 PR 06-MAY-1999; 99US-0132486.
 PR 06-MAY-1999; 99US-0132487.
 PR 07-MAY-1999; 99US-0132863.
 PR 11-MAY-1999; 99US-0134256.
 PR 14-MAY-1999; 99US-0134218.
 PR 14-MAY-1999; 99US-0134219.
 PR 14-MAY-1999; 99US-0134221.
 PR 14-MAY-1999; 99US-0134370.
 PR 18-MAY-1999; 99US-0134768.
 PR 19-MAY-1999; 99US-0134941.
 PR 20-MAY-1999; 99US-0135124.
 PR 21-MAY-1999; 99US-0135353.
 PR 24-MAY-1999; 99US-0135629.
 PR 25-MAY-1999; 99US-0136021.
 PR 27-MAY-1999; 99US-0136392.
 PR 28-MAY-1999; 99US-0136782.
 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137528.
 PR 04-JUN-1999; 99US-0137502.
 PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.
 PR 10-JUN-1999; 99US-0138547.
 PR 10-JUN-1999; 99US-0138847.
 PR 14-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139452.
 PR 16-JUN-1999; 99US-0139453.
 PR 17-JUN-1999; 99US-0139492.
 PR 18-JUN-1999; 99US-0139454.
 PR 18-JUN-1999; 99US-0139455.
 PR 18-JUN-1999; 99US-0139456.

Db 128 VLXVLACTSIWAHLISAVLLGLMLTQSAVVGDSGHVTVSTKPCNKLIQLISGNCLTG 187
 QY 200 LSIAMWKCNHNTHTIACNSLDHDPDLQHMPLFAVSPKLFGNIMSYFYORTLAFDAASKFE 259
 Db 188 ISIAMWKTHNAHNSLDHDPDLQHTLPIFAVSTKFEKQTSKRYGRKLTDPDLARFL 247
 QY 260 ISYQHTFYPVNCIARINLQAQALFVLTKEKVPORLEIAGVATFWMVYPLLVASLPNW 319
 Db 248 ISYQHTFYPVNCVGINLFIQTFELLFSKRHPDRLNAGILVMTWTFPLVSLPNW 307
 QY 320 WERVAVLFSFTICGIGHVQFCINHPSSDVYVGPFGNDWFEKQTAGTIDILCSPMMDWF 379
 Db 308 QEFIFVFPVFAVTAIQHVFCLNHPAADVYTGPPGNDWFEKQTAGTIDILCSPMMDWF 367
 QY 380 HGGLOFQIEHHLFPRRLPRCHLRKVAAPVARDLCKKHGLTYSATFPGANVLTWTLRAAAL 439
 Db 368 FGGLOFQIEHHLFPRRLPRCHLRKVAAPVARDLCKKHGLTYSATFPGANVLTWTLRAAAL 427
 QY 440 QARTATSGAPKRLVWEAVNTHG 462
 Db 428 QARDATN-PVLKRLWEAVNTHG 449
 RESULT 5
 AAY51333
 ID AAY51333 standard; Protein; 449 AA.
 AC AAY51333;
 XX
 DT 27-APR-2000 (first entry)
 XX
 DE B. napus sld1 protein.
 XX
 KW Sphingolipid desaturase, sld1; sphingobase; ceramide; capnoid;
 KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
 KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KW pharmaceutical; food; chemical raw material.
 XX
 OS Brassica napus.
 XX
 PN DE19828850-A1.
 XX
 PD 30-DEC-1999.
 XX
 PF 27-JUN-1998; 98DE-1028850.
 XX
 PR 27-JUN-1998; 98DE-1028850.
 XX
 PA (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
 PI Heinz E, Zaehring U, Schmidt H, Sperling P;
 XX
 DR MPI; 2000-127549/12.
 DR N-PSDB; AA244832.
 XX
 PT New sphingolipid desaturase that selectively introduces double bond
 into sphingolipid and capnoids -
 PS Claim 8; Fig 2; 62pp; German.
 XX
 CC This invention describes a novel sphingolipid desaturase that selectively
 CC introduces a double bond into the sphingobase of the ceramide residue of
 CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to
 CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered
 CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
 CC compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or

CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 CC materials. This sequence represents the Brassica napus sphingolipid
 CC desaturase sld1 protein described in the method of the invention.
 CC
 SQ Sequence 449 AA;
 Query Match 56 7%; Score 1429; DB 21; Length 449;
 Best Local Similarity 57.3%; Pred. No. 1,1e-138;
 Matches 254; Conservative 66; Mismatches 121; Indels 2; Gaps 2;
 QY 21 RMISSELRRAHASADDLWISISGDVYVTPMLPHRPGCDPLTLTAGODATPAFAAYHP 80
 Db 8 RITTSDDLKKNQPGDLWISIGKYVDVSHWKSHPGSAALINLAGOVTDFAIYHNG 67
 QY 81 SARPLIRRFVQ-RUSDVAVSPASADYRRLAQLSAGLPERVGPPTPKVQLVMAVLPYA 139
 Db 68 TAWRHLENLHNGVYHVVDHVSVDVSRDYRLAEPFKRGFLFDKKGHTLYTLTCVAAMLA 127
 QY 140 ALYVLACASAMAHLLAGLIGFWTQSGMGMHDSGHHITGHPVLDRIYVQVLSGNCITG 199
 Db 128 VYGVVACTSIWAHLISAVLLGLMLTQSAVVGDSGHVTVSTKPCNKLVQLISGNCLTG 187
 QY 200 LSIAMWKCNHNTHTIACNSLDHDPDLQHMPLFAVSPKLFGNIMSYFYORTLAFDAASKFE 259
 Db 188 ISIAMWKTHNAHNSLDHDPDLQHTLPIFAVSTKFEKQTSKRYGRKLTDPDLARFL 247
 QY 260 ISYQHTFYPVNCIARINLQAQALFVLTKEKVPORLEIAGVATFWMVYPLLVASLPNW 319
 Db 248 ISYQHTFYPVNCVGINLFIQTFELLFSKRHPDRLNAGILVMTWTFPLVSLPNW 307
 QY 320 WERVAVLFSFTICGIGHVQFCINHPSSDVYVGPFGNDWFEKQTAGTIDILCSPMMDWF 379
 Db 308 QEFIFVFPVFAVTAIQHVFCLNHPAADVYTGPPGNDWFEKQTAGTIDILCSPMMDWF 367
 QY 380 HGGLOFQIEHHLFPRRLPRCHLRKVAAPVARDLCKKHGLTYSATFPGANVLTWTLRAAAL 439
 Db 368 FGGLOFQIEHHLFPRRLPRCHLRKVAAPVARDLCKKHGLTYSATFPGANVLTWTLRAAAL 427
 QY 440 QARTATSGAPKRLVWEAVNTHG 462
 Db 428 QARDVTN-PVLENLWEALNTHG 449
 RESULT 6
 AAY51348
 ID AAY51348 standard; Protein; 458 AA.
 AC AAY51348;
 XX
 DT 27-APR-2000 (first entry)
 XX
 DE Sphingolipid desaturase protein.
 XX
 KW Sphingolipid desaturase, sld1; sphingobase; ceramide; capnoid;
 KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
 KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KW pharmaceutical; food; chemical raw material.
 XX
 OS Unidentified.
 XX
 PN DE19828850-A1.
 XX
 PD 30-DEC-1999.
 XX
 PF 27-JUN-1998; 98DE-1028850.
 XX
 PR 27-JUN-1998; 98DE-1028850.
 XX
 PA (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
 PI
 XX

PI Heinz E, Zaehring U, Schmidt H, Sperling P;
 XX MPI: 2000-127549/12.
 DR N-PSDB; AA244851.
 XX
 XX New sphingolipid desaturase that selectively introduces double bond
 PT into sphingolipids and capnoids -
 XX
 XX Disclosure; Fig 15; 62pp; German.
 PS
 XX This invention describes a novel sphingolipid desaturase that selectively
 CC introduces a double bond into the sphingobase of the ceramide residue of
 CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to
 CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered
 CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
 CC compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 CC materials. This sequence represents a sphingolipid desaturase protein
 CC described in the method of the invention.
 CC
 XX
 SQ Sequence 458 AA;
 Query Match 56.6%; Score 1427.5; DB 21; Length 458;
 Best Local Similarity 55.1%; Pred. No. 1.7e-138;
 Matches 254; Conservative 77; Mismatches 123; Indels 7; Gaps 3;
 QY 3 PSYDAMPAPEDDAAGADWMSKSELRANASADLWISIGDYVDTWLPNHPGGDLPL 62
 DB 4 PSIEVNSIADGK-----KYTSKELKKNPNPDLWISIGKYVNTWNAKEHGGAPL 58
 QY 63 LTLAAGDADTAPAFYHPPSARPLRRPFVG-RISDVAVSPASADYRLLAQSLGFER 121
 DB 59 INLAGODVDAFAFHPTAMKLDLFGYHKLKDQVSDISRDKLASFPKAGMFEK 118
 QY 122 VGPFPYQVLMAVLAFLVLAACASAWAHLAAGLIGFWIQSGMGGHSGHRTG 181
 DB 119 KKGIVYISLCFVSLLSACVGYLVGSGFWIHLSAIIIGLAWQIAYLGHDAHQMA 178
 QY 182 HVALDRVQVLSGNCUTGLSIAMKCNHNTHTIACNSLDHDPDLOHMPLEFVSGNT 241
 DB 179 TEGMNFAGIFIGNCTGISIAMWKTHNHTIACNSLDYDPLQHLPMALVSSKLFNSI 238
 QY 242 WGFYFQRTLAFLDASKFEISYOHMTFYPVWCIRINILNOSALFVLTEKVPQRLLEIAG 301
 DB 239 TSFVYFQRLTFDLARFVSYOHLYLVYIMCVARVNLVLTILLISKRKIPRGNTILG 298
 QY 302 VAFWMAFPLVSLNPMERVAFLVFSFTICIQHVFCLNHFSSDYYVGPCKGDMFE 361
 DB 299 TILFWMFPLVSLNPMERVAFLVFSFVTGICQIHQFTLNHFSGDYYVGPCKGDMFE 358
 QY 362 KQTAAGLILICSPWDMFHGLOFQIEHLFPLPRCHLRKVAFAVADLCCKHGLTYSAA 421
 DB 359 KQTRGITDIACSSMMWDFGGLQFQLEHHLFPLPRCHLASISPRICELCKYTNLPVSL 418
 QY 422 TFMGAVLVTKTLRAALQARTSGAPRGLVWEAVNTIG 462
 DB 419 SFYDANVTTLKTLRTALQARDLTN-PAPONLAMEAENTIG 458

DT 15-SEP-1996 (first entry)
 XX
 DE Borage delta-6-desaturase.
 XX
 XX Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;
 KM polyunsaturated fatty acid; octadecatretraenoic acid;
 KM chilling resistance; oilseed.
 XX
 OS Borage officinalis.
 XX
 FH Key Location/Qualifiers
 FT Region 156..163
 FT /label= Lipid_box
 FT 196..200
 FT /label= Metal_box-1
 FT Region 372..377
 FT /label= Metal_box-2
 XX
 PN MO9621022-A2.
 XX
 PD 11-JUL-1996.
 XX
 PF 28-DEC-1995; 95MO-IB01167.
 XX
 PR 30-DEC-1994; 94US-0366779.
 XX
 PA (RHON) RHONE POULENC AGROCHIMIE.
 XX
 PI Freyassinet GL, Nuccio M, Nunberg AN, Reddy AS, Thomas TL;
 DR WPI; 1996-333997/33.
 DR N-PSDB; AAT30395.
 XX
 PT Transgenic plants comprising the borage delta-6-desaturase gene
 PT show increased production of gamma linolenic acid and having
 PT increased resistance to chilling
 XX
 PS Claim 3; Page 52-53; 75pp; English.
 XX
 CC Borage delta-6-desaturase (AAR98455) catalyzes the conversion of
 CC linoleic acid to gamma-linolenic acid (GLA). Its sequence was
 CC deduced from that of the delta-6-desaturase gene (AAT30395) isolated
 CC from a borage membrane-bound polyosomal library. The sequence is
 CC distinct from that of Synchocystis delta-6-desaturase (AAR98456).
 CC Expression of the desaturase in transgenic plants, esp. sunflower,
 CC soybean, maize, tobacco, peanut, carrot or oilseed rape, results in
 CC increased GLA prodn. Alteration of the plant membrane lipids as a
 CC result of expression of the desaturase may also result in increased
 CC resistance to chilling.
 CC
 XX
 SQ Sequence 448 AA;
 Query Match 55.3%; Score 1393; DB 17; Length 448;
 Best Local Similarity 55.8%; Pred. No. 5.9e-135;
 Matches 247; Conservative 73; Mismatches 121; Indels 2; Gaps 2;
 QY 21 RMISSEKELAHNASADLWISIGDYVDTWLPNHPGGDLPLTLAAGDADTAPAFYH 80
 DB 7 KITSDLELNHKKPPGLWISIGKAYVSDWVKDHFSGSPRLKSLAQEVTDAFVAFHRA 66
 QY 81 SARPLRRPFVG-RISDVAVSPASADYRLLAQSLGFERVGPFPYQVLVMAVLFYA 139
 DB 67 STWKNDKFFGTGYLVDYSEVSKDYRLVPEFSKMGYDKKHGIMFATLCIAMLFAM 126
 QY 140 ALTVLACASAWAHLAAGLIGFWIQSGMGGHSGHRTGHPVLDREVQVLSGNCUTG 199
 DB 127 SVYGVLCFSGVLVHLFSGCLMGFLWIQSGWIGHDAGYVWVSDSRLNKFGIIPAANCLSG 186
 QY 200 LSIAMKCNHNTHTIACNSLDHDPDLOHMPLEFVSGNTSYGYQTLADDAASKFP 259
 DB 187 ISIGMKNHNAHRIACNSLDYDPLQHLPMALVSSKLFNSHPEKRLTFDSLSRFP 246
 QY 260 ISYQHWTFYPVWCIRINILNOSALFVLTEKVPQRLLEIAGVATFAMVYPLVLVSLPNW 319

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Db      247 VSYQHTFYPICARLNMVYQSLIMLTKRNVSYRAOELGLVFSIWYPLIVSCLPWN 306
Qy      320 WERVAFVLFSTICIGIHOVQFCLNHSSDYVGPCKGNMFKEKQTGTLIDILCSPPMMDWF 379
Db      307 GERIMFVIASLSTGMOVOFSLNHFSSVYVGPCKGNMFKEKQTGTLIDILCSPPMMDWF 366
Qy      380 HGGLOFOIEHHLPRLPRCHLRKVA PAVRDLCKKHGLTVSAATFPGANVLTWKTLEAAAL 439
Db      367 HGGLOFOIEHHLPRLPRCHLRKVA PAVRDLCKKHGLTVSAATFPGANVLTWKTLEAAAL 426
Qy      440 QARTATSGAPKXNLWEAVNTG 462
Db      427 QARDITK-PLPKNLWEALHTHG 448

RESULT 8
AAW67471
ID      AAW67471 standard; Protein; 448 AA.
AC      AAW67471;
DT      02-MAR-1999 (first entry)
DE      Borage delta-6 desaturase protein.
XX      Upstream region; regulatory region; sunflower; albumin; seed; expression;
KW      lipid metabolism; delta-6 desaturase; transgenic plant.
XX      Borage officinalis.
FH      Key
FT      Region
FT      Location/Qualifiers
FT      40..44 "cytochrome b5 haem-binding motif"
FT      156..163 /note= "his-rich metal binding motif"
FT      196..200 /note= "his-rich metal binding motif"
FT      373..377 /note= "his-rich metal binding motif"
FT      Domain
FT      /note= "his-rich metal binding motif"
XX      WO9845460-A1.
XX      15-OCT-1998.
XX      09-APR-1998; 98WO-US07178.
XX      09-APR-1997; 97US-0831570.
XX      (RHON ) RHONE-POULENC AGROCHIMIE.
XX      Beremand PD, Nunberg AN, Thomas TL;
XX      WPI; 1998-583201/49.
XX      N-PSDB; AAV34398.
XX      New sunflower albumin 5' regulatory region - useful for directing
XX      altered lipid metabolism in plant seeds
XX      Example 2; Fig 1; 38pp; English.
XX      This sequence corresponds to the borage (Borage officinalis) delta-6
XX      desaturase enzyme. The encoding lipid metabolism gene is an example
XX      of a heterologous gene which can be expressed at high levels in a
XX      seed-specific manner in transgenic plants, when placed under control
XX      of the sunflower albumin gene 5' regulatory region (AAV34397).
SQ      Sequence 448 AA;
Query Match 55.3%; Score 1393; DB 19; Length 448;
Best Local Similarity 55.8%; Pred. No. 5..9e-135;
Matches 247; Conservative 73; Mismatches 121; Indels 2; Gaps 2;

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Qy      21 RMISSEKELRAHASADDLWISGVDYDTYPMLPNHHGSDLPULLTAGODATDAFAAYHBP 80
Db      7 KYITSDLELNKNDKPDIMWISIGKAYDVSDWKDHPGGSFPLKSLAQGVETAFAVAFHBA 66
Qy      81 SARPLRRFPVVG-RLSDBAVSPASADYRRLAQLSAGLPERVGPPTPKQVLYMAVLFYA 139
Db      67 STWKNLDKFPFGTYLKDYSVEVSVDYRKLVEFSPMGILYDKKHIMFATLCEFIAMLFPM 126
Qy      140 ALYVLACASAAVHLLAGSLIGFWNIQSGMGMHDSGHHRTGHPVLDRAVOYLISGCLNG 199
Db      127 SVYGVLPCEGVVHLPSGCLMGFLMIQSGWIGHDGHYVSDSLNKKFMGIFPAACLSG 186
Qy      200 LSIAMWKNHNTHTIACNSLDHPDLQHMPLFAVSPKLFGNISYFYQRTLAFDAASKFE 259
Db      187 ISIGWKKNNHNAHIAACNSLBYDPLQYIPLVVSKEFGSLSHYERGLTFDSLSRF 246
Qy      260 ISYQHTFYPVNCIARINLLAQSALFVLTKEVPORLIEIAGVATFMAVYPLIVASLPMW 319
Db      247 VSYQHTFYPICARLNMVYQSLIMLTKRNVSYRAOELGLVFSIWYPLIVSCLPWN 306
Qy      320 WERVAFVLFSTICIGIHOVQFCLNHSSDYVGPCKGNMFKEKQTGTLIDILCSPPMMDWF 379
Db      307 GERIMFVIASLSTGMOVOFSLNHFSSVYVGPCKGNMFKEKQTGTLIDILCSPPMMDWF 366
Qy      380 HGGLOFOIEHHLPRLPRCHLRKVA PAVRDLCKKHGLTVSAATFPGANVLTWKTLEAAAL 439
Db      367 HGGLOFOIEHHLPRLPRCHLRKVA PAVRDLCKKHGLTVSAATFPGANVLTWKTLEAAAL 426
Qy      440 QARTATSGAPKXNLWEAVNTG 462
Db      427 QARDITK-PLPKNLWEALHTHG 448

RESULT 9
AAW98130
ID      AAW98130 standard; Protein; 448 AA.
AC      AAW98130;
DT      21-JUN-1999 (first entry)
DE      Borage delta-6 desaturase.
XX      Delta-6 desaturase; borage; oleosin; Afs21; promoter;
XX      transgenic plant; seed; lipid; fatty acid; oilseed; vegetable oil;
XX      gamma-linolenic acid; octadecatrienoic acid.
XX      Borage officinalis.
FH      Key
FT      Binding-site
FT      Location/Qualifiers
FT      40..44 "cytochrome b5 haem-binding motif"
FT      156..163 /note= "metal binding, histidine-rich motif"
FT      196..200 /note= "metal binding, histidine-rich motif"
FT      373..377 /note= "metal binding, histidine-rich motif"
FT      Binding-site
FT      /note= "metal binding, histidine-rich motif"
XX      WO9845461-A1.
XX      15-OCT-1998.
XX      09-APR-1998; 98WO-US07179.
XX      09-APR-1997; 97US-0831575.
XX      (RHON ) RHONE-POULENC AGROCHIMIE.
XX      Li Z, Thomas TL;
XX      WPI; 1999-180333/15.
XX      N-PSDB; AAX24917.

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XX Nucleic acid containing oleosin 5'-regulatory region - useful for
PT modulating fatty acid synthesis and lipid metabolism in plants,
PT particularly to increase content of gamma-linolenic acid

XX Example 2; Page 61; 101pp; English.

XX The present sequence is borage delta-6 desaturase, an enzyme that
CC catalyses the conversion of linoleic acid to gamma-linolenic acid
CC (Gla). Delta-6 desaturase cDNA (see AAX24917) was isolated from a
CC borage membrane-bound polysomal cDNA library using a partial clone,
CC obtained from an EST database search, as probe. The borage delta-6
CC desaturase nucleic acid can be operably linked to the seed-specific
CC 5' regulatory region (see AAX24916) of the Arabidopsis thaliana
CC oleosin At5g1 gene in claimed expression cassettes of the invention.
CC Transgenic plants, e.g. sunflower, soybean, maize, tobacco, cotton,
CC peanut, oilseed rape or Arabidopsis are obtained that show increased
CC levels of GLA or octadecatrienoic acid. The levels of desirable
CC fatty acids in oilseed crops can be manipulated to provide seed
CC oils of use in human health and industrial applications.

XX Sequence 448 AA;

XX Query Match 55.3%; Score 1393; DB 20; Length 448;
XX Best Local Similarity 55.8%; Pred. No. 5.9e-135;
XX Matches 247; Conservative 73; Mismatches 121; Indels 2; Gaps 2;

QY 21 RMISSELRNHAASADLWISISGVDYDVTWMLPHHFGDLPULTLAGODATDAFAAYHPP 80
DB 7 KYTSELKNDKPRGDMISIQKAYDVSDVMDHPGSGFPLKSLAQEVTDAFVAFHRA 66
QY 81 SARPLRRFVVG-RLSDYAVSPASADYRRLAQLSAGLPERVGPPTKVQVLMVAFYA 139
DB 67 STWKNDKFTGYLLDYDVSSEVSKYRKLVEFSKRGKLYDKKHIMFATLCTIAMLFPAM 126
QY 140 ALTYVLACASAMHLLAGLIGFWITQSGMGHDSGHHRTTGHPRVLDRAVQVLSGNCITG 199
DB 127 SVYGVLFCEGVLVHLPFGCLMGFLWIOSGWIQGDAGHYVWVSDRLNKFGIFPAANCLSG 186
QY 200 LSTAMWKCNHNTHTIACNSLDHDPDLOHMPFAVSPFLFGNITSYFQRTLADASKFF 259
DB 187 ISIGMMKMNNAHNAHICNSLDYDPLQYIFPLVSSKFFSLSHFEKRLTSDLSRFP 246
QY 260 ISYQHTFFYPWMCIAINLTAOSALFVLTERRVPORLLEAGVATFAMVPLVASTLPM 319
DB 247 VSQHTFFYPIMCAALNMYVQSILMLTKRANYSRAQELGCLVPSIMPLVSCILPM 306
QY 320 WERVAFLPSFTTCGIGHVQFCINHFSSDYVGPCKGDMFEKQTAGTLDILCSPMMDWF 379
DB 307 GERIMFVIASLSTGMQOVQFSLNHFSSVYVGPKGNMFEKQTGTLDILCSPMMDWF 366
QY 380 HGGLOIOTIEHNLPRRLPRCHLRKVAAPVRLCKKHGTLTAAATFGWANVLTWTLRAAL 439
DB 367 HGGLOIOTIEHNLPRKPRCMRLRKISPVVIELCKKHNLPRVYASFSKANEMTLTTLRTAL 426
QY 440 QARTATSGAPKRLWMEAVNTHG 462
DB 427 QARDITK-PLPKRLWMEALHTHG 448

RESULT 10

AAVS1349
ID AAVS1349 standard; Protein: 448 AA.

AC AAVS1349;

DT 27-APR-2000 (first entry)

DE Sunflower HADES protein.

KW sphingolipid desaturase; sldi; sphingobase; ceramide; capnoid;
KM transgenic plant; crop plant; delta-8-unsaturated long-chain base;
tolerance; resistance; soil salinity; ion stress; toxicity; drought;

KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
KM pharmaceutical; food; chemical raw material.

XX Helianthus annuus.

XX DE19828850-A1.

XX 30-DEC-1999.

XX 27-JUN-1998; 98DE-1028850.

XX 27-JUN-1998; 98DE-1028850.

XX (GVS-) GVS GES ERWERB & VERM LANDWIRTSCHAFTLICH.

PI Heinz E, Zehringer U, Schmidt H, Sperling P;

DR WPI; 2000-127549/12.

PT New sphingolipid desaturase that selectively introduces double bond
PT into sphingolipids and capnoids -

XX Disclosure; Page 33-34; 62pp; German.

XX This invention describes a novel sphingolipid desaturase that selectively
CC introduces a double bond into the sphingobase of the ceramide residue of
CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
CC desaturase, or a vector containing the DNA sequence, can be used to
CC produce transgenic plants, especially crop plants, with an increased or
CC decreased delta-8-unsaturated long-chain base content or an altered
CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
CC compensate for a delta-8-unsaturated long-chain base deficiency, to
CC exclude production of delta-8-unsaturated bases, to increase tolerance
CC or resistance to soil salinity, ion stress or toxicity, drought, wet
CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
CC alter size growth and flowering time. Cells, transgenic organisms or
CC plants containing the DNA sequence can be used to produce sphingolipids
CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
CC materials. This sequence represents a desaturase protein, HADES, isolated
CC from Helianthus annuus (sunflower) which is used in the method of the
CC invention.

XX Sequence 448 AA;

XX Query Match 55.2%; Score 1391; DB 21; Length 448;
XX Best Local Similarity 55.8%; Pred. No. 9.6e-135;
XX Matches 247; Conservative 73; Mismatches 121; Indels 2; Gaps 2;

QY 21 RMISSELRNHAASADLWISISGVDYDVTWMLPHHFGDLPULTLAGODATDAFAAYHPP 80
DB 7 KYTSELKNDKPRGDMISIQKAYDVSDVMDHPGSGFPLKSLAQEVTDAFVAFHRA 66
QY 81 SARPLRRFVVG-RLSDYAVSPASADYRRLAQLSAGLPERVGPPTKVQVLMVAFYA 139
DB 67 STWKNDKFTGYLLDYDVSSEVSKYRKLVEFSKRGKLYDKKHIMFATLCTIAMLFPAM 126
QY 140 ALTYVLACASAMHLLAGLIGFWITQSGMGHDSGHHRTTGHPRVLDRAVQVLSGNCITG 199
DB 127 SVYGVLFCEGVLVHLPFGCLMGFLWIOSGWIQGDAGHYVWVSDRLNKFGIFPAANCLSG 186
QY 200 LSTAMWKCNHNTHTIACNSLDHDPDLOHMPFAVSPFLFGNITSYFQRTLADASKFF 259
DB 187 ISIGMMKMNNAHNAHICNSLDYDPLQYIFPLVSSKFFSLSHFEKRLTSDLSRFP 246
QY 260 ISYQHTFFYPWMCIAINLTAOSALFVLTERRVPORLLEAGVATFAMVPLVASTLPM 319
DB 247 VSQHTFFYPIMCAALNMYVQSILMLTKRANYSRAQELGCLVPSIMPLVSCILPM 306
QY 320 WERVAFLPSFTTCGIGHVQFCINHFSSDYVGPCKGDMFEKQTAGTLDILCSPMMDWF 379
DB 307 GERIMFVIASLSTGMQOVQFSLNHFSSVYVGPKGNMFEKQTGTLDILCSPMMDWF 366


```
QY 380 HGGLOFOIEHHLPRLPRCHLRKVAAYVDLCKKHGLTYSATPFMGANVLTWKTLPAAAL 439
DB 367 HGGLOFOIEHHLPRLPRCHLRKVAAYVDLCKKHGLTYSATPFMGANVLTWKTLPAAAL 426
QY 440 QARTATSGGAPKRLVWEAVNTHG 462
DB 427 QARDITK-PLPKNLVWEALHTHG 448

RESULT 11
AAU79830
ID AAU79830 standard; Protein; 448 AA.
XX
XX AAU79830;
AC
XX
XX 15-JUL-2002 (first entry)
DT
XX
XX Borage officinalis delta6-desaturase.
DE
XX
XX delta6-desaturase; sunflower; soybean; maize; tobacco;
KW peanut; carrot; oil seed rape; gamma linolenic acid; GLA;
KM chilling tolerance; borage.
XX
XX Borage officinalis.
OS
XX
XX Key
FH Location/Qualifiers
FT 156..163
FT /label= Lipid_box
FT 196..200
FT /label= Metal_box_1
FT 372..377
FT /label= Metal_box_2
FT
XX
XX US6355861-B1.
PN
XX
XX 12-MAR-2002.
PD
XX
XX 19-SEP-1997; 97US-0934254.
PF
XX
XX 13-OCT-1992; 92US-0959952.
PR 10-OCT-1991; 91US-0774475.
PR 08-JAN-1992; 92US-0817919.
PR 14-SEP-1994; 94US-0307382.
PR 28-JAN-1997; 97US-0789936.
XX
XX (RHON ) RHONE-POULENC AGROCHIMIE.
PA
XX
XX Thomas TL;
XX
XX WPI; 2002-380944/41.
DR N-PSDB; ABK49502.
XX
XX
XX Novel nucleic acid encoding evening primrose delta6-desaturase which
PT converts linoleic acid to gamma linolenic acid useful for producing
PT gamma linolenic acid in transgenic plant or bacteria
XX
XX
XX Example 9; Column 31-34; 53pp; English.
PS
XX
XX The invention describes an isolated nucleic acid encoding an evening
CC primrose Delta6-desaturase. The nucleic acid and a vector expressing the
CC nucleic acid are useful for producing a plant such as sunflower, soybean,
CC maize, tobacco, peanut, carrot or oil seed rape plant, with increased
CC gamma linolenic acid (GLA) content, and also for inducing or increasing
CC production of GLA in a bacteria or plant deficient, lacking in or
CC producing low levels of GLA. The nucleic acid is also useful for inducing
CC chilling tolerance in plants. This is the amino acid sequence of the
CC borage delta6 desaturase involved in the production of gamma linolenic
CC acid.
XX
XX
XX Sequence 448 AA;
SQ
XX
XX Query Match 55.0%; Score 1387; DB 23; Length 448;
XX
XX Best Local Similarity 55.5%; Pred. No. 2.5e-134;
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Matches 246; Conservative 73; Mismatches 122; Indels 2; Gaps 2;
QY 21 RMISSEKLEAAHASADDLWISISGDVYDTPMLPHHGGDLPLTLTLAGODATDAFAAYHP 80
DB 7 KIITDELKNHDKPGDLMWISIOGKAYDVSDWKDHPGSGFLKSLAGQVTLTAFVAFHRA 66
QY 81 SARPLLRFPFVG-RLSDYAVSPASADYRRLLAQLSSAGLFERVGPTPKVQLVMAVLYA 139
DB 67 STMKQLDKRFETGYLKDYSVSEVSXDYRLVPEFSKMGLYDKKHIMFATLCFIAMLFPAM 126
QY 140 ALIYVLACASAMAHLAGGLIFWVWIOSGMMGHDSGHRITHPVLDRVVQVLSGCLTG 199
DB 127 SVYGVLPCEGYLVHPSGCLMGFLWIQSGWIGHDAGHYVWVSDSLNKKMGIFAANCISG 186
QY 200 LSIAMWKCHNTHHIAACNSLDHDPDLQHPPLFAVPKLEGNISYFYORTLAFDAASKFE 259
DB 187 ISIGMKNNHNAHHIACNSLEIDPDQYIFLVVSKSPFGSLTSHFYEKRLTFDSLSRFF 246
QY 260 ISYQHTFYPVNCIARINLLAQSLFVLTERRVQRLLEIAGVATFWAWYPLLVASLPNW 319
DB 247 VSYQHTFYPICARLNNVQSLIMLTKRNVSYRAQELGLCVFSIWYPLLVSCLPNW 306
QY 320 WERVAPVLFSPITIGIOHVOFLNHPSSDYVYGPCKNDMEFKQTAGTIDLCSPMDWF 379
DB 307 GERIMEVIALSLVTMOQVQFSLNHFSSVYGVKSGKNWFEKQYDGTDLDISCPMDWF 366
QY 380 HGGLOFOIEHHLPRLPRCHLRKVAAYVDLCKKHGLTYSATPFMGANVLTWKTLPAAAL 439
DB 367 HGGSOFOIEHHLPKMPKPRCLRKISPYVIELECKKNLPYNYASFSAKAMNTLTTLRNTAL 426
QY 440 QARTATSGGAPKRLVWEAVNTHG 462
DB 427 QARDITK-PLPKNLVWEALHTHG 448

RESULT 12
ABG73095
ID ABG73095 standard; Protein; 448 AA.
XX
XX
XX ABG73095;
AC
XX
XX 17-APR-2003 (first entry)
DT
XX
XX Borage delta-6-desaturase #1.
DE
XX
XX Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower; soybean;
KW maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
KW octadecatrienoic acid; alpha-linolenic acid; delta-15-desaturase;
XX
XX Borage officinalis.
OS
XX
XX Key
FH Location/Qualifiers
FT Misc-difference 370
FT /note= "Encoded by TTG"
FT
XX
XX
XX US2002108147-A1.
PN
XX
XX 08-AUG-2002.
PD
XX
XX 21-DEC-2001; 2001US-0029756.
PF
XX
XX 13-OCT-1992; 92US-0959952.
PR 19-SEP-1997; 97US-0934254.
PR 10-OCT-1991; 91US-0774475.
PR 08-JAN-1992; 92US-0817919.
PR 14-SEP-1994; 94US-0307382.
PR 28-JAN-1997; 97US-0789936.
XX
XX (THOM/) THOMAS T L.
PA
XX
XX Thomas TL;
XX
XX
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DR WPI; 2003-06659/06.
DR N-PSDB; ABX15366.
XX
PT Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
PT for producing plant with increased gamma linolenic acid content, and
XX for inducing octadecatrienoic acid production in plant
XX
PS Example 9; Fig 5B; 55pp; English.
XX
XX The invention relates to a nucleic acid encoding an evening primrose
CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
CC for producing a plant (such as sunflower, soybean, maize, tobacco,
CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
CC acid (GUA) content by transforming a plant cell with the nucleic acid or
CC vector and regenerating a plant with increased GUA content from the plant
CC cell, for inducing or increasing production of GUA in an organism lacking
CC in or producing low levels of GUA and for inducing production of
CC octadecatrienoic acid in at least one of a plant deficient or lacking
CC in or producing low levels of octadecatrienoic acid, a bacterium which
CC produces alpha-linolenic acid or a bacterium which exhibits a
CC delta-15-desaturase activity on a GUA substrate. This sequence represents
CC a borage delta-6-desaturase polypeptide.
XX
SQ Sequence 448 AA;
Query Match 55.0%; Score 1387; DB 24; Length 448;
Best Local Similarity 55.5%; Pred. No. 2.5e-134;
Matches 246; Conservative 73; Mismatches 122; Indels 2; Gaps 2;
QY 21 RMISSELRARASADLMIISGDDVYVDTWMLPHHFGDPLRLTLGQDADFAAHP 80
DB 7 KYTSDBLKXNDPRGDMISIGKAYDVSDVNDHFGSGSPFLSLAGQETDAFVAFHPA 66
QY 81 SAPPRLRRFVVG-RLSDYAVSPASADYRLLAQLSSAGLFERYVPTPKQVLVMAVLEYA 139
DB 67 STWKNDLKFPTGYLLKDYSEVSKDYRKLVFEESSKGLYDKKHIMFATLCFIAMLFAM 126
QY 140 ALVLVLAASAMHLAGLIGFVWIOSGMGHDGSHNRITGHPVDLDRVVOVLSGNLTG 139
DB 127 SVGVLFCEGVLVHLFSGCLMGFLMIQSGWIGHDAGHYVAVSDSRLLKFGIIPAACLSG 186
QY 200 LSIAMWKCNHTNHAIACNSLIDHDPDLOHMPDLFAVSPFLFGNINSYFYORTLAFDAASKPF 259
DB 187 ISIGMKMKHNAHIAHICNSLEYPDLOIYIFLVVSSKFFSLSHFBEKLTDSLSRF 246
QY 260 ISYQHTFYPVNCIARIINLLAQSALFVLTREKVPQRLLEIAGVATFWAWYPLLVASLPNV 319
DB 247 VSYQHTFYPVIMCAARLNMVYQSLIMLTTRKNSYRAOELLGCLVFSIWPPLVSLPNV 306
QY 320 WERVAVFLPSFTICGIONHFCINHFSSDYVGPVKNDMPFEKOTAGTLDILCSPMWDF 379
DB 307 GERIMFVIALSVTGMQVOFSLNHFSYVVGPKNNMFEKOTDITDISCPWMDWF 366
QY 380 HGLLOFQIEHNLFPRLPRCHLRKVPARVRLCKKGGITVYAAATFWGANVLTWTKRAAL 439
DB 367 HGSQSQIEHNLFPKRCRLKISPYVIELCKKHLPIYASFSKANEVTLTLRTAL 426
QY 440 QARTATSGAPKXULWEAVNTHG 462
DB 427 QARDITK-PLPKXULWEALHTHG 448
RESULT 13
AAG53861
ID AAG53861 standard; Protein; 449 AA.
XX
AC AAG53861;
XX
XX 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68613.
XX

KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
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XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
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XX 16-JUN-1999; 99US-0139453.
XX 17-JUN-1999; 99US-0139492.
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XX 18-JUN-1999; 99US-0139455.
XX 18-JUN-1999; 99US-0139456.
XX 18-JUN-1999; 99US-0139457.
XX 18-JUN-1999; 99US-0139458.
XX 18-JUN-1999; 99US-0139459.
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XX 18-JUN-1999; 99US-0139462.
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PR	10-AUG-1999;	99US-0147935;
PR	11-AUG-1999;	99US-0148171;
PR	12-AUG-1999;	99US-0148341;
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PR	30-AUG-1999;	99US-0151303;
PR	31-AUG-1999;	99US-0151438;

PR	17-SEP-1999;	99US-0151930;
PR	07-SEP-1999;	99US-0152363;
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PR	26-OCT-1999;	99US-0161360;
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PR	28-OCT-1999;	99US-0161923;
PR	29-OCT-1999;	99US-0162149;

Query Match	55.0%;	Score 1387;	DB 21;	Length 449;
Best Local Similarity	55.8%;	Pred. No. 2.5e-134;		
Matches 247; Conservative	69;	Mismatches 125;	Indels 2;	Gaps 2;

```

0Y 21 RMISKEIARAASADMLTISGDYUDATPYLBNHPCGDLPLTLLAGODATAPAAUYNP 80
Db 8 KYITNEDIKKHNKSSDLMIALOGKAYUNSDWIKTHPGSGTVLNLVGODVTDFAIENHPG 67
0Y 81 SARPLRFFVFG-RSDYAVSPASADYRRLTLQSSAGLFEHVGPPYKQOLVLMAYFYA 139
Db 68 TAMHHLDLFTGYNHRDFOVSEVSXDYRMALEFFKLGIFEKKGHTLTTLTFAAAMFLG 127
0Y 140 ALYVLACASAWAHLLAGGLIGFWMIQSGMCHDSGHRITGHPVLDRVQVLSGCLTG 199
Db 128 VLUGVLACTSVFAHQIAAALLGLTIQSAVYIGHDSGHVYIMSNKSYNRFPAQLLSGCLTG 187
0Y 200 LSIAMKKNHTHTHIAACNSLDHDPLOHMPFAYVSKJFGNIMSYQOTLTFADASKPF 259
Db 188 ISIAWMKTHNAHHLACNSLDVDPLOHIVFAVASTKFPSSILTSRKYDKLTFDPVAREL 247
0Y 260 ISOHWTFYPWVCILRINMLAOSALFVLTEKVPORLIEIAGVATFWANYPPLIVASLPMW 319
Db 248 VSYGFTLYYPWVCIFRINLFIOTFLLPSPKREVPBALNFAGILVWMTFFPLIVSCLPMW 307
0Y 320 WERVAFLVFSPTTICGIIHQVQCLNHFSSDVGPPKGNDFEKQTAGTLIDILCSPMWDF 379

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DB 308 PERFFVFTSFVTALQHIQFTLNHPADYVGPPTGSDWFEKQAAGTIDISCRSYMDWF 367
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 DB 368 FGGLQFOLEHNLPRRLPRCHLRKAPAVRDLCKHGILTYSAATFGANVLTWTLRAAL 427
 QY 440 QARTATSGAPKNLWMEAVNTTG 462
 DB 428 QARD-VANPVVKNLWMEALNTHG 449
 RESULT 14
 ID AAY51334 standard; Protein; 449 AA.
 AC AAY51334;
 DT 27-APR-2000 (first entry)
 DE A. thaliana sld1 protein.
 XX Shingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
 KM transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KM tolerance; resistance; soil salinity; ion stress; toxicity; drought;
 KM cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KM pharmaceutical; food; chemical raw material.
 OS Arabidopsis thaliana.
 PN DE19828850-A1.
 XX 30-DEC-1999.
 PD 27-JUN-1998; 98DE-1028850.
 PF 27-JUN-1998; 98DE-1028850.
 PR 27-JUN-1998; 98DE-1028850.
 XX (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
 PA Heinz E, Zaehring U, Schmidt H, Sperling P;
 PI WPI; 2000-127549/12.
 DR N-PSDB; AA244833.
 XX New sphingolipid desaturase that selectively introduces double bond
 PT into sphingolipids and capnoids -
 PS Claim 8; Fig 4; 62pp; German.
 XX This invention describes a novel sphingolipid desaturase that selectively
 CC introduces a double bond into the sphingobase of the ceramide residue of
 CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to
 CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered
 CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
 CC compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 CC materials. This sequence represents the Arabidopsis thaliana sphingolipid
 CC desaturase sld1 protein described in the invention.
 SO Sequence 449 AA;
 Query Match 55.0%; Score 1387; DB 21; Length 449;
 Best Local Similarity 55.8%; Pred. No. 2.5e-134;
 Matches 247; Conservative 69; Mismatches 125; Indels 2; Gaps 2;

QY 21 RMISSEKELRAHASADDLMTISIGDYYVDTPTMLPHRPGDLPLTLTAGODATDAFAAYHPP 80
 DB 8 KYITNEDLKKHNSGDLMTALIGKVVNVSDWMLKTHRGDVTILNLVGQDVTDAFIAPHG 67
 QY 81 SARPLLRRFPVG-RSDYVSPASADYRRLAQLSAGLPERVGPPTKQVLMAVLFPA 139
 DB 68 TAWHHDHLFTGYHIDFQVSEVSRDYRMAAEFRRLGFEKNGHTLYTLAEVAAAFGL 127
 QY 140 ALYLVACASAMVHLLAGLIGFWTIQSGMGGHSHRITGHPVLDRVVOVLSGCLTG 129
 DB 128 VLYGVLAFTSVFHAQALALGLMTQSAVYIGDSGHVYIMSKSYNRRFQQLSGCLTG 187
 QY 200 LSIAMWKCNHNTTHIACNSLDHDPDLQHNPLFAVSPKLGNTWYFQRTLAFDAASKPE 259
 DB 188 ISIAMWKTHMAHNLACNSLDYDPDLQHPVFAVSTKTFSSLSRSRYDKLTFDPVAFRL 247
 QY 260 ISYQHWTFYPVNCIARINILAQSAFLVTEKRYPORLEIAGVATWANYPLVASLPPW 319
 DB 248 VSYQHTFYFVWCFGRINIFIQTFLLFSKREVPDRLNPFAGILVFWTFPLVSLPPW 307
 QY 320 MERVAVLFSFTTCGLOHVOFCLNHFSDDYVGPBKNDMFEKOTAGTLDILCSPMWDMF 379
 DB 308 PERFFVFTSFVTALQHIQFTLNHPADYVGPPTGSDWFEKQAAGTIDISCRSYMDWF 367
 QY 380 HGLQFOIEHNLPRRLPRCHLRKAPAVRDLCKHGILTYSAATFGANVLTWTLRAAL 439
 DB 368 FGGLQFOLEHNLPRRLPRCHLRKAPAVRDLCKHGILTYSAATFGANVLTWTLRAAL 427
 QY 440 QARTATSGAPKNLWMEAVNTTG 462
 DB 428 QARD-VANPVVKNLWMEALNTHG 449
 RESULT 15
 ID AAG07392 standard; Protein; 449 AA.
 AC AAG07392;
 DT 17-OCT-2000 (first entry)
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 4528.
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KM hybridisation assay; genetic mapping; gene expression control; promoter;
 KM termination sequence.
 OS Arabidopsis thaliana.
 PN EP1033405-A2.
 XX 06-SEP-2000.
 PD 25-FEB-2000; 2000EP-0301439.
 PF 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
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 PR 21-APR-1999; 99US-0130449.
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PR 02-JUL-1999; 99US-0142055.
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PR 18-AUG-1999; 99US-0149426.
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PR 25-AUG-1999; 99US-0150566.
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PR 27-AUG-1999; 99US-0151065.
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PR 31-AUG-1999; 99US-0151438.
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PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0158923.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
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PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.

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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 17.3885 Seconds
(without alignments)
2555.128 Million cell updates/sec

Title: US-09-857-524B-4
Perfect score: 2521
Sequence: 1 MPPSVDAAMPADAGAGDV.....TATSGAPKLVWEAVNTHG 462

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1466	58.2	449 2	hypotheical prote
2	1429	56.7	449 2	delta-8 sphingolip
3	1427.5	56.6	458 2	delta8 sphingolip
4	1387	55.0	449 2	delta-8 sphingolip
5	735	29.2	523 2	linoleoyl-CoA dea
6	454.5	18.0	473 1	linoleoyl-CoA dea
7	408	16.2	444 2	linoleoyl-CoA dea
8	400	15.9	444 2	linoleoyl-CoA dea
9	370.5	14.7	447 1	Delta5 fatty acid
10	358	14.2	454 2	Delta5 fatty acid
11	247.5	9.8	359 2	protein T13f2.1 [1
12	245.5	9.7	345 2	Delta6 fatty acid
13	226	9.4	368 2	probable Delta6 fa
14	185.5	7.4	864 1	linoleoyl-CoA dea
15	184.5	7.3	135 2	hypotheical prote
16	183.5	7.3	387 2	omega-6 desaturase
17	181	7.2	140 2	cytochrome b5 [imp
18	180	7.1	134 2	cytochrome b5 [imp
19	180	7.1	139 2	cytochrome b5 [imp
20	179.5	7.1	427 2	probable desat pro
21	178.5	7.1	894 2	probable desat pro
22	176.5	7.0	905 1	nitrate reductase
23	175.5	7.0	443 2	nitrate reductase
24	175	6.9	443 2	omega-3 fatty acid
25	173	6.9	134 2	cytochrome b5 - w1
26	172.5	6.8	877 2	nitrate reductase
27	172	6.8	318 2	nitrate reductase
28	170	6.7	489 2	probable heme bind
29	170	6.7	904 1	nitrate reductase

30	169.5	6.7	911 2	T08105	nitrate reductase
31	168.5	6.7	448 2	D85362	hypotheical prote
32	167	6.6	904 1	R02MNS	nitrate reductase
33	166.5	6.6	920 2	S52301	nitrate reductase
34	166	6.6	347 2	S43771	phosphatidylcholin
35	166	6.6	917 2	S35228	nitrate reductase
36	166	6.6	917 2	E96807	nitrate reductase
37	164.5	6.5	911 2	T08108	nitrate reductase
38	164.5	6.5	982 1	S16292	nitrate reductase
39	163.5	6.5	134 2	T00796	nitrate reductase
40	162.5	6.4	443 2	T08136	cytochrome b5 At2g
41	162	6.4	917 1	R02MNS	probable omega-6 d
42	161.5	6.4	370 2	B83034	nitrate reductase
43	161.5	6.4	889 2	T02240	conserved hypothe
44	161	6.4	926 1	R02MNS	nitrate reductase
45	160	6.3	135 1	CBRTSM	nitrate reductase

ALIGNMENTS

RESULT 1
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hypotheical protein At2g46210 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #ext_change 02-Feb-2001
C/Accession: A84900
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:1061197
A/Accession: A84900
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-449 <STO>
A/Cross-references: GB:AB002093; NID:g3702328; PIDN:AAC62885.1; GSPDB:GN00139
C/Genetics:
A/Gene: At2g46210
A/Map position: 2

Query Match	Score	58.2%	Score	1466	DB 2	Length	449
Best Local Similarity	59.1%	Pred. No.	4.9e-119				
Matches	262	Conservative	63	Mismatches	116	Indels	2
QY	21	RMISSEKLEPAHASADLWISISGDVYDTPWLRPHPGDLPYLLAGDADTAFAAYHPP	80				
DB	8	RYVTSDDLKGNKPGDLWISIGKYYDVSDWKSHPGGAATLNLACGVDTDAFIYHFG	67				
QY	81	SARPLRRPFVG-RISDVAVSPASADYRRLAQLSAGLFEKVGPTPKQVLMAYLFYA	139				
DB	68	TAMHLEKLNQYVHDHVSVDYRRLAELFSGKGLFDDKGVHTLYTLTCVGMFLAA	127				
QY	140	ALYVLACASAAHLLAGGLIGFWIISGMMHDSGHHITGHPVLDRVVOVLGNCLLG	199				
DB	128	VLYGVLACTSIWAHLISAVLLGLMTIQSAVYVGHDSGHVYVITKPCNKIQLSLCTLG	187				
QY	200	LSIAWKKCNHTNHTIACNSLDHDPDLOHMPLEPAVSPKLGNIWSYFYQTTLAFAASKEF	259				
DB	188	ISIAWKKTHNHNHIAACNSLDHDPDLOHPIPAVSTKPFNSMTSRVYKGLTFDPLARFL	247				
QY	260	ISYQHTTFYPVNCIARINILAQSLFVLTKEKVPORLEIAGVATFAMVYPLLVASLPMW	319				
DB	248	ISYQHTTFYPVNCVGRINLFIQTFLLFSKRVHPRALINAGILVFWTFPLVSLPMW	307				
QY	320	WERVAFLVLESTICGHOVQCLNHFSSDYVYGPKNQWFEKQAGTDIICSPMDF	379				
DB	308	QSRFLFVVSFAVYTAIQHQPCLNHPADVYGGPKNQWFEKQAGTDIICSRPMDF	367				
QY	380	HGLOFQLEHNLFPRLPRCHLRKVAFAVDLCCKGLTSAATFPGANVLTAKTLRAAL	439				
DB	368	FGLOFQLEHNLFPRLPRCHLRKVAFAVDLCCKGLTSAATFPGANVLTAKTLRAAL	427				

Db RNSDATHIFHAFHSSGQAYKQDLLKKHGEHDEPLEKOLEKRLDKVDINVASDVSAQ 128
 QY 104 -----ADYRRLAQLQSAG-----LPERVGPTRKQVLMVAFLF---YALYIVLA 146
 Db 129 EKQVESFEKLRLKLDHDDGMKANETFLFKALIS---TLSTMAFAYLYQYLGWYITSA 183
 QY 147 CASAMWHLLAGLIGFVWISGMWGHDSGHRTGHEVLDLVVQVLSGNCITGLSIAMWK 206
 Db 184 C-----LLALAQPGFWLTHFPCQOPTKRPPLADTSLPFGNLTQGSFRMWK 232
 QY 207 CNNTHTIACNSLDHDDLOHMLFAVSPKLFNGISYFYORTLAPDAASKPISTQHT 266
 Db 233 DKNTHTAATNVLDHGDIDLALFAFIP---GDLCKY---KASFEKALIKTIVPYOHLY 285
 QY 267 FYVVMCIARINLAQSLFPLTEKRVQRLL-----ELAGVATFMAWYLLVASLPMW 320
 Db 286 FTALMLPLRFSTWGQSQVWPKENQMKYQORNAFWEQATVGHMAWVFYQFLLETPW 345
 QY 321 ERVAFVLFSTICG--IOHVQCLNHPSSDVYVGPVK--NDWFEKQTAGTLDILCSPM 375
 Db 346 LRVAFLISQMGGLIAHY-VTFNHSVUKY--PANSRLINPALQILITRMTPSPF 402
 QY 376 MDVFGLOFOIHHLPRLPRCHLRKVAVDLCKKGLTYSAAFTWGANVLTWKTLR 435
 Db 403 IDWLMGGLANYQIEHHLEPTWPRCNLACMKYKWKCKENMLPYLVDDYFDGYAMNLIQOLK 462
 QY 436 --AAALQART 444
 Db 463 NMAEHIQAKA 473

RESULT 7

110155
 110155 l1noeol1-CoA desaturase (EC 1.14.19.3) [validated] - human
 N:Alternate names: Delta6 fatty acid desaturase; protein DKFZp586C201.1
 C:Species: Homo sapiens (man)
 C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 03-Jun-2002
 C:Accession: T13155; T08765
 R:Cho, H.P.; Nakamura, M.T.; Clarke, S.D.
 J. Biol. Chem. 274, 471-477, 1999
 A:Title: Cloning, expression, and nutritional regulation of the mammalian Delta-6 desaturase
 A:Reference number: Z17612; MUID:99085046; PMID:9867867
 A:Accession: T13155
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-444 <CHO>
 A:Cross-references: EMBL:AF126799; NID:94406527; PID:94406528; PIDN:AAD20018.1
 R:Mambuti, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 Submitted to the Protein Sequence Database, March 1999
 A:Reference number: Z16471
 A:Accession: T08765
 A:Molecule type: mRNA
 A:Residues: 'RTG', '138-428', 'D', '430', 'W', '432-444' <MAN>
 A:Residues: 'RTG', '138-428', 'D', '430', 'W', '432-444' <MAN>
 A:Cross-references: EMBL:AL050118
 A:Experimental source: adult uterus; clone DKFZp586C201
 C:Genetics:
 A:Gene: GDB:FADS6
 A:Cross-references: GDB:9956652
 A:Note: DKFZp586C201.1
 C:Superfamily: cytochrome b5 core homology
 C:Keywords: cytochrome; heme; iron; metalloprotein; oxidoreductase; unsaturated fatty
 F:18-94/Domain: cytochrome b5 core homology <CB5>
 F:53,76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 16.2%; Score 408; DB 2; Length 444;
 Best Local Similarity 26.7%; Pred. No. 1.9e-27;

Matches 122; Conservative 63; Mismatches 172; Indels 100; Gaps 19;

QY 12 GDAAGAGDVMM--ISSKELRAHSAADLMISISGDVDTVPWLPNHPGGLPLTLTAGOD 69
 Db 8 GEGAABREVSVPTFSWEIOKHLRTDRMLVIDRKVYNITKWSIOHFGGQGVIGHYAGED 67
 QY 70 ATAPAPAYNH-----PSARPLLRPFVGRLS-----DYAV-SPASADYRRLAQLSSA 116

Db 68 ATDAFAHFDLEFVGKFLKPLL-----IGELAPESPQDHGKSKITEDFALRKTAEDM 123
 QY 117 GLFERVGPTRKQVLMVAFLF---ALYVLACASAM-AHLLAGLIGFVWISGMWK 171
 Db 124 NLFK-----TNHVFLLLAHIALLESIAFWFYFPGNGMIFLITAFVATGQAQGMQ 179
 QY 172 HDGHHRTGHPFLDRVVOVLSGNCITGLSIAMWKCNHTHTIACNSLDHDDPLQAMPLF 231
 Db 180 HDYGLSTVYRKPRKNLHKFVYGLKASAMWNRHGHAKRPIFKKDPVNMHLNF 239
 QY 232 AVSPKLFNGISYFYORTLAPDAASKPISTQHTFYPVWCIAIRINLAQSLFVLTEKR 291
 Db 240 VLGE-----W-----QPIEYKKKLYLPYNH-----QHEYFLIG-- 270
 QY 292 VPORLLEIAGVATFMAWYLLVASL--PW---WERYAVFLFSPT-----ICG-----I 335
 Db 271 -PRLIPM-----YFOYQIMTMIVKKNWVDLAWVSYYIRFYIYIFPYGLALPL 323
 QY 336 OHVQCLNHP-----SSDVYVGPVKGNDFEKKOTAGTLDILCSPMQMPFG 381
 Db 324 NFRFLSHFWVWVTOHNIWVEIDQAY-----RDMSSQLTATCNVQSFNDMFSG 377
 QY 382 GLQFOIHHLPRLPRCHLRKVAVDLCKKGLTYSAAFTWGANVLTWKTLR 418
 Db 378 HNFQIEHLLFTWPRHNLHKTIALPLVKSICAKHGIEY 414

RESULT 8

UG0180
 Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
 C:Accession: UG0180
 R:Aki, T.; Shimada, Y.; Inagaki, K.; Higashimoto, H.; Kawamoto, S.; Shigeta, S.; Ono, K.;
 Biochem. Biophys. Res. Commun. 255, 575-579, 1999
 A:Title: Molecular cloning and functional characterization of rat delta-6 fatty acid desaturase
 A:Reference number: JG0180; MUID:99160394; PMID:10049752
 A:Accession: JG0180
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-444 <AKI>
 A:Cross-references: DDBJ:AB021980; NID:94514721; PIDN:BA75496.1; PID:94514722
 C:Superfamily: cytochrome b5 core homology
 C:Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid biosynthesis
 F:18-94/Domain: cytochrome b5 core homology <CB5>
 F:53,76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 15.9%; Score 400; DB 2; Length 444;
 Best Local Similarity 26.4%; Pred. No. 9.6e-27;

Matches 115; Conservative 68; Mismatches 166; Indels 86; Gaps 15;

QY 26 KELRAHSAADLMISISGDVDTVPWLPNHPGGLPLTLTAGODATDAFAAYH-----P 79
 Db 24 BEIQGNLRTDRMLVIDRKVYNITKWSIOHFGHRTGHSGBDATDAFAFLDLPVG 83
 QY 80 PSARPLLRPFVGRLSDY-----AVSPASADYRRLAQLSSAGLFEKVGTPRKQVLY 132
 Db 84 KFLKPLL-----IGELAPESPQDHGKSKITEDFALRKTAEDMNLFK-----T 128
 QY 133 MAVLFPYAL-YVLACASAMWHLLAGLIGFVWISGMWKCNHTHTIACNSLDHDDLOHMLFAVSPK 237
 Db 129 NHLPFLLSHITWESIMFLL--SYGNGHIFPVITAFVATGQAQGMQOHYGLH 185
 QY 178 RITGHVLDLVVVOVLSGNCITGLSIAMWKCNHTHTIACNSLDHDDLOHMLFAVSPK 237
 Db 186 SVYKSIWNIHVKFVYGLKASAMWNRHGHAKRPIFKKDPVNMHLNF 239
 QY 238 FGNISYFYORTLAPDAASKPISTQHTFYPVWCIAIRINLAQSLFVLTEKVPQR 295
 Db 244 ---W-----QPIEYKKKLYLPYNHQHEFFLIPPLIPYFOYQIMTMIR--RD 292
 QY 296 LLEIAGVATFMAWYLLVASLPMWERYAVFLFSPT-----ICGIGHV--QFCLN 343

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Db      293 WVDLAIASVYARF--FYTYIPFYGILGALVFNINFRLESHFWVAVTQNMHIWMEIDD 350
QY      344 HFSDDVYVPRPKNDMEFEQTAGTLDILCSPMWDMHGGLQPOIEHHLPRRLPRCHLRKY 403
Db      351 HY-----RDWFSSQLATACNVEOSFFNDWFGHLNFQIEHHLPTPRRHRLHKI 399
QY      404 APARVLDCKKGLTY 418
Db      400 APLVKSLSCKHGLE 414

RESULT 9
T4319
Deltas fatty acid desaturase (EC 1.14.99.-) T13F2.1 [validated] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C:Accession: T4319; T24875
R:Michaelsen, L.V.; Napier, J.A.; Lewis, M.; Griffiths, G.; Lazarus, C.M.; Stobart, A.K.
FEBS Lett. 439, 215-218, 1998
A:Title: Functional identification of a fatty acid deltas desaturase gene from Caenorhab
A:Reference number: Z22422; MIMD:99059458; PMID:9845325
A:Accession: T4319
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-447 <MIC>
A:Cross-references: EMBL:AF078796; NID:94003522; PIDN:AAC95143.1; PID:94003523
R:Swindburn, J.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19947
A:Accession: T24875
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-197; VSHIFNN', 198-447 <WIL>
A:Cross-references: EMBL:Z81122; PIDN:CA03352.1; GSPDB:GN00022; CESP:T13F2.1
A:Experimental source: clone T13F2
C:Genetics:
A:Gene: CESP:T13F2.1; des-5
A:Map position: 4
A:Insertions: 48/3; 80/3; 197/3; 295/3; 318/2; 349/1; 384/3
C:Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match: 14.7%; Score 370.5; DB 1; Length 447;
Best Local Similarity 26.2%; Pred. No. 3.5e-24;
Matches 117; Conservative 61; Mismatches 177; Indels 91; Gaps 17;

QY      35 DDLWISISGDVYDVTWMLPHHPGDLPLTLTAGDATTDAFAAYHP----- 79
Db      16 DGMKQCIDDAV-----LRSHPGGS-AITTYKMDATTYFHTHGSKEAYOMTELKKE 68
QY      80 -PSARP-----LRRFPVGRISDVAVSPASADYR-RLAQ--LSSAGLF 119
Db      69 CPTQBEIPDIKDDPKIGIDVNMGTGFNISSEKRSQINIKSFTDLRRVRABGLMDGSPLE 128
QY      120 ERGGRFPKQVLMAVLF-----YALYLVLACASAMAHLLAGLIGFWIWSGWMGHDS 174
Db      129 Y-----IRKLEITFTILFAFYLYQHTYILPSAI-----LMGVAMQOLGWLIIHF 173
QY      175 GHHRTIGHVLDLVVQVLSGNCLTGLSIAMWKCNHNTTHIACNSLDHDPDLQHPPLFAVS 234
Db      174 AHHQLFKRRYNDLASFYVGNFLQVSHIFNNFGSSGWMKEQHNHAAATNVVGRDGLDLPVRYAYV 233
QY      235 PKLGNWISFYQRTLAFDAASKFPISYOHTFYPVMCIARINLALQSAALFVLEKRVQ 294
Db      234 AEHLNYSQDSVMTL-----FRMQVHWTF--MLPFLRLSWLLQSIIFV---SQMPF 281
QY      295 R-----LLEIAGVATPMAYRPLVLVASLPNMMERVAFLVFSFTICG--IOHVOFCLN 343
Db      282 HYYDYRNATAIYQVGLSLHMASLQGLYFLPDMSTRIMFVLVSHVVGGLLSHV--VTFN 340
QY      344 HFSDDVY-VGPRKNDMEFEKOTAGTLDILCSPMWDMHGGLQPOIEHHLPRRLPRCHLRK 402

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Db      341 HYSVEKFAISSNINSNVACLAQIMTTRNNRPGRFIDWLGNGLYQIEHHLPTPRHRLNT 400
QY      403 VAPAVRDLCKKGLTYSA-----ATFM 424
Db      401 VMLPVEPAANGLPYMVDYFTFGW 426

RESULT 10
H88791
protein T13F2.1 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: H88791
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MIMD:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_eleg
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: H88791
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-454 <STO>
A:Cross-references: GB:chr_IV; PIDN:CA03352.1; PID:93879828; GSPDB:GN00022; CESP:T13F2.1
C:Genetics:
A:Gene: T13F2.1
A:Map position: 4
C:Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase

Query Match: 14.2%; Score 358; DB 2; Length 454;
Best Local Similarity 25.8%; Pred. No. 4.3e-23;
Matches 117; Conservative 61; Mismatches 177; Indels 98; Gaps 18;

QY      35 DDLWISISGDVYDVTWMLPHHPGDLPLTLTAGDATTDAFAAYHP----- 79
Db      16 DGMKQCIDDAV-----LRSHPGGS-AITTYKMDATTYFHTHGSKEAYOMTELKKE 68
QY      80 -PSARP-----LRRFPVGRISDVAVSPASADYR-RLAQ--LSSAGLF 119
Db      69 CPTQBEIPDIKDDPKIGIDVNMGTGFNISSEKRSQINIKSFTDLRRVRABGLMDGSPLE 128
QY      120 ERGGRFPKQVLMAVLF-----YALYLVLACASAMAHLLAGLIGFWIWSGWMGHDS 174
Db      129 Y-----IRKLEITFTILFAFYLYQHTYILPSAI-----LMGVAMQOLGWLIIHF 173
QY      175 GHHRTIGHVLDLVVQVLSGNCL-----TGLSIAMWKCNHNTTHIACNSLDHDPDLQ 227
Db      174 AHHQLFKRRYNDLASFYVGNFLQVSHIFNNFGSSGWMKEQHNHAAATNVVGRDGLDLP 233
QY      228 MLEFVSPKLFENINISYFQRTLAFDAASKFPISYOHTFYPVMCIARINLALQSAALFVL 287
Db      234 VPFYATVAEHLNYSQDSVMTL-----FRMQVHWTF--MLPFLRLSWLLQSIIFV-- 283
QY      288 TEKRVFOR-----LLEIAGVATPMAYRPLVLVASLPNMMERVAFLVFSFTICG--IQ 336
Db      284 --SQMPHTYDYRNATAIYQVGLSLHMASLQGLYFLPDMSTRIMFVLVSHVVGGLLS 341
QY      337 HVQFCLNHSSDDVY-VGPRKNDMEFEKOTAGTLDILCSPMWDMHGGLQPOIEHHLPRRL 395
Db      342 HV-VTFNHSYVEKFAISSNINSNVACLAQIMTTRNNRPGRFIDWLGNGLYQIEHHLFPM 400
QY      396 PRCHLRKVAAPVADLCKKGLTYSA-----ATFM 424
Db      401 PRHNLNTWMLPVEPAANGLPYMVDYFTFGW 433

RESULT 11
S35157
Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - Synechocystis sp.
C:Species: Synechocystis sp.
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C:Accession: S35157; S76243
R:Reddy, A.S.; Nuccio, M.L.; Gross, L.M.; Thomas, T.L.

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Db 289 NFIIIMVYGGLNYQVTHLPHICH1HYPKIAPILAEVCEBQVNVAVHQTFFGALANY 348
 QY 432 KTLRAALQART 443
 Db 349 SWLKQKMSINPEF 360

RESULT 14

JCI422
 nitrate reductase (NADH) (EC 1.7.1.1) - Volvox carteri

C:Species: Volvox carteri

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002

C:Accession: JCI422; S22192

R:Gruber, H.; Goeltz, S.D.; Kirk, D.L.; Schmitt, R.

Gene 120, 75-83, 1992

A:Title: The nitrate reductase-encoding gene of Volvox carteri. Map location, sequence

A:Reference number: JCI422; WUID:93013022; PMID:1398126

A:Accession: JCI422

A:Molecule type: DNA

A:Residues: 1-864 <GR2>

A:Cross-references: EMBL:X64136; NID:g21993; PIDN:CAA45497.1; PID:g21994

A:Note: submitted to the EMBL Data Library, January 1992

A:Gene: nltA

A:Map position: linkage group IX

A:Function: 183/3; 234/2; 295/1; 339/1; 372/1; 425/2; 521/3; 593/3; 677/3; 797/2

A:Description: catalyzes the reduction of nitrate to nitrite

C:Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 redu

C:Keywords: dimer; electron transfer; FAD; flavoprotein; heme; iron; metalloprotein; mol

F:36-425/Domain: molybdopterin-binding domain homology <PCO>

F:497-571/Domain: cytochrome b5 core homology <CB5>

F:613-864/Domain: cytochrome-b5 reductase homology <CBR>

F:139/Binding site: molybdopterin (Cys) (covalent) #status predicted

F:532,555/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 7.4%; Score 185.5; DB 1; Length 864;

Best Local Similarity 36.4%; Pred. No. 7,9e-08;

Matches 48; Conservative 22; Mismatches 57; Indels 5; Gaps 3;

QY 7 AMPAPGDAAGA-GDYRMISSEKELRAHASADDLWISIGDYDVTPLPHHGGDLPLTL 65

Db 483 AAPPPVAAANAGGPRQYMEVAAHNTBESCMFVHGKVDATPLDHPGABSLIV 542

QY 66 AGQDXTDAAYHPSARPLRRFFVGRU--SDYAVSPASADYRRLAQLSSAGLFERY- 122

Db 543 AGADATDEFNSIHSSKAKMLAQYIGDVLVASKPAAGATVPEPQVASTSSPAVDPLV 602

QY 123 -GPTPKVQLVLM 133

Db 603 LNPQKVKLPLI 614

RESULT 15

A86390
 hypothetical protein TK7_28 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001

C:Accession: A86390

R:Theologis, A.; Ecker, J.R.; Palm, C.U.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizier, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; WUID:21016719; PMID:11130712

A:Accession: A86390

A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-135 <STO>
 A:Cross-references: GB:A8005172; NID:g9797763; PIDN:AAF98581.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

C:Superfamily: cytochrome b5; cytochrome b5 core homology

C:Keywords: heme; iron; metalloprotein

F:40,64/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 7.3%; Score 184.5; DB 2; Length 135;

Best Local Similarity 36.5%; Pred. No. 1.1e-08;

Matches 46; Conservative 23; Mismatches 48; Indels 9; Gaps 4;

QY 21 RMISSEKELRAHASADDLWISIGDYDVTPLPHHGGDLPLTLAGODATDAPA-AVHP 79

Db 6 KLYSHEEATNKKQDDCWVIDGKYVDSYNDHEPGDDVLLAVAGKDATDDEFDAGHS 65

QY 80 PSARPLRRFPVGRUSDYAVS--PASADYRRLAQLSSAGLFER----VGPTPKVQL-V 131

Db 66 KDARELMKRYFGLDESSLPETPELKTKYKKQPDQSVQKLPDLTKQYVWVVSITISV 125

QY 132 LMAVLF 137

Db 126 AVSVLF 131

Search completed: January 1, 2004, 06:39:40

UDD time : 18.385 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 10.1656 Seconds
(without alignments)
2137.240 Million cell updates/sec

Title: US-09-857-524B-4
Perfect score: 2521
Sequence: 1 MPPSYDAMPAPDPAAGADV.....TATSGAPKLVWEAVNTHG 462

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	424	16.8	444	1	FADS_BRARE
2	247.5	9.8	359	1	L1CD_SYNY3
3	185.5	7.4	864	1	NIA_VOICA
4	183.5	7.3	387	1	FD61_SOYBN
5	180	7.1	134	1	CYS1_ARATH
6	180	7.1	136	1	CYSB_TOBAC
7	178.5	7.1	894	1	NIA_BEABA
8	176.5	7.0	905	1	NIA_FUSOX
9	175	6.9	134	1	CYSB_BRAOL
10	172.5	6.8	318	1	NIA_CHLVU
11	170	6.7	881	1	NIA_HORVU
12	170	6.7	904	1	NIA_TOBAC
13	169.5	6.7	911	1	NIA_BRANA
14	168.5	6.7	448	1	FD6C_ARATH
15	167	6.6	904	1	NIA2_TOBAC
16	166.5	6.6	930	1	NIA_CICIN
17	166	6.6	917	1	NIA1_ARATH
18	164.5	6.5	911	1	NIA2_BRANA
19	164.5	6.5	982	1	NIA_NEUCR
20	163.5	6.5	134	1	CYS2_ARATH
21	163	6.5	146	1	CYS5_RAT
22	162.5	6.4	443	1	FD6C_BRANA
23	162	6.4	917	1	NIA2_ARATH
24	161.5	6.4	889	1	NIA1_MAIZE
25	161	6.4	926	1	NIA_SPIOLE
26	160	6.3	135	1	CYS5_TOBAC
27	160	6.3	909	1	NIA_PENNY
28	159	6.3	132	1	CYSB_BOROF
29	158.5	6.3	916	1	NIA1_ORISA
30	158	6.3	137	1	CYSB_ORISA
31	157	6.2	902	1	NIA1_PHYIN
32	157	6.2	881	1	NIA1_PHAVU
33	155	6.1	424	1	FD6C_SOYBN

34	155	6.1	911	1	NIA_LYCES	P17570 lycopersico
35	154.5	6.1	414	1	CYBR_DROME	P19967 drosophila
36	154	6.1	890	1	NIA2_PHAVU	P19866 phaseolus v
37	153.5	6.1	912	1	NIA2_HORVU	P27869 hordeum vul
38	153.5	6.1	915	1	NIA1_HORVU	P27867 hordeum vul
39	152	6.0	900	1	NIA1_LOTJA	P39869 lotus japon
40	151.5	6.0	988	1	NIA_BETVE	P27783 betula verr
41	151	6.0	573	1	CYB2_HANAN	P09437 hansenula a
42	151	6.0	908	1	NIA_USTMA	O05531 ustilago ma
43	150.5	6.0	893	1	NIA_LERMC	P36842 leprospnaer
44	149	5.9	890	1	NIA2_SOYBN	P39870 glycine max
45	148.5	5.9	147	1	YDAA_SCHPO	O10352 schizosacch

ALIGNMENTS

RESULT 1	ID	FADS_BRARE	STANDARD	PRT	444 AA.
AC	09DEX7	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Delta-5/delta-6 fatty acid desaturase (EC 1.14.19.-).				
GN	FADS2 OR FADS2D6.				
OS	Brachydanio rerio (Zebrafish) (Danio rerio).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;				
OX	Cyprinidae; Danio.				
NCBI	TaxID=7955;				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RX	MEDLINE=21592990; PubMed=11724940;				
RA	Hastings N., Agaba M., Tocher D.R., Leaver M.J., Dick J.R.,				
RA	Sargent J.R., Teale A.J.;				
RT	"A vertebrate fatty acid desaturase with deltas and deltas				
RT	activities."				
Proc. Natl. Acad. Sci. U.S.A.	98:14304-14309(2001).				
CC	-1- FUNCTION: Fatty acid desaturase with both delta-5 and delta-6				
CC	activities. May represent a component of the polyunsaturated fatty				
CC	acid biosynthesis pathway.				
CC	-1- PATHWAY: Polyunsaturated fatty acid biosynthesis.				
CC	-1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.				
CC	-1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
DR	EMBL: AF309556; AAC25710.1; -.				
DR	HSSP: P00173; JEX.				
DR	ZFIN: ZDB-GENE-011212-1; fads2.				
DR	InterPro: IPR001199; Cyt B5.				
DR	InterPro: IPR005804; FA_desat fam.				
DR	Pfam: PF00487; FA_desaturase; 1.				
DR	Pfam: PF00173; heme_1; 1.				
DR	Prodom: PD000612; Cyt_B5; 1.				
DR	Prodom: PD001081; FA_desat fam; 2.				
DR	PROSITE: PS00191; CYTOCHROME_B5_1; FALSE_NEG.				
DR	PROSITE: PS00255; CYTOCHROME_B5_2; 1.				
KW	Fatty acid biosynthesis; Oxidoreductase; Heme.				
FT	DOMAIN 18 95				
FT	DOMAIN 53 53				
FT	DOMAIN 76 76				
FT	METAL				
FT	SEQUENCE 444 AA; 52032 MW; 6AA25A1DCIDC0F65 CRC64;				
Query Match	16.8%; Score 424; DB 1; Length 444;				

CC	between the Swiss Institute of Bioinformatics and the EMBL outstation on its
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.ebi.ch/announcement/
CC	or send an email to licence@ebi.ac.uk).
CC	EMBL; L11421; AAA27286.1; -
DR	EMBL; D90914; BA18502.1; -
DR	InterPro; IPR005804; FA_desat_fam.
DR	Pfam; PF00487; FA_desaturase; 1.
DR	ProDom; PD001081; FA_desat_fam; 1.
KW	Oxidoreductase; Iron; Complete proteome.
SW	SEQUENCE 359 AA; 41425 MW; 33FB165AB9BC05F CRC64;
CC	Query Match 9.8%; Score 247.5; DB 1; Length 359;
CC	Best Local Similarity 23.9%; Pred. No. 5e-13;
CC	Matches 92; Conservative 57; Mismatches 137; Indels 99; Gaps 19;
OY	106 YRLLAQLSSA-----GLPFRVGTTPKVLVLAIVFLYALVYLACASAMAHLLAG--- 157
DB	15 FRRVLNQRVDAVFAHEGLTQRDHS-----MYLKTLLITVLMFSAMAFVLFAPVI 64
OY	158 ---GLISFPMIQ-----SGMGGDSGHHRTGHPVLDVRVVOVLSGNCGLGSLIAWKKCN 208
DB	65 FPRVLLGCMVLATLALAAFSFVGGHDANNAVSSNPHINRLGKMTYD--PVGLSFLMKRYR 122
OY	209 HN-THHIACSLSDH-----PDLQHNPLFAVSPKLFNGNIWSEYFQRTLAFDA 255
DB	123 HNVLHHTYNTLIGHDEVIHGDAVRMSPEQEHGIVYFQGFY---INGLY----- 169
OY	256 SKFTISQHTFFYVWCIAINLLAQSALVYLKRY-----PQLLEIAGVATFW 306
DB	170 --LPIPR-YWFLYDV-----YLVNKGKXNDHKIIPPOPLRLASLLGLTLW 213
OY	307 AMY-----PLVVA-SLPN--WMERYAVFLFSFTIGIQHVGFCLNHPESDYYVGPKG--- 356
DB	214 LGVYFGPLPAIGFSIPVLLIGASTYTTGIVCTI---FMLAHVLESTFELTPDQESG 269
OY	357 ---NDWEKQTAGTLDLDC-SPMWDMFHGGLQFQIEHNLPRRLRCHLRKARVAPVDLCK 412
DB	270 AIDDEMAICQRTTANPATNNPFWNFCGGLNQVTHLPRNCHIHVQLDENIKDVQC 329
OY	413 KHGLTYSA-ATFWGANVLTWKTLEA 436
DB	330 EFGVEKYKYPTEFKAALIASNYRMLEA 354
CC	RESULT 3
CC	NIA_VOLCA STANDARD; PRT; 864 AA.
CC	ID NIA_VOLCA STANDARD; PRT; 864 AA.
AC	P36841;
DT	01-JUN-1994 (Rel. 29, Created)
DT	01-JUN-1994 (Rel. 29, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Nitrate reductase [NADH] [EC 1.7.1.1] (NR).
GN	NITR.
OS	Volvox carteri.
OC	Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC	Eukaryota; Volvox.
OX	NCBI_TaxID=3067;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=f. Nagariensis / HK10;
RX	MEDLINE=93013022; PubMed=1396126;
RA	Gruber H., Goetnick S.D., Kirk D.L., Schmitt R.,
RT	"The nitrate reductase-encoding gene of Volvox carteri: map location,
RT	sequence and induction kinetics.";
RL	Gene 120;75-83(1992).
CC	-1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC	step of nitrate assimilation in plants, fungi and bacteria.
CC	-1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H2O = nitrate + NADH.
CC	-1- COPACTOR EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,

CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
 CC GROUP IS CALLED CYTOCHROME B-557.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- INDUCTION: By nitrate.
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 CC N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
 CC C-TERMINAL DOMAIN.
 CC -----
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 CC -----
 CC EMBL; X64136; CAA45497.1; -.
 CC PIR; JCI422; JCI422.
 CC HSP; P04166; 1B5M.
 CC InterPro: IPR001199; Cyt_B5.
 CC InterPro: IPR001834; Cyt_B5_reductase.
 CC InterPro: IPR000572; Bmk_Mb_oxred.
 CC InterPro: IPR001709; FPN_Cyt_reductase.
 CC InterPro: IPR005066; Mo-co_dimer.
 CC InterPro: IPR004433; Oxred_FAD/NAD(P).
 CC Pfam; PF00970; FAD_binding_6; 1.
 CC Pfam; PF00173; heme_1; 1.
 CC Pfam; PF03404; Mo-co_dimer; 1.
 CC Pfam; PF00175; NAD_binding_1; 1.
 CC Pfam; PF00174; oxidored_molyd; 1.
 CC PRINTS; PR00406; CYTBSRDTASE.
 CC PRINTS; PR00363; CYTOCHROMEBS..
 CC PRINTS; PR00407; EMOPTERIN..
 CC PRINTS; PR00371; FPNCR.
 CC ProDom; PD000612; Cyt_B5; 1.
 CC PROSITE; PS00191; CYTOCHROME_B5_1; 1.
 CC PROSITE; PS00191; CYTOCHROME_B5_2; 1.
 CC PROSITE; PS00559; MOLYBDOTERIN_EUK; 1.
 CC Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
 CC Nitrile assimilation.
 CC FT METAL 139 139 MOLYBDENUM-PTERIN (POTENTIAL).
 CC FT METAL 193 193 MOLYBDENUM-PTERIN (POTENTIAL).
 CC FT DISULFID 376 376 INTERCHAIN (POTENTIAL).
 CC FT METAL 532 532 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC FT METAL 555 555 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC SQ SEQUENCE 864 AA; 96402 MW; 499529652CDDIC7 CRC64;
 CC -----
 CC Query Match 7.4%; Score 185.5; DB 1; Length 864;
 CC Best Local Similarity 36.4%; Pred. No. 1.7e-07;
 CC Matches 48; Conservative 22; Mismatches 57; Indels 5; Gaps 3;
 CC
 CC QY 7 AMPAPGADAGA-GDVWISSKELRAHASADLWISISGDVYDVYTPMLPHHGGDLPLTLT 65
 CC Db 483 AARPVVAANAANGPRQYTMEEVAHNTBSCMFVHGCKYDAPYIDEPHGAESLIIV 542
 CC QY 66 AGQDADTAPAAVPPSARPLLRFFVGRLL--SDVAVSPASADYRRLIAQLSSAGLFERY- 122
 CC Db 543 AGADADTDEFNSIHSSKAKMLAQYIGDLVASKRAAGATVPBPQVASTSSDAVPLIV 602
 CC QY 123 -GPTKQVQLVM 133
 CC Db 603 LNPQKVKPLPI 614
 CC
 CC RESULT 4
 CC FD61_SQYBN STANDARD; PRT; 387 AA.
 CC AC P48650;
 CC DT 01-FEB-1996 (Rel. 33, Created)
 CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 1
 DE (EC 1.14.19.-).
 GN FAD2-1.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 ON NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Seed;
 RX MEDLINE=96151506; PubMed=8587990;
 RA Heppard E.P., Kinney A.J., Stecca K.L., Miao G.H.;
 RT Developmental and growth temperature regulation of two different
 RT microsomal omega-6 desaturase genes in soybeans.";
 RL Plant Physiol. 110:311-319(1996).
 CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
 CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
 CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN DEVELOPING SEEDS.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; I43920; AAB0859.1; -.
 CC PIR; T07687; T07687.
 CC InterPro: IPR005804; FA_desat_fam.
 CC Pfam; PF00487; FA_desaturase; 1.
 CC ProDom; PD001081; FA_desat_fam; 2.
 CC Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
 CC Transmembrane.
 CC FT TRANSMEM 54 74 POTENTIAL.
 CC FT TRANSMEM 87 107 POTENTIAL.
 CC FT TRANSMEM 121 141 POTENTIAL.
 CC FT TRANSMEM 183 203 POTENTIAL.
 CC FT TRANSMEM 227 247 POTENTIAL.
 CC FT TRANSMEM 251 271 POTENTIAL.
 CC FT DOMAIN 109 113 HISTIDINE BOX-1.
 CC FT DOMAIN 145 149 HISTIDINE BOX-2.
 CC FT DOMAIN 319 323 HISTIDINE BOX-3.
 CC SQ SEQUENCE 387 AA; 44662 MW; 49068805C2IALC31 CRC64;
 CC -----
 CC Query Match 7.3%; Score 183.5; DB 1; Length 387;
 CC Best Local Similarity 23.1%; Pred. No. 9.8e-08;
 CC Matches 96; Conservative 53; Mismatches 165; Indels 101; Gaps 22;
 CC
 CC QY 80 PSARPLLRFFVGRLLSDVAVSPASADYRRLIAQLSSAGLFERYGPPKYQLVMAVLFYA 139
 CC Db 30 PNTKP---PFTYGQLK--KAIRPHCFGRSLNLSFSIV-----YDLSFAIFPI 73
 CC QY 140 AL-----YLVLAASAMALLAGLIGFVWISQGMWGHDSGHRITGHPVLDVVQ 190
 CC Db 74 ATTYFHLPPPSLILMPITY--VLGGCLLTGVWV---IAHCGHARSKYQWVDVVG 127
 CC QY 191 VLSGNCLTGLSLAMWKCNTNTHIACNSIDHPDLOHMLFAVSPRL-----F 238
 CC Db 128 LTLHSTLL-VYPFSWKISHRHHSNTGSLDRD-----EVFVPKPSKVAMPSKYLNPL 180
 CC QY 239 GNWISYFQRT-----LAFDAASKFFISY-QHWTFYPMWCARIMLT--AQSALEFVLT 288

Db 181 GRAVSLVLTLLTGMPTLAFVNSGRPYDSFASHYHPAPYISNRERLLIYVSVALFSVT 240
 QY 289 EKRPVRLLEIAGVATWAWY--PLVVASLPMWNERAPFLFSFTICIGIHQFCINHS 346
 Db 241 YSV--YRVATLTKGLVWLLCYGVPLLVN-----GFLVTTIYVLOHTHPALPHYD 287
 QY 347 SDVYVGPKNQDNMFKEKOTAGTLDILCSPMMDW-----FHGQLQFOIENHLPRLPRCHL 400
 Db 288 SSSW-----DWL-KGALATMD-----RDYGLNVFHHIDTVAHHLFSTMPHYHA 333
 QY 401 RKVAPAVRDLCKHGLTYSATWGANVLTWKTLPAAALQARTATSGAPKPLVW 455
 Db 334 MEATNAIKPIGLEY-YQFDDTPEYKA--LMREARECLYV--EPDEGTSEKGYW 382

RESULT 5
 CY51_ARATH STANDARD; PRT; 134 AA.
 ID CY51_ARATH STANDARD; PRT; 134 AA.
 AC Q42342; Q9SB05;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5 isoform 1.
 GN AT5G53560 OR MNC6.10.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=99087071; PubMed=9880378;
 RA Fukuchi-Mizutani M., Mizutani M., Tanaka Y., Kusumi T., Ohta D.;
 RT "Microsomal electron transfer in higher plants: cloning and
 RT heterologous expression of NADH-cytochrome b5a reductase from
 RT Arabidopsis.";
 RL Plant Physiol. 119:353-361 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=99087489; PubMed=9872454;
 RA Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VII.
 RT Sequence features of the regions of 1,013,767 bp covered by sixteen
 RT physically assigned P1 and TAC clones.";
 RL DNA Res. 5:297-308 (1998).
 RN [3]
 RP SEQUENCE OF 1-113 FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Cooke R., Laurie M., Raynal M., Delseny M.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases (By similarity).
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC
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 CC
 CC EMBL: AB007801; BA74839.1; -
 CC EMBL: AB015476; BAB09732.1; -
 CC EMBL: F20001; CAA23377.1; -
 CC PIR: T52469; T52469.
 CC HSSP: P00171; IEHB.
 CC InterPro: IPR001199; Cyt_B5.

DR Pfam; PF00173; heme 1; 1.
 DR PRINTS: PR00363; CYTOCHROME5.
 DR PRODOM: PD000612; Cyt_B5; 1.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE: PS0255; CYTOCHROME_B5_2; 1.
 KW Electron transport; Transmembrane; Heme; Iron; Microsome;
 KW Multigene family.
 FT TRANSMEM 107 127 POTENTIAL.
 FT METAL 40 40 IRON (HEME AXIAL LIGAND) (By similarity).
 FT METAL 64 64 IRON (HEME AXIAL LIGAND) (By similarity).
 FT CONFLICT 1 3 MS -> AKA (IN REF. 3).
 SQ SEQUENCE 134 AA; 15084 MW; 9CC01C60FC7C873FD CRC64;
 Query Match 7.1%; Score 180; DB 1; Length 134;
 Best Local Similarity 39.6%; Pred. No. 5.5e-08;
 Matches 36; Conservative 21; Mismatches 32; Indels 2; Gaps 2;
 QY 17 AGDVPMISSKELRFAHSAADLWISIGDYVDYTPMLPHHGGDLPLTLAAGDADTAFV- 75
 Db 2 SDRKVLSPFEVSKNKTKDCWLLISGKYVDYTPMDHGGDEVLSTGKDATNDFED 61
 QY 76 AYHPSPARPLRFEPVGRUSDVAVSPASADY 106
 Db 62 VGHSDTARDMDKCYFGEIDSSSV-PATRY 91

RESULT 6
 CYB5_TOBAC STANDARD; PRT; 136 AA.
 ID CYB5_TOBAC STANDARD; PRT; 136 AA.
 AC P49098;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
 NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RX MEDLINE=94325476; PubMed=8049375;
 RA Smith M.A., Stobart A.K., Shewry P.R., Nadler J.A.;
 RT "Tobacco cytochrome b5: cDNA isolation, expression analysis and in
 RT vitro protein targeting.";
 RL Plant Mol. Biol. 25:527-537 (1994).
 CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
 CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
 CC OXYGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY
 CC DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH IN
 CC THE DEVELOPING SEED IS UTILIZED FOR MEMBRANE SYNTHESIS AND IN THE
 CC DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE
 CC LIPIDS. IS INVOLVED IN THE REDUCTION OF CYTOCHROME P-450 AND
 CC MAY THEREFORE BE INVOLVED IN FLAVONOID BIOSYNTHESIS IN THE PETALS.
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (By similarity).
 CC -1- TISSUE SPECIFICITY: IS HIGHLY EXPRESSED IN DEVELOPING SEEDS,
 CC MODERATELY EXPRESSED IN FLOWERS, AND IS EXPRESSED AT LOW
 CC LEVELS IN THE LEAF.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC
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 CC
 CC EMBL: X71441; CAA50575.1; ALT_INIT.
 CC EMBL: X68140; CAA48240.1; -
 CC HSSP: P04166; 1BSM.

DR InterPro; IPR001199; Cyt_B5.
 DR Pfam; PF00173; heme 1; 1.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
 DR Electron transport; Transmembrane; Heme; Iron; Microsome;
 KW Multigene family.
 FT TRANSMEM 107 127 POTENTIAL.
 FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT CONFLICT 10 11 LA -> EF (IN REF. 1; CAA48240).
 FT CONFLICT 105 105 MISSING (IN REF. 1; CAA48240).
 SQ SEQUENCE 136 AA; 14979 MW; DACE9AE695B2835F CRC64;
 Query Match 7.1%; Score 180; DB 1; Length 136;
 Best Local Similarity 43.3%; Pred. No. 5.6e-08;
 Matches 39; Conservative 14; Mismatches 35; Indels 2; Gaps 2;
 QY 18 GDVWMSKELRAHASADLMTISGDYDVTPLPHHPCGDLPLTLTGADATDAFA-A 76
 DB 3 GERTKFTLAEVSGHNAKCMVLISGRVYDTKFDHDPGDEVLSATGKATIDFEDV 62
 QY 77 YHPSAPPLRRFFVGRSLSDVAVSPASADY 106
 DB 63 GHSSSARAMLDEYVGDVDSATIPRTKTY 91
 RESULT 7
 ID NIA_BEABA STANDARD; PRT; 894 AA.
 AC P43100;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Nitrate reductase [NADPH] (EC 1.7.1.3) (NR).
 GN NIA.
 OS Beauveria bassiana (Trichothium shioteae).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Cordyceps.
 OX NCBI_TaxId=176275;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=BB147;
 RA Maurer P.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
 CC step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NADP(+) + H(2)O = nitrate + NADPH.
 CC -1- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
 CC AND ONE MOLYBDENUM ATOM.
 CC -1- SUBUNIT: Homodimer (by similarity).
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 CC N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
 CC C-TERMINAL DOMAIN.
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 CC -----
 CC EMBL; X84950; CAA59336.1; -
 CC PIR; S52857; S52857.
 CC HSSP; P04166; 1EUE.
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR001834; Cyt_B5_reductase.
 DR InterPro; IPR000572; Bux_Mb_oxred.
 DR InterPro; IPR001709; FPN_Cyt_reductase.
 DR InterPro; IPR005066; Mo-co_dimer.

DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00970; FAD binding_6; 1.
 DR Pfam; PF00173; heme 1; 1.
 DR Pfam; PF03404; Mo-co_dimer; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR Pfam; PF00174; oxidored_molyb; 1.
 DR PRINTS; PR00406; CYTB5RDTASE.
 DR PRINTS; PR00363; CYTOCHROME_B5.
 DR PRINTS; PR00407; EUMOPTERIN.
 DR PRINTS; PR00371; FPNCR.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE; PS0255; CYTOCHROME_B5_2; 1.
 DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
 KW Oxidoreductase; Flavoprotein; FAD; NADP; Heme; Molybdenum;
 KW Nitrate assimilation.
 FT METAL 169 169 MOLYBDENUM-PTERIN (POTENTIAL).
 FT METAL 220 220 MOLYBDENUM-PTERIN (POTENTIAL).
 FT DISULFID 418 418 INTERCHAIN (POTENTIAL).
 FT METAL 570 570 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 593 593 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 894 AA; 99934 MW; D0ED234BF1B1322B CRC64;
 Query Match 7.1%; Score 178.5; DB 1; Length 894;
 Best Local Similarity 36.3%; Pred. No. 6.7e-07;
 Matches 37; Conservative 21; Mismatches 35; Indels 9; Gaps 1;
 QY 20 VWMISKELRAHASADLMTISGDYDVTPLPHHPCGDLPLTLTGADATDAFAAHP 79
 DB 535 VVILSLEELKAHEGMEFWFVNGHYVNGTPLYLDHPCGATSIINAAQDATEEFWTIHS 594
 QY 80 PSAPPLRRFFVGRSLSDVAVSPASADYRRLAQQ 112
 DB 595 ENAKAMPQYHIGTLNDAARKALBGSABESPASDPTRAVFLQ 636
 RESULT 8
 ID NIA_FUSOX STANDARD; PRT; 905 AA.
 AC P39863;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Nitrate reductase [NADPH] (EC 1.7.1.3) (NR).
 GN NIA.
 OS Fusarium oxysporum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
 OX NCBI_TaxId=5507;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=FOM24;
 RX MEDLINE=93380674; PubMed=8370541;
 RA Dolez A., Langin T., Gerlinger C., Brygoo Y., Daboussi M.-J.;
 RT "The nia gene of Fusarium oxysporum: isolation, sequence and
 RT development of a homologous transformation system".
 RL Gene 131:61-67(1993).
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
 CC step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NADP(+) + H(2)O = nitrate + NADPH.
 CC -1- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
 CC AND ONE MOLYBDENUM ATOM.
 CC -1- SUBUNIT: Homodimer (by similarity).
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 CC N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
 CC C-TERMINAL DOMAIN.
 CC -----
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DR EMBL; Z22549; CA90270.1; -
 DR PIR; JN0803; JN0803.
 DR HSSP; P04166; 1EUE.
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR001834; Cyt_B5_reductase.
 DR InterPro; IPR000572; Bk_Mb_oxired.
 DR InterPro; IPR001709; FFW_Cyt_redctase.
 DR InterPro; IPR005066; Mo-co_dimer.
 DR InterPro; IPR001433; Oxired_FAD/NAD(P).
 DR Pfam; PF00970; FAD binding_6; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR Pfam; PF03404; Mo-co_dimer; 1.
 DR Pfam; PF00175; NAD binding_1; 1.
 DR Pfam; PF00174; oxidored_molyp; 1.
 DR PRINTS; PR00406; CYTB5RDTASE.
 DR PRINTS; PR00363; CYTOCHROME B5.
 DR PRINTS; PR00407; EUMOPTERIN.
 DR PRINTS; PR00371; FENCR.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME B5_2; 1.
 DR PROSITE; PS00559; MOLYBDOTERIN_EUK; 1.
 DR Oxidoreductase; Flavoprotein; FAD; NADP; Heme; Molybdenum;
 KM Nitrate assimilation.
 FT DOMAIN 3
 FT METAL 179 179 POLY-THR.
 FT METAL 230 230 MOLYBDENUM-PTERIN (POTENTIAL).
 FT DISULFID 428 428 MOLYBDENUM-PTERIN (POTENTIAL).
 FT DOMAIN 550 620 INTERCHAIN (POTENTIAL).
 FT METAL 581 581 HEME-BINDING (BY SIMILARITY).
 FT METAL 604 604 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 604 604 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT DOMAIN 645 905 FLAVIN-BINDING DOMAIN (BY SIMILARITY).
 FT NP BIND 875 884 NADP (BY SIMILARITY).
 SQ SEQUENCE 905 AA; 101898 MW; D5DBE23F7971ACDA CRC64;

Query Match 7.0%; Score 176.5; DB 1; Length 905;
 Best Local Similarity 31.4%; Pred. No. 9.9e-07;
 Matches 36; Conservative 26; Mismatches 44; Indels 13; Gaps 2;

QY 21 RMISSEKELRAHNSADDLWISGSDVYDTPMLPHHPCGDDPLTLTGADATDAFAAHP 80
 DB 547 RKITIELKHAHSGEPEFVVKGEVYDCTPLSGHGAASIFGAAGDADIEEFMAHSE 606

QY 81 SARPLRRFVGRSLDYAVSPASADYR-----LLAQLSSAGLPER--VGPTPK 127
 DB 607 NAKAMLPYHIGTDESRAILSGDATKTNDDADREVFLOAKTKSKALIDKTSISPTK 666

QY 128 V 128
 DB 667 I 667

RESULT 9
 CYB5_BRAOL STANDARD; PRT; 134 AA.
 ID CYB5_BRAOL
 AC P40934;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cytochrome B5.
 GN CYB5.
 OS Brassica oleracea (Cauliflower).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC Eusteroideae; Brassicales; Brassicaceae; Brassica.
 CC NCBI_TaxID=3712;
 RN [1]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 6-47 AND 75-89.
 RC STRAIN=cv. Cauliflora;

RA Kearns E.V., Kack P., Somerville C.R.;
 RT "Nucleotide sequence of cDNA for cytochrome b5 from cauliflower
 RT (Brassica oleracea L.).";
 RL Plant Physiol. 99:1254-1257(1992).

CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases.
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

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DR EMBL; M87514; AAA32990.1; -
 DR PIR; T14454; T14454.
 DR HSSP; P00171; 1EHB.
 DR InterPro; IPR001199; Cyt_B5.
 DR Pfam; PF00173; heme_1; 1.
 DR PRINTS; PR00363; CYTOCHROME B5.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME B5_2; 1.
 DR Electron transport; Transmembrane; Heme; Iron; Microsome.
 KM TRANSMEM 107 127 POTENTIAL.
 FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT VARIANT 5 5 K -> N.
 SQ SEQUENCE 134 AA; 15062 MW; 764DC24A4CDD591 CRC64;

Query Match 6.9%; Score 175; DB 1; Length 134;
 Best Local Similarity 37.4%; Pred. No. 1.4e-07;
 Matches 34; Conservative 22; Mismatches 33; Indels 2; Gaps 2;

QY 17 AGDVRMISSEKELRAHNSADDLWISGSDVYDTPMLPHHPCGDDPLTLTGADATDAFA- 75
 DB 2 ASKKVGLGFEVEVSQHNKTKDCLWILISGKYDVPFMDHFGGDEVLISSTGKATNDPFD 61

QY 76 AVHPSARPLRRFVGRSLDYAVSPASADY 106
 DB 62 VGHSDTARDMEKXYIGET-DSSTVPRATRY 91

RESULT 10
 NIA_CHLVU STANDARD; PRT; 318 AA.
 ID NIA_CHLVU
 AC G01170;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR) (Fragment).
 OS Chlorella vulgaris.
 CC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
 CC Chlorellaceae; Chlorella.
 CC NCBI_TaxID=3077;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91354204; PubMed=188330;
 RA Cannons A.C., Tida N., Solomonson L.P.;
 RT "Expression of a cDNA clone encoding the haem-binding domain of
 RT Chlorella nitrate reductase.";
 RL Biochem. J. 278:203-209(1991).
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
 CC step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
 CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
 CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
 CC GROUP IS CALLED CYTOCHROME B-557.
 CC -1- SUBUNIT: Homodimer.

CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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CC -----
CC EMBL: X56771; CAA40090.1; -
CC PIR: S17197; S17197.
CC HSSP: P04166; 1BSW.
CC InterPro: IPR001199; Cyt_B5.
CC InterPro: IPR000572; Euk_Mb_oxred.
CC InterPro: IPR005066; Mo-co_dimer.
CC Pfam: PF00173; heme_1; 1.
CC Pfam: PF03404; Mo-co_dimer; 1.
CC PRINTS: PR00363; CYTOCHROMEBS.
CC PRINTS: PR00407; EUMOPTERIN.
CC ProDom: PD000612; Cyt_B5; 1.
CC PROSITE: PS00191; CYTOCHROME_B5_1; 1.
CC PROSITE: PS00255; CYTOCHROME_B5_2; 1.
CC PROSITE: PS00559; MOLYBDOPTERIN_EUK; PARTIAL.
CC Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
CC Nitrate assimilation.
CC FT METAL 251 251 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC FT METAL 274 274 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC FT NON_TER 318 318
CC SQ SEQUENCE 318 AA; 34830 MW; E60D82FE1E98292A CRC64;
Query Match 6.8%; Score 172.5; DB 1; Length 318;
Best Local Similarity 36.5%; Pred. No. 6,2e-07;
Matches 38; Conservative 17; Mismatches 38; Indels 11; Gaps 3;
QY 2 PRSDAMPAPGAGAGDVAMISSKELRAHASADLMISGVDYDTPMLPHHGGADLP 61
DB 209 PP-----PAP---AGA---KSFTMAVEHTHTWESAMFVVDGKYDAPFLKDHPCGADS 257
QY 62 LLTLAGODATDAFAAHPPSARPLRRFFVGRISDVAVSPASAD 105
DB 258 ILVAGIDATDEFNAHSLKAKKQLLEYIIGELAEBCQEAASD 301
RESULT 11
NIA7_HORVU STANDARD; PRT; 891 AA.
ID NIA7_HORVU STANDARD; PRT; 891 AA.
AC P27968;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NAD(P)H] (EC 1.7.1.2).
GN NAR-7.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OC NCBI_TaxID=4513;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Himalaya;
RX MEDLINE=91375416; PubMed=1896007;
RA Miyazaki J., Juricek M., Angelis K., Schnorr K.M., Kleinholz A.,
RT Warner R.L.;
RT Characterization and sequence of a novel nitrate reductase from
RL Mol. Gen. Genet. 228:329-334(1991).
-1- FUNCTION: Nitrate reductase is a key enzyme involved in the first

CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(P)(+) + H(2)O = nitrate +
CC NAD(P)H.
CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
CC GROUP IS CALLED CYTOCHROME B-557.
CC -1- SUBUNIT: Homodimer.
CC -1- INDUCTION: By nitrate.
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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CC -----
CC EMBL: X60173; CAA42739.1; -
CC PIR: S16895; RDBHNP.
CC HSSP: P15711; 2CND.
CC InterPro: IPR001199; Cyt_B5.
CC InterPro: IPR001834; Cyt_B5_reductase.
CC InterPro: IPR000572; Euk_Mb_oxred.
CC InterPro: IPR001709; FPN_cyt_redctse.
CC InterPro: IPR005066; Mo-co_dimer.
CC InterPro: IPR001433; Oxred_FAD/NAD(P).
CC InterPro: IPR001221; Phe_hydroxylase.
CC Pfam: PF00970; FAD_binding_6; 1.
CC Pfam: PF00173; heme_1; 1.
CC Pfam: PF03404; Mo-co_dimer; 1.
CC Pfam: PF00175; NAD binding_1; 1.
CC Pfam: PF00174; oxidored_molyb_1.
CC PRINTS: PR00406; CYTB5RDYASE.
CC PRINTS: PR00363; CYTOCHROMEBS.
CC PRINTS: PR00407; EUMOPTERIN.
CC PRINTS: PR00371; PPNCR.
CC PRINTS: PR00410; PHEHYDRXKLASE.
CC ProDom: PD000612; Cyt_B5; 1.
CC PROSITE: PS00191; CYTOCHROME_B5_1; 1.
CC PROSITE: PS00255; CYTOCHROME_B5_2; 1.
CC PROSITE: PS00559; MOLYBDOPTERIN_EUK; 1.
CC Oxidoreductase; Flavoprotein; FAD; NAD; NADP; Heme; Molybdenum;
CC Nitrate assimilation; Multigene family.
CC FT METAL 168 168 MOLYBDENUM-PTERIN (POTENTIAL).
CC FT METAL 221 221 MOLYBDENUM-PTERIN (POTENTIAL).
CC FT DISULFID 406 406 INTERCHAIN (POTENTIAL).
CC FT METAL 550 550 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC FT METAL 573 573 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC SQ SEQUENCE 891 AA; 98630 MW; AA47EC52FC1EFD13 CRC64;
Query Match 6.7%; Score 170; DB 1; Length 891;
Best Local Similarity 44.6%; Pred. No. 3.3e-06;
Matches 37; Conservative 10; Mismatches 32; Indels 4; Gaps 1;
QY 27 ELRAVASADLMISGVDYDTPMLPHHGGADLP LTLAAGDADTDAFAAHPPSARPL 86
DB 522 EVRRHASKDSAMIVVGHVYDCTAFLKDHPCGADSLINAGSDCTEEFPAIHSAKRGLL 581
QY 87 RRFVGR L-----SDYAVSPASAD 105
DB 582 EMYRVGELIVTNDYSPSSNAD 604
RESULT 12
NIA1_TOBAC STANDARD; PRT; 904 AA.
ID NIA1_TOBAC STANDARD; PRT; 904 AA.
AC P1605;
DT 01-OCT-1989 (Rel. 12, Created)

DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS00255; CYTOCHROME B5_2; 1.
 DR PROSITE; PS00559; MOLYBDOTERIN EUK; 1.
 KM Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
 Nitrate assimilation; Multigene family;
 FT METAL 191 191 MOLYBDENUM-PTERIN (POTENTIAL).
 FT METAL 245 245 MOLYBDENUM-PTERIN (POTENTIAL).
 FT DISULFID 430 430 INTERCHAIN (POTENTIAL).
 FT METAL 574 574 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 597 597 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 911 AA; 102253 MW; BBA4E19635B03D8C CRC64;
 Query Match 6.7%; Score 169.5; DB 1; Length 911;
 Best Local Similarity 34.7%; Pred. No. 3.7e-06;
 Matches 41; Conservative 17; Mismatches 47; Indels 13; Gaps 3;
 DB 540 KMSMEVRKGNHSAESAMITVHGHIYDCTFLKDHFGSGSITILNMGDTSEFEFAIHS 599
 QY 21 RMSSSELRHAAADLMISGDVDTVFWLPHHFGDLPLTLGQATDPAAYVHP 80
 DB 540 KMSMEVRKGNHSAESAMITVHGHIYDCTFLKDHFGSGSITILNMGDTSEFEFAIHS 599
 QY 81 SARPRLRFVGRRL--SDYAVSP-----ASADYRRLIAQLQSAGLPERVGPTEKQLV 131
 DB 600 KAKKLIEDYRIGELITTTGYDSFNVSVHGSSVMSLAPI-----RQLAPYKIALV 651
 RESULT 14
 FD6C ARATH STANDARD; PRT; 448 AA.
 AC P46312; O9M094; 32, Created)
 DT 01-NOV-1995 (Rel. 16-OCT-2001 (Rel. 41, last sequence update)
 DT 28-FEB-2003 (Rel. 41, last annotation update)
 DE Omega-6 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).
 GN FAD6 OR FAD6 OR ATG30950 OR F6118.140.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxId=3702;
 RN (1)
 RP SEQUENCE OF 1-418 FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=95148736; PubMed=7846158;
 RA Falcone D.L., Gibson S., Lemieux B., Somerville C.R.;
 RT "Identification of a gene that complements an Arabidopsis mutant
 RT deficient in chloroplast omega 6 desaturase activity.";
 RL Plant Physiol. 106:1453-1459(1994).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wandutt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
 RA Harris B., Anstorge W., Brandt P., Grivell L., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
 RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
 RA Reichert B., Portelelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hohnsbeil U., Zimmermann W., Weiler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
 RA Van der Schuren J., Grymoprez B., Chuang Y.-J., Vandenbussche F.,
 RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Weitsengger T., Bothe G., Rampersger U., Hilbert H., Brann M.,
 RA Holzner E., Brandt A., Peters S., van Staveren M., Dirke W.,
 RA Moolman P., Klein Lankhorst R., Rose W., Haut J., Koeltter P.,
 RA Bernieris S., Hempel S., Feldpausch M., Lambersch S., Van den Daele H.,
 RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Leonard N., Mcclay K., Mayes R.,
 RA Pettit A., Rajandream M.A., Lyne M., Bens V., Reichmann S.,
 RA Borkova D., Blocher H., Scharte M., Grimm M., Loehner T.-H.,
 RA Dose S., De Haan M., Maarse A., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Partmann B., Grandenath K., Dauner D., Herzi A.,
 RA Neumann S., Argiriou A., Vitale D., Ligouri R., Piravandi E.,

MASSNET O., Quigley F., Clabaud G., Muendlein A., Felber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lechman A., Aubourg S.,
 RA Chefor F., Cooke R., Berger C., Monfort A., Caasaburga E.,
 RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacón D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bietke C.,
 RA Fishman D., Haase D., Lemcke K., Mewes H.-W., Stoeck S.,
 RA Zaccaria P., Bavan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dehla N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Shee P., Cordes M., Abu-Threiden U.,
 RA Steneking T., Kallick J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Min P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramar J., Fulton L., Mardie E., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Splich J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Bergoff A., Jones K., Drome K., Cotton M., Joshi C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamer B., Yordan C.,
 RA Ma P., Zhong Y., Preston R., Vill D., Shekher M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
 RA Granat S., Shohdy N., Haegawa A., Hameed A., Lodhi M., Johnson A.,
 RA Chen E., Marra M., Martienssen R., McCombie W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 402:769-777(1999).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinzaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 RT SSP consortium (Salk/Stanford/PDEC)."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBS databases.
 CC -1- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE. INTRODUCES
 CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
 CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST. MEMBRANE-BOUND (PROBABLY).
 CC -1- DEVELOPMENTAL STAGE: HIGHEST LEVELS FOUND IN EXPANDING LEAVES.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 CC
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 CC
 CC EMBL; U09503; AAA92800.1; -
 CC EMBL; AL022198; CA18198.1; -
 CC EMBL; AL161578; CAB79813.1; -
 CC EMBL; AY045621; AAK73979.1; -
 CC EMBL; AY058078; AAL24186.1; -
 CC EMBL; AY058852; AAL24240.1; -
 CC EMBL; AY058852; AAL24240.1; -
 CC PIR; D85362; D85362.
 CC InterPro; IPR005804; FA desat fam.
 CC Pfam; PF00487; FA desaturase; 1.
 CC Prodom; PD001081; FA desat fam; 2.
 DR Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
 KM Transist peptide.
 FT TRANSIT 1 69 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 70 448 OMEGA-6 FATTY ACID DESATURASE.
 FT DOMAIN 171 175 HISTIDINE BOX-1.
 FT DOMAIN 207 211 HISTIDINE BOX-2.
 FT DOMAIN 367 371 HISTIDINE BOX-3.
 SQ SEQUENCE 448 AA; 51225 MW; C3AC72PB28F8287 CRC64;
 Query Match 6.7%; Score 169.5; DB 1; Length 448;
 Best Local Similarity 21.8%; Pred. No. 2e-06;
 Matches 87; Conservative 64; Mismatches 140; Indels 109; Gaps 22;

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QY 84 PLTRFFVGRLLSDYA--VSPADYRRLAQLSSAGLFEERV-----PTPK 127
DB 59 PVKRR--IGCIKAVAPAPPSADSDREQLAESYFROIGEDLPENNTLKDIMTLPK 116
QY 128 -----VOLVMAVLEFYAALVYLVLACASAMHLLAGLIGFWVIOGSM-----M 170
DB 117 EVEIEDLKLKSLVLSVTSY-FLGLFMIAKSPVY-----LLPLAAMTGTATIGPFVI 169
QY 171 GHDSGHHRIIGHVLDRLVNOVLSGNCITGSIAM-----KCNTHHIIACNSLDHDDLQ 226
DB 170 GHDCAKHSFKGNLVEDIV-----GTLAFLPLVYPYEPMPFKIDRHAKTNMIVHDPAWQ 224
QY 227 HMLPFAVSPCLFGNMSYFQRTIAPD--AAKFFISYQHTFYPVWCITARIINLAQSLF 285
DB 225 PIV-----PEEFS--SPVKKAIIFGYPGRIPRLSLAHVNM-----HPLKKPRA-- 269
QY 286 VLTEKVPORLLIAGVATFWA--WYPLLV--ASLPNM-----WERVAFVLSFTICG1 335
DB 270 -----SEVNRVKISILACVFAFMAVGMPLIVYKVGILGVKFMPLMPLGXYHFMGSTFTM--- 332
QY 336 QHVQCLNHESSDYVGPFGKNDW--PEKQTAGTLDILCSPPMDWFGGLQFOIENHLP 393
DB 323 -----VHHTAPRIPEKP--ADEMNAAQAOQINGTVHCDYPSWTEILCHDINVHI PHRIISP 374
QY 394 RLPRCHLRKVAAPAVRDLCCKGGLTYSATFWG--ANVLTM 431
DB 375 RIPSYNLRRAHESIQE-----NMGKTYLATM 401

RESULT 15
NIA2_TOBAC STANDARD; PRT; 904 AA.
ID NIA2_TOBAC STANDARD; PRT; 904 AA.
AC P08509;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] 2 (EC 1.7.1.1) (NR2).
GN NIA2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_Taxid=4097;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=cv. Xanthi; TISSUE=Leaf;
RA Vaucheret H., Kronenberger J., Rouze P., Caboche M.;
RT "Complete nucleotide sequence of the two homologous tobacco nitrate
RT reductase genes.";
RT plant Mol. Biol. 12:597-600(1989).
RN [2]
RP SEQUENCE OF 171-724 FROM N.A.
RA Calza R., Huttner E., Vincentz M., Rouze P., Galangau F.,
RA Vaucheret H., Chereil I., Meyer C., Kronenberger J., Caboche M.;
RT "Cloning of DNA fragments complementary to tobacco nitrate reductase
RT mRNA and encoding epitopes common to the nitrate reductases from
RT higher plants.";
RN Mol. Gen. Genet. 209:552-562(1987).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
CC GROUP IS CALLED CYTOCHROME B-557.
CC -1- ENZYME REGULATION: REGULATED BY THE NITROGEN SOURCE AND CONTROLLED
CC BY THE CIRCADIAN RHYTHM.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.

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CC between the Swiss Institute of Bioinformatics and the EMBL, outstation -
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CC or send an email to license@sb-sib.ch).
CC -----
CC EMBL: X14059; CA32217.1; -.
CC EMBL: X06134; CA29497.1; -.
CC PIR: S04839; RDNTNS.
CC HSSP: P17571; 2CND.
CC DR InterPro: IPR001189; Cyt B5.
CC DR InterPro: IPR001834; Cyt B5.
CC DR InterPro: IPR000572; Euk_Mb_oxred.
CC DR InterPro: IPR001709; FPN_cyt_redctase.
CC DR InterPro: IPR005066; Mo-co_dimer.
CC DR pfam: PF00970; FAD_binding_6; 1.
CC DR pfam: PF00173; heme_1; 1.
CC DR pfam: PF03404; Mo-co_dimer; 1.
CC DR pfam: PF00175; NAD_binding_1; 1.
CC DR pfam: PF00174; oxidored_molyb; 1.
CC DR PRINTS: PR00406; CYTB5RDYASE.
CC DR PRINTS: PR00363; CYTOCHROME5.
CC DR PRINTS: PR00407; EUMOPTERIN.
CC DR PRINTS: PR00371; FPNCR.
CC DR ProDom: PD000612; Cyt_B5; 1.
CC DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
CC DR PROSITE: PS0255; CYTOCHROME_B5_2; 1.
CC DR PROSITE: PS00559; MOLYBDOPTERIN_EUK; 1.
CC KW Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
CC Nitrate assimilation; Multigene family;
CC FT METAL 183
CC FT METAL 237
CC FT DISULFID 422
CC FT METAL 566
CC FT METAL 589
CC SQ SEQUENCE 904 AA; 101957 MW; 75196875A3561D69 CRC64;

Query Match 6.6%; Score 167; DB 1; Length 904;
Best local Similarity 44.6%; Pred. No. 5.9e-06;
Matches 33; Conservative 10; Mismatches 31; Indels 0; Gaps 0;

QY 21 RMSSKELRAHASADLWISGSDYDVTPMLPHNGGDLPLTLTAGQATDAFAAYHP 80
DB 532 KMTSMSEVKHSSADSDAWITVGHIVDTRFLNDHGGTDSILINAGTCTEERFAIHS 591
QY 81 SARPLRRFFVGRLL 94
DB 592 KAKKLEDFRIGEL 605

```

Search completed: January 1, 2004, 06:30:54
 Job time : 11.1656 sec

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 41.465 Seconds
(without alignments)
2875.205 Million cell updates/sec

Title: US-09-857-524B-4
Perfect score: 2521
Sequence: 1 MPPSYDAMPAPGDAGAGDV.....TATSGAPKLVWEAVNTHG 462

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2061	81.8	469	10 Q92T08	Q92T08 triticum ae
2	1500.5	59.5	446	10 Q92T09	Q92T09 rictinus com
3	1457	57.8	448	10 Q8VZ22	Q8VZ22 echium gent
4	1443	57.2	448	10 Q8VZ21	Q8VZ21 echium pita
5	1429	56.7	449	10 Q92R08	Q92R08 brassica na
6	1427.5	56.6	458	10 Q92R08	Q92R08 brassica na
7	1424.5	56.5	446	10 Q92R08	Q92R08 brassica na
8	1393	55.3	448	10 Q92R08	Q92R08 brassica na
9	1392	55.2	448	10 Q92R08	Q92R08 brassica na
10	1387	54.8	449	10 Q92R08	Q92R08 brassica na
11	1382	54.8	449	10 Q92R08	Q92R08 brassica na
12	1363.5	54.1	446	10 Q92R08	Q92R08 brassica na
13	1340	53.2	448	10 Q92R08	Q92R08 brassica na
14	738	29.3	523	3 Q9HDG8	Q9HDG8 mucor rouxi
15	620	24.6	568	3 Q8NKG9	Q8NKG9 saccharomyc
16	612	24.3	459	10 Q944W4	Q944W4 psidium ltr

17	605.5	24.0	573	3 Q8NKG8	Q8NKG8 kluyveromyc
18	564.5	22.4	483	10 Q9LENO	Q9LENO ceratodon p
19	552	21.9	520	10 Q9LENO	Q9LENO ceratodon p
20	536	21.3	457	3 Q8X173	Q8X173 mortierella
21	535	21.2	457	3 Q9UVY3	Q9UVY3 mortierella
22	535	21.2	477	10 Q8RXB0	Q8RXB0 phaeodactyl
23	532	21.1	457	3 Q9HEV1	Q9HEV1 mortierella
24	532	21.1	457	3 Q8X174	Q8X174 mortierella
25	523	20.7	457	3 Q9UVV3	Q9UVV3 mortierella
26	521	20.7	457	3 Q9HEV4	Q9HEV4 mortierella
27	506.5	20.1	467	3 Q96VC3	Q96VC3 mucor circi
28	495.5	19.7	525	10 Q92NM2	Q92NM2 physcomitri
29	462.5	18.3	443	5 Q61388	Q61388 caenorhabdi
30	461.5	18.3	443	5 Q23221	Q23221 caenorhabdi
31	437	17.3	452	13 Q8UMM5	Q8UMM5 oncorhynch
32	435	17.3	357	3 Q9HDF4	Q9HDF4 mortierella
33	433	17.2	454	13 Q98SW7	Q98SW7 oncorhynch
34	431.5	17.1	445	4 Q9Y5Q0	Q9Y5Q0 homo sapien
35	431.5	17.1	445	13 Q8AY64	Q8AY64 sparus aura
36	429	17.0	454	13 Q90ZEB	Q90ZEB oncorhynch
37	425	16.9	454	13 Q8QGE2	Q8QGE2 salmo salar
38	414.5	16.4	444	4 Q96T10	Q96T10 homo sapien
39	414	16.4	501	4 Q8NCG0	Q8NCG0 homo sapien
40	413.5	16.4	449	11 Q9JUE7	Q9JUE7 mus musculu
41	413.5	16.4	449	11 Q8K1P9	Q8K1P9 rattus norv
42	413	16.4	444	4 Q96T13	Q96T13 homo sapien
43	412.5	16.4	449	11 Q8CDZ4	Q8CDZ4 mus musculu
44	412.5	16.4	449	11 Q8C4Y5	Q8C4Y5 mus musculu
45	412	16.3	444	4 Q60427	Q60427 homo sapien

ALIGNMENTS

RESULT 1	ID	Q92T08	PRELIMINARY;	PRT;	469 AA.
AC	Q92T08	01-MAY-1999 (TREMREL. 10, Created)			
DT	01-MAY-1999 (TREMREL. 10, Last sequence update)				
DT	01-MAR-2003 (TREMREL. 23, Last annotation update)				
DE	S276.				
GN	S276.				
OS	Triticum aestivum (wheat).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;				
OC	Triticaceae; Triticum.				
OX	NCBI_TaxID=4565;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=cv. ET3;				
RA	Delhalize E., Hebb D.M., Gardner R.C., Richards K.D.;				
RT	"Aluminum tolerance in yeast conferred by over-expression of wheat				
RT	genes."				
RL	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.				
CC	-I- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.				
DR	EMBL; AF031194; AAD10250.1; -.				
DR	HSSP; P00171; 115U.				
DR	InterPro; IPR001199; Cyt B5.				
DR	InterPro; IPR005804; FA_desat fam.				
DR	InterPro; IPR001092; HLI_bact.				
DR	Pfam; PF00487; FA_desaturase; 1.				
DR	Pfam; PF00173; heme_1; 1.				
DR	PRINTS; PR001363; CYTOCHROME B5.				
DR	ProDom; PD000612; Cyt B5; 1.				
DR	ProDom; PD001081; FA_desat fam; 1.				
DR	PROSITE; PS00255; CYTOCHROME_B5_2; 1.				
DR	PROSITE; PS00038; HLI_1; 1.				
KW	Heme.				
SQ	SEQUENCE 469 AA; 52617 MW; 16F223CC1F79740D CRC64;				
Query Match	81.8%; Score 2061; DB 10; Length 469;				
Best Local Similarity	80.7%; Pred. No. 5.8e-169;				

Matches	371; Conservative	36; Mismatches	51; Indels	2; Gaps	1
Qy	3	PSVAMPAFGDAAGDYRMISSEKRLAAASADLDLMISGIVYDTWPLPHNPGGDLPL	62		
Db	12	PEADMPAA--SKDAADVRMISTKELQAAADADLMISGIVYDTWPLPHNPGGEEVPL	69		
Qy	63	LTLGQADATDAFAAYTHPPSARPLRRFFGVGRISDPAVSPASADYRRLLAQLSSAGLFEVY	122		
Db	70	ITLGGQADATDAFMAVTHPPSVRPLRRFFGVGRITDTPVPASADFRLLLAQLSSAGLFEVY	129		
Qy	123	GPTPEVQVLVMAVLYFVLAALYLVLACASAMAHLLAGLIGFWITQSGMGHDSGHHRIYTH	182		
Db	130	GHTPEFLLLVAMSVLFECIALYCVLACSSGGAHMFAGLIGFWITQSGMGHDSGHHQOITIH	189		
Qy	183	PVLDERVVOVLSCNCLCTGASIAWKNHNTHTHACNSLDHPDPLQHPPLPAVSPKLFGNTH	242		
Db	190	PALNRLLQVNVSGNCLCTGIGIAWKNHNTHTHSCNSLDHPDPLQHPPLPAVSTKLFENLIM	249		
Qy	243	SYEFORTLAFDAASKFPTISYQHWTFYPMWCARINLLAQSLFVLTEKRVFORLLEIAGV	302		
Db	250	SVCEYERTLAFPAISKFPVSYQHWTFYPMVGFARINLLVOSIVELITQKVRORWEIAGV	309		
Qy	303	ATFMAWYPLVLASLDNMWMEVAVFLVFSPTIGCIOHYOFCINHFSSDYVYVGPDKGDMWEK	362		
Db	310	AAFWWTYPLVLASCPLNMWMEVAVFLASFTYITGICHOYFCINHFSSAVYVGPDKGDMWEK	369		
Qy	363	QTAGTLIDLCSPPMDMFEHGLQFOIETHHLFPLPLPCHLAKVAPAVADLCCKKHGLTYSAA	422		
Db	370	QTAGTLIDLKCSPPMDMFEHGLQFOVEBHHLFPLPLPCHYEMVAVPIVADLCCKKHGLSYGAA	429		
Qy	423	FMGANVLTWTKTLRAAALQARTTSGAPRNULVWBAVNTHG	462		
Db	430	FWEANVMTWTKTLRAAALQAREKITTAAPRNULVWBAVNTHG	469		

Query Match	Best Local Similarity	59.5%	Score 1500.5	DB 10	Length 446
		63.0%	Pred. No. 9.3e-121		
RESULT 2					
092TV9					
ID	092TV9	PRELIMINARY;	PRT;	446	AA.
AC	092TV9;				
DT	01-MAY-1999	(TRMBLrel, 10, Created)			
DT	01-MAY-1999	(TRMBLrel, 10, Last sequence update)			
DT	01-OCT-2002	(TRMBLrel, 22, Last annotation update)			
DE	Desaturase/cytochrome b5 protein.				
OS	Ricinus communis (Castor bean).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid				
OC	eurosid 1; Malpighiales; Euphorbiaceae; Ricinus.				
OX	NCBI_TaxID=33981;				
RP	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Seed endosperm;				
RX	MEDLINE=97268723; PubMed=9108131;				
RA	Savanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,				
RA	Christie W.W., Shewry P.R., Napier J.A.;				
RT	"Expression of a borage desaturase cDNA containing an N-terminal				
RT	cytochrome b5 domain results in the accumulation of high levels of				
RT	delta-desaturated fatty acids in transgenic tobacco."				
RL	Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).				
CC	-1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.				
DR	EMBL; AF005096; AAD01240.1; -				
DR	HSSP; P00171; IISU.				
DR	InterPro; IPR001199; Cyt B5.				
DR	InterPro; IPR005804; FA_desat.fam.				
DR	Pfam; PF00487; FA_desaturase; 1.				
DR	Pfam; PF00173; heme_1; 1.				
DR	ProDom; PD000612; Cyt B5; 1.				
DR	ProDom; PD001081; FA_desat.fam; 1.				
DR	PROSITE; PS50255; CYTOCHROME_B5_2; 1.				
KW	Heme.				
SEQUENCE	446 AA; 51418 MW; A1954FDB32DB600F CRC64;				

	Matches	279;	Conservative	49;	Mismatches	112;	Indels	3;	Gaps	3																																														
QY	21	RMIS	SKELRA	HA	SAD	LD	LM	IS	SG	VD	TP	PL	PH	PG	DD	L	PL	TL	AG	DA	DA	PA	AA	YP	80																															
Db	6	KY	IR	DE	LE	KNN	GG	DM	IS	IG	KI	YN	TD	WS	KD	PG	GV	S	PL	LH	AG	OD	VD	DA	FA	YP	65																													
QY	81	SAR	PL	RR	F	P	G	-	R	L	S	D	Y	A	S	P	A	D	A	D	R	L	L	A	O	S	A	G	L	F	R	V	P	T	P	P	V	O	L	M	A	L	P	Y	A	139										
Db	66	T	A	Q	Y	D	K	F	F	G	Y	L	K	D	O	Y	S	V	E	T	S	K	D	O	R	L	A	E	R	S	K	G	-	F	E	K	G	H	I	A	T	L	V	S	M	L	L	A	124							
QY	140	A	L	I	V	L	A	C	A	S	A	M	A	L	L	A	G	G	L	I	G	P	W	I	O	S	G	M	G	H	S	G	H	R	I	T	G	H	P	L	D	R	V	O	L	S	N	C	I	T	G	199				
Db	125	S	V	Y	G	L	S	N	S	T	W	V	H	I	S	G	L	M	G	F	W	I	O	S	G	M	G	H	S	G	H	I	G	Q	V	M	S	R	R	F	N	L	A	O	I	L	S	N	C	I	A	G	184			
QY	200	L	S	I	A	M	M	C	N	N	H	T	H	I	A	C	N	S	D	H	D	D	L	O	M	P	L	F	A	V	S	P	K	L	F	G	N	I	M	S	Y	F	O	R	T	A	F	D	A	S	K	F	259			
Db	185	I	S	I	A	M	M	C	N	N	H	T	H	I	A	C	N	S	D	F	D	D	L	O	M	P	F	A	V	S	K	F	S	S	I	T	S	T	F	Y	R	K	N	F	D	C	A	A	F	L	244					
QY	260	I	S	Y	O	H	M	T	P	P	P	W	C	I	A	R	I	N	L	A	O	S	A	F	V	L	T	E	K	R	V	P	O	R	L	E	I	A	G	V	A	T	P	M	A	Y	P	L	L	A	S	L	P	N	319	
Db	245	V	S	Y	O	H	L	T	P	P	P	W	C	E	A	R	I	N	L	F	A	O	S	I	S	L	L	S	K	R	V	A	N	R	G	O	E	I	G	V	I	V	F	W	I	M	P	P	L	S	C	L	P	N	304	
QY	320	W	E	R	A	F	L	P	S	T	T	G	I	O	H	V	O	F	C	L	N	H	F	S	D	V	V	G	P	P	K	G	M	D	E	K	O	T	A	G	L	D	I	L	C	S	P	M	D	M	F	379				
Db	305	G	E	R	M	F	P	A	A	S	S	V	R	I	Q	H	V	O	F	C	L	N	H	F	S	S	V	L	G	L	L	I	A	N	D	E	N	O	T	K	G	L	D	I	T	C	S	M	D	M	F	364				
QY	380	H	G	L	O	F	O	I	E	H	L	L	P	R	L	P	R	C	H	L	R	K	V	A	P	A	V	R	D	I	C	K	H	G	L	T	T	S	A	T	F	W	A	N	L	T	W	K	T	L	R	A	A	L	439	
Db	365	H	G	L	O	F	O	M	E	H	L	L	P	R	L	P	R	V	K	R	K	V	S	P	E	V	E	L	C	K	G	H	N	L	P	Y	O	S	A	S	F	W	M	A	N	E	L	T	K	T	L	R	A	A	L	424
QY	440	Q	A	R	T	A	T	S	G	A	P	R	I	N	L	V	E	A	V	N	T	H	G	462																																
Db	425	Q	A	R	D	-	L	S	N	P	L	P	K	N	L	W	E	A	V	N	T	H	G																																	

	RESULT 3
Q8VZZ2	
ID Q8VZZ2	PRELIMINARY; PRT; 448 AA.
AC Q8VZZ2;	
DT 01-MAR-2002 (TREMBLrel. 20, Created)	
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)	
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)	
DE Delta-6-desaturase.	
GDN D6DES.	
OS Echinium gentianoides.	
OC Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC Spermatophytes; Magnoliopsida; eudicotyledons; core eudicots;	
OX Asceridae; lamids; Boraginaceae; Echium.	
NB NCBI_TaxID=173991;	
RN [1]	
RP SEQUENCE FROM N.A.	
RA Maroto F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz J.R.;	
RT "Cloning and Molecular Characterization of the D6-Desaturase from	
RL Echium: Functional Expression in Yeast and Tobacco.";	
RU Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.	
CC -I- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.	
DR EMBL; AY055117; AAL23580.1;-	
DR InterPro; IPR001199; Cyt_B5.	
DR InterPro; IPR005804; FA_desac_fam.	
DR Pfam; PF00487; FA_desaturase; 1.	
DR Pfam; PF00173; heme_1; 1.	
DR ProDom; PD000612; Cyt_B5; 1.	
DR ProDom; PD001081; FA_desac_fam; 1.	
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.	
KW Heme.	
SQ SEQUENCE 448 AA; 51428 MW; CZA937951E87C183 CRC64;	
Query Match 57.8%; Score 1457; DB 10; Length 448;	
Best Local Similarity 57.8%; Pred. No. 5.2e-117;	
Matches 256; Conservative 76; Mismatches 109; Indels 2; Gaps 2;	
CY 21 RMISKELRANASADLLMISTSGVVYVTPLPHHGGDRLTLAGODATDAFAAYR RP 80	
: ::::: : : : : : : :	

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Db      7 KITTAELKHDKEGDLWISIOGKYVDSDMLKDHPGKFPLLSLAGOEVTDAFVAHSG 66
Qy      81 SARPLRRFFVVG-RLSDYAVSPASADYRRLLAQLSSAGLFEERYGPTPKVOLVMAVLFA 139
Db      67 STMKLDSFFTYGLKDYDVSSEVSKDYRKLVFEFNKMGFLDKKHGHLVLTVEFIAMFPM 126
Qy      140 ALYVLACASAMAHLLAGLIGFWMIOSGMWHDGHHRTGHPVLDRVOVLSGNCITG 199
Db      127 SVYGVLFCEGVVLHLLAGLGMFWMIOSGMIGHDAGHYTMENPKLTKMLGIVAGNCLSG 186
Qy      200 LSIAMWKCNHNTHTACNSLDHDPDLQHPMLFAVSPKLGNIWISYFYQRTLAFDAASKFP 259
Db      187 ISIGMKNHNAHNTACNSLDYDQYIPFLVSSKLPSSLSHFEKKLTFDSLSRFF 246
Qy      260 ISYQWTFYPVWCARINILNLAOSALFVLTKEKVPORLLEIAGVATFMAVPLVLSLPMW 319
Db      247 VSHQWTFYPVWCASARVNFVQSLIMLTGRNVFYSQELGLVFWIWPPLVSCLPWM 306
Qy      320 WERVAFLPESFTICGLOHVOFCLNHPSDYYVGPCKGDMFEKOTAGTLDILCSPMWDMF 379
Db      307 GERIMEVVASLSTVGLOQVQFSLNHFSAVYVGPCKGDMFEKOTAGTLDILCSPMWDMF 366
Qy      380 HGGLOFOIEHHLFPLPLRCHLRKVAPAVDLCCKHGLTYSATFGANVLTWKTLLAAL 439
Db      367 HGGLOFOVEHHLFPLPLRCHLRKISPFVWELCKGNLSYNCSFSEANEMTLRTLDL 426
Qy      440 QARTATSGGAPKRLVMEAVNTHG 462
Db      427 QARDLTK-PLPKRLVMEALNTHG 448

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RESULT 4

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ID      08VZ21      PRELIMINARY;      PRT;      448 AA.
AC      08VZ21;
DT      01-MAR-2002 (TREMBLrel. 20, Created)
DT      01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT      01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE      Delta-6-deacaturase.
GN      D6DBS.
OS      Echium pitardii var. pitardii.
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC      Asteridae; lamiales; Boraginaceae; Echium.
OX      NCBI_TaxID=174255;
RN      (1)
RP      SEQUENCE FROM N.A.
RA      Marcelo F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz J.R.,
RT      "Cloning and Molecular Characterization of the D6-Deacaturase from
RT      Echium: Functional Expression in Yeast and Tobacco.";
RT      Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR      EMBL; AY055118; AL23581.1; -.
DR      InterPro; IPR001199; Cyt B5.
DR      InterPro; IPR005804; FA_deacat_fam.
DR      Pfam; PF00487; FA_deacaturase; 1.
DR      Pfam; PF00173; heme_1; 1.
DR      ProDom; PD000612; Cyt_B5; 1.
DR      ProDom; PD001081; FA_deacat_fam; 1.
DR      PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW      Heme.
SQ      SEQUENCE 448 AA; 51394 MW; 4B6DEA905DE263 CRC64;

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Query Match      57.2%; Score 1443; DB 10; Length 448;
Best Local Similarity 57.3%; Pred. No. 8.3e-116;
Matches 254; Conservative 76; Mismatches 111; Indels 2; Gaps 2;

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Qy      21 RMISSEKELRAHNSADLWISISGDYVDYTPMLPHHGGDLPLTLTAGODATPAFAAHP 80
Db      7 KITTAELKHDKEGDLWISIOGKYVDSDMLKDHPGKFPLLSLAGOEVTDAFVAHSG 66
Qy      81 SARPLRRFFVVG-RLSDYAVSPASADYRRLLAQLSSAGLFEERYGPTPKVOLVMAVLFA 139
Db      67 STMKLDSFFTYGLKDYDVSSEVSKDYRKLVFEFNKMGFLDKKHGHLVLTVEFIAMFPM 126

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Db      67 STMKLDSFFTYGLKDYDVSSEVSKDYRKLVFEFNKMGFLDKKHGHLVLTVEFIAMFPM 126
Qy      140 ALYVLACASAMAHLLAGLIGFWMIOSGMWHDGHHRTGHPVLDRVOVLSGNCITG 199
Db      127 SVYGVLFCEGVVLHLLAGLGMFWMIOSGMIGHDAGHYTMENPKLTKMLGIVAGNCLSG 186
Qy      200 LSIAMWKCNHNTHTACNSLDHDPDLQHPMLFAVSPKLGNIWISYFYQRTLAFDAASKFP 259
Db      187 ISIGMKNHNAHNTACNSLDYDQYIPFLVSSKLPSSLSHFEKKLTFDSLSRFF 246
Qy      260 ISYQWTFYPVWCARINILNLAOSALFVLTKEKVPORLLEIAGVATFMAVPLVLSLPMW 319
Db      247 VSHQWTFYPVWCASARVNFVQSLIMLTGRNVFYSQELGLVFWIWPPLVSCLPWM 306
Qy      320 WERVAFLPESFTICGLOHVOFCLNHPSDYYVGPCKGDMFEKOTAGTLDILCSPMWDMF 379
Db      307 GERIMEVVASLSTVGLOQVQFSLNHFSAVYVGPCKGDMFEKOTAGTLDILCSPMWDMF 366
Qy      380 HGGLOFOIEHHLFPLPLRCHLRKVAPAVDLCCKHGLTYSATFGANVLTWKTLLAAL 439
Db      367 HGGLOFOVEHHLFPLPLRCHLRKISPFVWELCKGNLSYNCSFSEANEMTLRTLDL 426
Qy      440 QARTATSGGAPKRLVMEAVNTHG 462
Db      427 QARDLTK-PLPKRLVMEALNTHG 448

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RESULT 5

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ID      09ZRP8      PRELIMINARY;      PRT;      449 AA.
AC      09ZRP8;
DT      01-MAY-1999 (TREMBLrel. 10, Created)
DT      01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Delta-8 sphingolipid deacaturase.
GN      SIDL.
OS      Brassica napus (Rape).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eurosida II; Brassicales; Brassicaceae; Brassica.
OX      NCBI_TaxID=3708;
RN      (1)
RP      SEQUENCE FROM N.A.
RA      STRAIN=cv. Drakkar; TISSUE=ripening embryos;
RC      MEDLINE=99003197; PubMed=9786850;
RX      Speiting P., Zaehring U., Heinz E.,
RT      "A Sphingolipid Desaturase from Higher Plants Identification of a New
RT      Cytochrome b5 Fusion Protein.";
RT      J. Biol. Chem. 273:28590-28596(1998).
CC      -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR      EMBL; AJ224160; CA11857.1; -.
DR      HSSP; P82291; ICXY.
DR      InterPro; IPR001199; Cyt B5.
DR      InterPro; IPR005804; FA_deacat_fam.
DR      Pfam; PF00487; FA_deacaturase; 1.
DR      Pfam; PF00173; heme_1; 1.
DR      ProDom; PD000612; Cyt_B5; 1.
DR      ProDom; PD001081; FA_deacat_fam; 1.
DR      PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW      Heme.
SQ      SEQUENCE 449 AA; 51490 MW; FEF637AF9D390C1 CRC64;

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Query Match      56.7%; Score 1429; DB 10; Length 449;
Best Local Similarity 57.3%; Pred. No. 1.3e-114;
Matches 254; Conservative 66; Mismatches 121; Indels 2; Gaps 2;

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Qy      21 RMISSEKELRAHNSADLWISISGDYVDYTPMLPHHGGDLPLTLTAGODATPAFAAHP 80
Db      8 RFTSDDLKGNQPGDLWISIOGKYVDSDMLKDHPGKFPLLSLAGOEVTDAFVAHSG 67
Qy      81 SARPLRRFFVVG-RLSDYAVSPASADYRRLLAQLSSAGLFEERYGPTPKVOLVMAVLFA 139
Db      68 TAMRHLNHNHNGYHKKHNDVSDYRDLRAAEFKRGFLDKKHGHLVLTVEFIAMFPM 127

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Oy		140	ALVYLACSAANAHLIAGLIGFWYQSGMMGHDSGHHITGHPVDRVQVYLSGCITG	197
Dd		128	VYGVAVACTSIWAHLISAVLLGLMTQSAVYVGSDSHYNWTSRKPCNKVLQVLLSNCITG	167
Oy		200	LSIAWMKCNENTHTHIAACNSLDHPDLOENMLPAVSFPLFGNIWSYYORTLAFDAASKFF	259
Dd		188	ISIAAMKWTHNAHHSICNSLDHPDLOHTPVLAVSNKFPEKSMTSRFYGRGLTFEDPLARFL	247
Oy		260	ISYOMTFFPVNVCIRINULAAOSAPLVLEKRPOLLELAGATFTMAWPLLVAISLPNW	319
Dd		248	ISYQMSSTPYPLICVGRINILFTOTLLLFSSRRYPDBALNLAGLVTWTMPELLVSLPNW	307
Oy		320	MERVAFLVFSFWTCGIOHVQCCLMHFSSDVVVGPFPKGNDMEFEKOTAGTLIDLCSPMWDMF	379
Dd		308	QERIIFVFLSMASVTAHQVFCLNHRAADVYGSPRGNMDMEFKQTGTIDISCRSYMDWF	367
Oy		380	HGGLOFOIEBHILPPRLPRCHLRKVADVPDLCKHGILTYSATFGWANVLTWKTLRAAL	439
Dd		368	FCGLOFOLEHHILPPRLPRCHLRKGVSPVOELCKHNLPKRSLSMEANVWLTLTKRAAV	427
Oy		440	QARTATSGAPPKULWEAVNTG	462
Dd		428	QARDVTN-PVENLMLERLNTG	449
RESULT	6			
ID	Q43469			
AC	Q43469.	PRELIMINARY;	PRT;	458 AA.
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Delta-8 sphingolipid desaturase.			
GN	Sld1.			
OS	Helianthus annuus (Common sunflower).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;			
OC	Heliantheae; Helianthus.			
XC	NCBI_TaxId=4232;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Inbred line HA89;			
RC	TISSUE=Cotyledons of developing sunflower fruits;			
RX	MEDLINE=96028121; PubMed=7588718;			
RT	Spearling P., Schmidt H., Heinz E.;			
RT	"A cytochrome b5-containing fusion protein similar to plant acyl lipid			
RT	desaturases."			
RL	Eur. J. Biochem. 232:798-805(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Inbred line HA89;			
RC	TISSUE=Cotyledons of developing sunflower fruits;			
RA	MEDLINE=21116801; Pubmed=11171153;			
RT	Spearling P., Blume A., Zaehlinger U., Heinz E.;			
RT	"Further characterization of delta 8-sphingolipid desaturases from			
RT	higher plants."			
RL	Biochem. Soc. Trans. 28:638-641(2000).			
CC	-1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.			
DR	EMBL; X87143; CAA60621.1; -.			
DR	HSSP; P00171; IFO3.			
DR	InterPro; IPRO01199; Cyt_B5.			
DR	InterPro; IPRO05804; FA_deeat_fam.			
DR	Pfam; PF00487; FA_desaturase; 1.			
DR	Pfam; PF00173; heme_1; 1.			
DR	ProDom; PD00612; Cyt_B5; 1.			
DR	ProDom; PD001081; FA_deeat_fam; 1.			
DR	PROSITE; PS50255; CYTOCHROME_B5_2; 1.			
KW	Heme.			
SEQ	SEQUENCE	458 AA;	52231 MW;	.DI82287ABOE99245 CRC64;

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Best Local Similarity 55.1%, Pred. No. 1,8e-114;
Matches 254; Conservative 77; Mismatches 123; Indels 7; Gaps 3

OY 3 PSVDAMPAGDAAGDVMTSSKELRAHASADDMISISGDVYDVTFWLRPHNPGGDLPL 62
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 4 PSIEVLNSIADGK-----KYITSKELKKNHNPNDLMSILCKVYVTEWAKENPGDAPL 58

OY 63 LTIAGGQATDAPFAVHPSPARPLRRFPVG-RISDYANVSPASDPRLLAQLSSAGLPER 121
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 59 INLGGQDVTDAFIHPHGETAKWHLDKLFPTYGHLXDYOVSISRDRKLASEPAKGMFEK 118

OY 122 VGPTPKVQVLVMAALFYAALYLVLACASAMAYHLLAGGLGCFVWISQGMWGHDSGHHRTG 181
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 119 KGHGVISLCLCVSILLSACVYGVLXSGSPFWIHLMSGALIGLAWQIALYLGHDAGHYQMA 178

OY 182 HPVLDRVVQVLSGNCITGLSLIAMWKCNHNTTHIACNSLDHDPDIQHPDLFAVSPKLGNI 241
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 179 TRGNKKFAGIFIGINCITGISIAMWKMTHAHIACNSLDYDPDLQHLPEMLAVSSKLFNSI 238

OY 242 WSYVYQRTLAPDAASKSPFISYQHTFPVVMCIATINLLAQSALFVLTETKRPQRLLETAG 301
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 239 TSVEYGRQLTDPILARFPVSYOHLTYPRMCVARNVLYLTQTLILISRKXIPDRGLNLTG 298

OY 302 VATFWAMPPLVLVASLPMWMEVAVFLFSFTICIGIQHVOFCUNHFSSDVYVGPCKGDMFE 361
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 299 TLIWTWPFPLVSLRPNMPERVAVLVSFCYTGIOHTIOPLTNHSRGDYVGPCKGDMFE 358

OY 362 KQTAGTIDILICSPMWDMEHGGLOFOIEHNLPRPLRCHLRKVAAPVRDLCKKGIITYSAA 421
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 359 KQTGTIDIACSSMWDMFEGGLQFOLEHNLPRPLRCHLRISIPICRELCCKYVLPVSL 418

OY 422 TFMGANVLWTKTLLRAALQARTATNSGAPKRLVMEAVNTHG 462
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 419 SFYDANVTTLKTRTALQARDLTN-PAPQNLWEAFNTHG 458

RESULT 7
OBLD7 PRELIMINARY; PRT; 446 AA.
ID OBLD7
AC OBLD7;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE SpHingolipid long chain base delta 8 desaturase.
OS Aquilegia vulgaris.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; eudicotyledons; Ranunculales;
OC Ranunculaceae; Aquilegia.
OX NCBI_TaxID=3451;
RN
RP
PP
RA Longman A.J., Michaelson L.V., Napier J.A.;
RT "Isolation and characterization of a cDNA encoding a delta 8
RT sphingolipid desaturase from Aquilegia vulgaris.";
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CTOCHROME B5 FAMILY.
DR EMBL; AF406816; AA03619.1; -.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase_1.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROME_B5.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ
SEQUENCE 446 AA; 51273 MW; 76366DB0EB956D09 CRC64;

Query Match 56.5%; Score 1424.5; DB 10; Length 446;
Best Local Similarity 56.8%; Pred. No. 3.2e-114;
Matches 251; Conservative 68; Mismatches 122; Indels 1; Gaps 1;

21 RMISKELRAHASADDMISISGDVYDVTFWLRPHNPGGDLPLTLAGQATDAPFAVHPSPARPLRRFPVG-RISDYANVSPASDPRLLAQLSSAGLPER 62

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21 RMISSELRAHASADDLWISISGDVYDVT P W L P H P G G D L P L L T L A G Q D A T D A F A A Y H P P 80

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Db      6 RETTSELKGNKGDWISIOGKIDVSEWIKDHPGGEAPLNLGQDVTDAFVAFHPG 65
QY      81 SARPLLRFRFVGLSDVAVSPASADYRRLAQLSSAGLFEFVGPTRPVOLVMAVLFYA 140
Db      66 SAKRTLDKFFITGLKDTTISEVSKDYRKLVAFESKALYDKGHHILFSLTFVTLMAIS 125
QY      141 LYLVLACASAMHLLAGGLIGFWVIOGMMGHDGSHHRTGHVPLDRVVOVLSGNCITGL 200
Db      126 VMGVLSGDKTKWHLASAAVGLMLMGIFVGHDSGHNNILTKLRNFMQIFGNCITGI 185
QY      201 SIAMKCNHNTHHIACNSLDHDDLOHMLFAVSPKLFENIMSYFQRTLAFAASKFT 260
Db      186 SIQMMKNNHNAHIAVNSLDYDPLQHIPELAVSSDIFSLTSKFGYRKMTFPIARFLI 245
QY      261 SYQHMTFYPVNCIARINILAQSLFVTEKRVPRQLLEIAGVATFMAVYLLVASLPNW 320
Db      246 SFQHMTFYPVMAIARINLFAQSFLILSKRPVDRALDELGLVFWCWSYLLACLPMWG 305
QY      321 ERVAVLFSTICIGIQHVFCLNHFSSDVYVPPKGNDFEKOAGTGLDILCSPPMDWPF 380
Db      306 ERAMVAVMSFVSGYQIOTCLNHFSAHTYVGPPCNDWFEKOTKGFPIDSCSTMDFH 365
QY      381 GGLQFOIEHHLFPRLPKRLKXVAPAVRDLCKKGLTYSATFGANVLTWKTLPRAALQ 440
Db      366 GGLQFOVEHHLFPRLPKRLKXISPYVKELCRKHNLPYISVSFEANXMTIATLRNALQ 425
QY      441 ARTATSGAPKXVLWEAVNTHG 462
Db      426 ARDLTN-PIPKNLWEAVNTHG 446

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RESULT 8

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ID      09SAUS      PRELIMINARY;      PRT;      448 AA.
AC      09SAUS;
DT      01-MAY-2000 (TEMBLrel. 13, Created)
DT      01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT      01-OCT-2002 (TEMBLrel. 22, Last annotation update)
DE      Delta 6-desaturase.
OS      Borage officinalis (Borraghe) (Borage).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC      Asteridae; lamiales; Boraginaceae; Borage.
OX      NCBI_TaxID=13363;
RN      [1]
RN      SEQUENCE FROM N.A.
RC      TISSUE=Seed.
RA      Nunberg A.N., Beremand P.D., Thomas T.L.;
RT      "Engineering of Plant Seed Oils to Produce Gamma Linolenic Acid
RT      (GLA).";
RL      Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC      - SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR      EMBL: AF007561; AAD01410.1; -
DR      InterPro: IPR001199; Cyt B5.
DR      InterPro: IPR005804; FA_desat. fam.
DR      Pfam: PF00487; FA_desaturase; 1.
DR      Pfam: PF00173; heme_1; 1.
DR      ProDom: PD000612; Cyt_B5; 1.
DR      ProDom: PD001081; FA_desat. fam; 1.
DR      PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KM      Heme.
SQ      SEQUENCE 448 AA; 51626 MW; EACJF0BF22E0DE00 CRC64;

Query Match      55.3%; Score 1393; DB 10; Length 448;
Best Local Similarity 55.8%; Pred. No. 1.7e-111;
Matches 247; Conservative 73; Mismatches 121; Indels 2; Gaps 2;

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Db      67 STWKNDKFFTYGLKDYVSVSEVSKDYRKLVFEFSKGLYDKKHIMFATLCFIAMLFAM 126
QY      140 ALYLVLACASAMHLLAGGLIGFWVIOGMMGHDGSHHRTGHVPLDRVVOVLSGNCITG 139
Db      127 SYGVGLFCGVLVHLFSSGLMGFLWIOGMIHGDACHVAVSDSRINKFMGTFIAAACLGG 186
QY      200 LSIAMKCNHNTHHIACNSLDHDDLOHMLFAVSPKLFENIMSYFQRTLAFAASKFT 259
Db      187 ISIGMMKNNHNAHIAVNSLDYDPLQHIPELAVSSDIFSLTSKFGYRKMTFPIARFLI 246
QY      260 ISYQHMTFYPVNCIARINILAQSLFVTEKRVPRQLLEIAGVATFMAVYLLVASLPNW 319
Db      247 VSYQHMTFYPVNCIARINILAQSLFVTEKRVPRQLLEIAGVATFMAVYLLVASLPNW 306
QY      320 WERVAVLFSTICIGIQHVFCLNHFSSDVYVPPKGNDFEKOAGTGLDILCSPPMDWPF 379
Db      307 GERIMFVIALSLATGQOVQFSLNHFSSSVYVGPCKGNWFEKOTGTDILSCPMDWPF 366
QY      380 HGLQFOIEHHLFPRLPKRLKXVAPAVRDLCKKGLTYSATFGANVLTWKTLPRAAL 439
Db      367 HGLQFOIEHHLFPRLPKRLKXISPYVKELCRKHNLPYISVSFEANXMTIATLRNAL 426
QY      440 QARTATSGAPKXVLWEAVNTHG 462
Db      427 QARDITK-PLPKNLWEALHTHG 448

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RESULT 9

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ID      004353      PRELIMINARY;      PRT;      448 AA.
AC      004353;
DT      01-JUL-1997 (TEMBLrel. 04, Created)
DT      01-JUL-1997 (TEMBLrel. 04, Last sequence update)
DT      01-OCT-2002 (TEMBLrel. 22, Last annotation update)
DE      Delta 6-desaturase.
OS      Borage officinalis (Borraghe) (Borage).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC      Asteridae; lamiales; Boraginaceae; Borage.
OX      NCBI_TaxID=13363;
RN      [1]
RN      SEQUENCE FROM N.A.
RX      MEDLINE=97268723; PubMed=9108131;
RA      Sayanova O., Smith M.A., Lapinatas P., Stobart A.K., Dobson G.,
RA      Christie W.W., Shewry P.R., Napier J.A.;
RT      "Expression of a borage desaturase cDNA containing an N-terminal
RT      cytochrome b5 domain results in the accumulation of high levels of
RT      delta6-desaturated fatty acids in transgenic tobacco.";
RL      Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
CC      - SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR      EMBL: U79010; AAC49700.1; -
DR      InterPro: IPR001199; Cyt B5.
DR      InterPro: IPR005804; FA_desat. fam.
DR      Pfam: PF00487; FA_desaturase; 1.
DR      Pfam: PF00173; heme_1; 1.
DR      ProDom: PD000612; Cyt_B5; 1.
DR      ProDom: PD001081; FA_desat. fam; 1.
DR      PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KM      Heme.
SQ      SEQUENCE 448 AA; 51635 MW; B62EEF701680909F CRC64;

Query Match      55.2%; Score 1392; DB 10; Length 448;
Best Local Similarity 55.8%; Pred. No. 2e-111;
Matches 247; Conservative 73; Mismatches 121; Indels 2; Gaps 2;

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QY 140 ATYLVACASAMAHLAGGLIGFVWIOSGMWGHDSGHRITGHPVLDRVVQVLSGNCITG 139
 DB 127 SVTGVLFCBEVLYHLHSGCLMGFMIOGSIIGHDAGHYVWSRLKMKGPANCLSG 186
 QY 200 LSIAMWKCNHNTTHIACNSLDHDPDLQHMPLFAVSPRLFGNINISYFQRTIAPDASKPF 259
 DB 187 ISIGWKMKNNAHIIACNSLEYPDLDIYIFLVVSAKFSFSLSHPEKRLTDPDSJRRF 246
 QY 260 ISYQHTFFVWMCARINLALQSLFVLTREKVPOLLEIAGVATFPAATPLVLAJPNW 319
 DB 247 VSYQHWTFEYIMCAARLNMVQOSILMLTKRNVSYRAHEHLLGCLVFSIWPPLVASCJPNW 306
 QY 320 WERVAFLFSPFTICGIIQHVQCLNHFSSDYVVGPKGNDWPEKOTAGTLDILCSPMWDMF 379
 DB 307 GERIMFVIALSTGMOQVPSLNHFSSSYVVGPKGNWPEKOTDGLDISCPMWDWF 366
 QY 380 HGGLOFQIEHHLPRRLPRCHLRKVAAPVBDLCKKGLTYSAAATFGANVLTWKTLPAAAL 439
 DB 367 HGGLOFQIEHHLPRKMRKRLKISPVVIELCKKNLPPYVASFSSKANTMTLRLTAL 426
 QY 440 QARTATSGAPKXULVWEAVNTHG 462
 DB 427 QARDITK-PLPKXULVWEALHTHG 448
 RESULT 10
 Q9ZRP7 PRELIMINARY; PRT; 449 AA.
 ID Q9ZRP7
 AC Q9ZRP7
 DT 01-MAY-1999 (TEMBLrel. 10, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE Delta-8 sphingolipid desaturase (AT3G61580/F2A19_180).
 GN SUD1 OR F2A19.180 OR AT3G61580.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Euphorbia II; Brassicales; Brassicaceae; Arabidopsis.
 NC NCBI_TaxID=3702;
 RX MEDLINE=99003197; Pubmed=9786850;
 RA Speeling P., Zehring U., Heinz E.;
 RT "A sphingolipid desaturase from higher plants. Identification of a new
 cytochrome b5 fusion protein.";
 RL J. Biol. Chem. 273:28590-28596(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA De Haan M., Maere A.C., Grievell L.A., Mewes H.W., Lemcke K.,
 Mayer K.F.X., Quetier F., Salanoubat M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narisaka M.,
 Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.U., Sakurai T.,
 Saitou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
 Becker J.R.;
 RT "Arabidopsis cDNA clones";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
 Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,

RA Deng J.M., Hayashizaki Y., Huan V.W., Lee J.M., Ishida J., Kamiya A.,
 RA Kawai J., Kim C.J., Narisaka M., Quach H.U., Sakurai T., Saitou M.,
 RA Seki M., Shin P., Tang C.C., Toriumi M., Wallender E.K., Wong C.,
 RA Wu H.C., Yamada K., Yu G., Yuan S., Shinzaki K., Becker J.,
 RA Theologis A., Davis R.W.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AJ224161; CAL1858.1; -;
 DR EMBL: AL132962; CAB71088.1; -;
 DR EMBL: AF428420; AAL16189.1; -;
 DR EMBL: BT000442; AAN17419.1; -;
 DR HSSP: P00171; 1150.
 DR InterPro: IPR001159; Cyt B5.
 DR InterPro: IPR005804; FA desat fam.
 DR Pfam: PF00487; FA desaturase_1.
 DR Pfam: PF00173; heme_1.1.
 DR ProDom: PD000612; Cyt_B5_1.
 DR ProDom: PD001081; FA desat fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KM Heme.
 SQ SEQUENCE 449 AA; 51675 MW; 145048F9F1D35964 CRC64;
 Query Match 55.0%; Score 1387; DB 10; Length 449;
 Best Local Similarity 55.8%; Pred. No. 5, 5e-111;
 Matches 247; Conservative 69; Mismatches 125; Indels 2; Gaps 2;
 QY 21 RMISKELEPAHASADLMTISGDYVDYTPWLPNHPGDLPLTLTAGODATDAFAAYHPP 80
 DB 8 KYTNEDLKKHNSGDLMTALIQKYNVSDWIKTHGGGTVLNLVGGDTDAFIAPHG 67
 QY 81 SARPLRPFVVG-RLSDYVWSPASADYRLRLAQLSSAGLFEVVGPPYQVLMVAVLFYA 139
 DB 68 TANHHDHLFTGHIHDPOVSEVSRDYRMAAFRLGGLFENKGHITLVTLAFVAAFLG 127
 QY 140 ATYLVACASAMAHLAGGLIGFVWIOSGMWGHDSGHRITGHPVLDRVVQVLSGNCITG 139
 DB 128 VLVGLVACTSVFPAHQIAAALLGLMTIOSAVYIGHDSGHVYIMSKSYNRPAQLISGNCITG 187
 QY 200 LSIAMWKCNHNTTHIACNSLDHDPDLQHMPLFAVSPRLFGNINISYFQRTIAPDASKPF 259
 DB 188 ISIAMWKCNHNTTHIACNSLDHDPDLQHMPLFAVSPRLFGNINISYFQRTIAPDASKPF 259
 QY 260 ISYQHTFFVWMCARINLALQSLFVLTREKVPOLLEIAGVATFPAATPLVLAJPNW 319
 DB 248 VSYQHTFFVWMCARINLALQSLFVLTREKVPOLLEIAGVATFPAATPLVLAJPNW 319
 QY 320 WERVAFLFSPFTICGIIQHVQCLNHFSSDYVVGPKGNDWPEKOTAGTLDILCSPMWDMF 379
 DB 308 PERFPVFTSFYVTAQIHLQFTLNHPADYVVGPPGSDWPEKOTAGTLDILCSPMWDMF 367
 QY 380 HGGLOFQIEHHLPRRLPRCHLRKVAAPVBDLCKKGLTYSAAATFGANVLTWKTLPAAAL 439
 DB 368 HGGLOFQIEHHLPRRLPRCHLRKVAAPVBDLCKKGLTYSAAATFGANVLTWKTLPAAAL 439
 QY 440 QARTATSGAPKXULVWEAVNTHG 462
 DB 428 QARD-VAAPVWVXULVWEALHTHG 449
 RESULT 11
 Q8LB96 PRELIMINARY; PRT; 449 AA.
 ID Q8LB96
 AC Q8LB96
 DT 01-OCT-2002 (TEMBLrel. 22, Created)
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE Delta-8 sphingolipid desaturase.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Euphorbia II; Brassicales; Brassicaceae; Arabidopsis.
 NC NCBI_TaxID=3702;
 RN [1]

RP SEQUENCE FROM N.A.
RA Haas B.J., Volkovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation."; 0:0-0(2002).
RL Genome Biol. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana."
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AY087345; AAM64895.1; -
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; PA_decat_fam.
DR Pfam; PF00467; PA_decat_fam.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; PA_decat_fam; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
DR Heme.
SQ SEQUENCE 449 AA; 51744 MW; A1EB57B8CE03E18 CRC64;
Query Match 54.8%; Score 1382; DB 10; Length 449;
Best Local Similarity 55.5%; Pred. No. 1.5e-110;
Matches 246; Conservative 69; Mismatches 126; Indels 2; Gaps 2;
QY 21 RMISSELRRAHSAADLMTISGSDYDVTWPLPHNGGDLPLTLTAGODATDAFAAYHP 80
DB 8 KYTNEDLKKHNSGDLMTAIOGKYNVSDWIKTHGCGDVTILNLVQDVTDAFIAPRG 67
QY 81 SARPLRRFVFG-RLSDYAVSPASADYRRLAQLSSAGLFEFVGPPTPKYQVLVMAVLFYA 139
DB 68 TANHLDHLFTGYHNDPOVSEVSRYRRRAAEFRKLGFEKNGHVTLYTLAFVAAFLR 127
QY 140 ALYVLACASAMAHLAGLIGFWIIOGMMGHDGSHRITGHPVLDVVQVLSGNCITG 199
DB 128 VLYGVLAAGSVFPAHQIAAALGLMLQSAIIGHDSGHVYVMSKYNRRPAQLISGNCITG 187
QY 200 LSIAMWKCHNTHHIAHNSLDHDPDLQHPMLFAVSPKLFNGINVSFYQRTLAFAAASKEF 259
DB 188 ISIAAMWKTHNHNHIAHNSLDHDPDLQHPMLFAVSPKLFNGINVSFYQRTLAFAAASKEF 247
QY 260 ISYQHTTFYVWMCIAINILAQSLFVLEKRPQRLLEIAGVATFWANVPLVLAAL 319
DB 248 VSQHTTFYVWMCIEGINLFIQFLILFSKREVPDALNFAGILVFWTFPLVSCIPW 307
QY 320 WERVAFLVFSFTICGIAHQVFCINHFSSDYVGPFGKNDWFEKQTAGTLDILCSPMWDMF 379
DB 308 PERFFVFGFTYALQHOIOTFLNHPADVYVGPFGSDWFEKQAAGTIDISCRSYMDF 367
QY 380 HGGLOFQIEHNLPRRLPRCHLRKVAAPVADLCKKHGLTYSATFWGANVLTWKTLPAAAL 439
DB 368 FGGLOFQIEHNLPRRLPRCHLRKVAAPVADLCKKHGLTYSATFWGANVLTWKTLPAAAL 427
QY 440 QARTATSGAPKVLWEAVNTHG 462
DB 428 QARD-VANPVVKLVWEALNTHG 449
RESULT 12
Q9FR82 PRELIMINARY; PRT; 446 AA.
AC Q9FR82;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Delta 8-sphingolipid desaturase.
GN SUD1.
OS Borage officinalis (Boraginaceae) (Borage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; lamiids; Boraginaceae; Borage.
OX NCBI_TaxId=13363;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092516; PubMed=11162428;
RA Liblisch B., Michaelson L.V., Lewis M.J., Shewry P.R., Napier J.A.;
RT "Chimeras of Delta6-fatty acid and Delta6-sphingolipid desaturases";
RL Biochem. Biophys. Res. Commun. 279:779-785(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2160464; PubMed=11368168;
RA Sperling P., Liblisch B., Zaehring U., Napier J.A., Heinz E.;
RT "Functional identification of a delta 8-sphingolipid desaturase from
RT Borage officinalis";
RL Arch. Biochem. Biophys. 388:293-298(2001).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AF133728; AAG43277.1; -
DR HSSP; P0171; 115U.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; PA_decat_fam.
DR Pfam; PF00467; PA_decat_fam.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; PA_decat_fam; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
DR Heme.
SQ SEQUENCE 446 AA; 50926 MW; EBD579F035A3AF0C CRC64;
Query Match 54.1%; Score 1363.5; DB 10; Length 446;
Best Local Similarity 55.4%; Pred. No. 5.8e-109;
Matches 247; Conservative 64; Mismatches 132; Indels 3; Gaps 2;
QY 18 GGVRRMISSELRRAHSAADLMTISGSDYDVTWPLPHNGGDLPLTLTAGODATDAFAAY 77
DB 3 GYRKQIYSGELKHNQQLGQVWISIQGKYNVTDWIKKHGQVPIPNMLAGODATDAFIAY 62
QY 78 HPSARPLRRFVFG-RLSDYAVSPASADYRRLAQLSSAGLFEFVGPPTPKYQVLVMAVLFYA 136
DB 63 HGTAMKLENLFTGYHLEDYLVSEISKDYRLASFSAAGLFEKKGHTVYICLSIALIL 122
QY 137 FYAALYVLACASAMAHLAGLIGFWIIOGMMGHDGSHRITGHPVLDVVQVLSGNC 196
DB 123 LGGCVYGVLCNSLWVHMLSGAMLCFQAAVLYGHDSGHVYVMSKYNRRPAQLISGNC 182
QY 197 LSGLSIAAMWKCHNTHHIAHNSLDHDPDLQHPMLFAVSPKLFNGINVSFYQRTLAFAAASKEF 256
DB 183 LSGLSIAAMWKTHNHNHIAHNSLDHDPDLQHPMLFAVSPKLFNGINVSFYQRTLAFAAASKEF 242
QY 257 KEFISQHTTFYVWMCIAINILAQSLFVLEKRPQRLLEIAGVATFWANVPLVLAAL 316
DB 243 RFLVSTQHTTYLVWIFGINLYVQFLFLFSKREVPDALNFIQILVYVWTFPLVSCIPW 302
QY 317 PMWERVAFLVFSFTICGIAHQVFCINHFSSDYVGPFGKNDWFEKQTAGTLDILCSPMWDMF 376
DB 303 PMWERVAFLVLCFSTYALQHOIOTFLNHPADVYVGPFGSDWFEKQAAGTIDISCRSYMDF 362
QY 377 DMFEGLOFQIEHNLPRRLPRCHLRKVAAPVADLCKKHGLTYSATFWGANVLTWKTLPAAAL 436
DB 363 DMFEGLOFQIEHNLPRRLPRCHLRKVAAPVADLCKKHGLTYSATFWGANVLTWKTLPAAAL 422
QY 437 AALQARTATSGAPKVLWEAVNTHG 462
DB 423 AALQARDLTV--VPQNLWEAVNTHG 446
RESULT 13
Q8L717 PRELIMINARY; PRT; 448 AA.
AC Q8L717;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Delta-6-desaturase.

	OC	Arganiaspirosea.
	OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
	OC	Ascertidae; Ericales; Sapotaceae; Argania.
	OX	NCBI_TaxID=85884;
	RN	[1]
	RP	SEQUENCE FROM N.A.
	RA	El Filiali A., Anderson M., Abbas K.;
	RT	"Characterization and cloning of delta-6-desaturase in Argania spinosa
	RT	fruct.,"
	RL	Submitted (JUL-2002) to the EMBL/genbank/DBJ databases.
	CC	-I- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
	DR	EMBL; AY131238; AA94345.1; -
	DR	InterPro; IPR001199; Cyt B5.
	DR	InterPro; IPR005804; FA_desat_fam.
	DR	Pfam; PF00487; FA_desaturase; 1.
	DR	Pfam; PF00173; heme_1; 1.
	DR	Prodrom; PD000612; Cyt B5; 1.
	DR	Prodrom; PD001081; FA_desat_fam; 1.
	DR	PROSITE; PS0255; CYTOCHROME_B5_2; 1.
	KM	Heme.
	SO	SEQUENCE 448 AA; 51304 MW; 0B46F81B7DEE29EF CRC64;
	Query Match	53.2%; Score 1340; DB 10; Length 448;
	Best Local Similarity	54.2%; Pred. No. 6,1e-107;
	Matches 240;	Conservative 72; Mismatches 129; Indels 2; Gaps 2
OY	21	RMISSEKELRAHASADDLWISIGDYYDTVPMHPHGGDLPLTLTAGDATDAFAAYHP 80
Db	7	KYTSDLELNKHNDKPDDLWISIGRAYDVSDWTDPGGSFLPKSLAGQVTDAPFAVAFPA 66
OY	81	SARPLRRFFPG-RLSADVSPASADYRRLLAQLSSAGLFERVGFTPKVOYLMAVLFYA 139
Db	67	STWKNLDFPFYGYYLKDYVSSEVSXDKLYVEFSKMGLYDAGHIMEPTALCFIAMLPAM 126
OY	140	ALYLVACASAWAHLLAGGLIGFWVIQSMMGHDSGHRHRTGHPVLDRVVQVLSGNCITG 199
Db	127	SVYGYLRREGVLYVHLFGSCLMGFMLTIOGMWIGHDGHWNVSDSKNKFMGIFAANCLSG 186
OY	200	LSIAMWKNHNTHIHACSNSLDHPDLQHMPLEFAPSFKLGNIWSYFOQTALFAASKRF 259
Db	187	ISIGSMKNNAHNAHIACNSLEXEDPDLOYIPLFVSSKFSGSLSHFEKRLLTIDLSPF 246
OY	260	ISYQWTVTPVMCIRINLLAOSALFVLTKEKVPORLLIEAGVATFMAFYPLLVASLPNW 319
Db	247	VSYQMTEYTTIMCARLNMVYOQLIMLLTKRVNSYRAHELLGLCLVESIWYPPLVSCIPNW 306
OY	320	MERVAVFVFESPTIGIQHVQFCNLNFSSDVYVGPBKGNMPEKOTAGTLDLCSPMDWF 379
Db	307	GERRIFEVNASVSTMQQOVSLSNFISSVYVKGKNGNNMFETQDGTDLDISCPMDWF 366
OY	360	HGGLQFOLEHHLFPRLPFRCHLRKVAPAVBDLCCKHGLTYSAATFGNAVLTWKTLPAAAL 439
Db	367	HGGLOFOLEHHLFPMGRPCNRNLTISPYLELCKKGNLPYNVASFKAKENMTLRTLRNAL 426
OY	440	QARTATSGAPKRLWEAVNTHG 462
Db	427	QARDITK-PLPKNLVMEALHTHG 448
RESULT 14	ID	Q9HDG8 PRELIMINARY; PRT; 523 AA.
AC	Q9HDG8;	
DT	01-MAR-2001 (TREMBLrel. 16, Created)	
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
D8	Delta-6 desaturase.	
OS	Mucor rouxi.	
OC	Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;	
OC	Mucor	
OX	NCBI_TaxID=29923;	
RN	[1]	

RP	SEQUENCE FROM N.A.
RC	STRAIN=ATCC 24905;
RX	MEDLINE=20563795; PubMed=11112411;
RA	Lactenz K., Mammotarat R., Tanticharoen M., Cheevadhanarak S.;
RT	"Delta(6)-desaturase of Pucor rouxi with high similarity to plant
RT	delta(6)-desaturase and its heterologous expression in Saccharomyces
RT	cerevisiae.";
RL	Biochem. Biophys. Res. Commun. 279:17-22(2000).
DR	-I- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC	EMBL; AF296076; AACG6960.1; -
DR	EMBL; AF290983; AAG36959.1; -
DR	HSSP; P00173; IJEX.
DR	InterPro; IPR001525; C5 DNA meth.
DR	InterPro; IPR001199; Cyte B5_
DR	InterPro; IPR005804; PA_desat fam.
DR	Pfam; PF00487; FA_desaturase; 1.
DR	Prodrom; PD000612; Cyte B5; 1.
DR	Prodrom; PD001081; PA_desat fam; 1.
DR	PROSITE; PS00095; C5_MTASE_2; 1.
DR	PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR	PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW	Heme.
SQ	SEQUENCE 523 AA; 60622 MW; A0372AF3EB7857 CRC64;
Query Match	29.3%; Score 738; DB 3; Length 523;
Best Local Similarity	31.4%; Pred. No. 4.7e-55;
Matches 164; Conservative	78; Mismatches 175; Indels 106; Gaps 10.
OY	1 MPSPVDMPAPRGDAAGADVMISKEELAH-----ASADDLWISGDVVDV 48
Dd	1 MPPT-----AAD-RLLSSTGRSSNITVEKFOELINQSGSVFL-YEQKYRV 47
OY	49 TWPLRNHPCGDLRYLLTAGODATDAFAAHPPSA----- 82
Dd	48 NNFMAKRPGGAALRSALGRDVTDEIRTMHRPYUEKMINLYCIGDYMPDIVRBSMKQ 107
OY	83 -----RPLRRFVGLSDVAVPASAD-----Y 106
Dd	108 HTTPKRKEDKKVLPAATWEGFTVQAYDDAIODLNHNSHDIKDVALOKDINGQIRNAV 167
OY	107 RLTAQISSAGLF-----RVGPTRPVQLMAVLFYAALLYLVCASAMHLAAGL 159
Dd	168 RKLAZELYAKGLFCNKWTAKAREG-----CKTLRLFSLMTLKGTETMNMAGAFA 220
OY	160 IGFWIGSGMWGHDGSHNRITGNHLDLRVVUOLVSGNCITGLSIAMWKCNHTNHIIACNSL 219
Dd	221 MAMFMHQDLVFPAHDAGNEIKSEIDHIVGILLIANFIGSLGWKNKHNVHHIVTHNP 280
OY	220 DHDDLDLMPLFAVSFKLFGNIWSYFORLTAFDAASKFPFISYONHTFYPMCTARIYLL 279
Dd	281 EHDDIDIHVPMAITTTKFENNIYSTYYKRVLPDAAASFVRHNDHYULLLSFGFRFLH 340
OY	280 AQSLAPVLETKRVQRRLLETLAGVATPFAMAUYRLVASIPNNMERAVAFVLFSTIGIOHV 339
Dd	341 RLSPAVALICANVTRTILELGITFFFWFGSSLSTIEPTNIRIAYIWSIMLPPRLHVQ 400
OY	340 FCLNHFSSDVVVGPPKND-WPEKQTAGTLDICSPMMDMFGLOFOLEHNPRLR 397
Dd	401 ITLSHFGNST---BDRGDBEPFPAKMRLRTMDVDCREPLDIFHGLOLVQAVNHLFRLR 457
OY	398 CHLRKVARAVDLCCKNGILTYSAATFENGANYLTKTLEAALQ 440
Dd	458 HNLRCVPLVKKFCDEVGLHYMYNFSGNGVULGITLSKVADQ 500
RESULT 15	
Q8NKG9	PRELIMINARY; PRT; 568 AA.
Q8NKG9	
AC	Q8NKG9;
DT	01-OCT-2002 (Tremblrel. 22, Created)
DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT	01-MAR-2003 (Tremblrel. 23, Last annotation update)

DE Putative delta 8-ephiingolipid desaturase.
 OS Saccharomyces kluyveri (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxId:4934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IFO 1685;
 RA Takakuwa N., Kinoshita M., Oda Y., Ohnishi M.;
 RT "Isolation and characterization of the genes encoding delta 8-
 RT ephiingolipid desaturase from Saccharomyces kluyveri and Kluyveromyces
 RT lactis";
 RT Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 CC -! SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AB085689; BAB93117.1; -
 DR InterPro: IPR001199; Cyt B5.
 DR InterPro: IPR005804; PA_desat_fam.
 DR Pfam: PF00487; PA_desat_fam.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD001081; PA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KM Heme
 SQ SEQUENCE 568 AA, 66465 MW, 115887B876D68EC CRC64;

 Query Match 24.6%; Score 620; DB 3; Length 568;
 Best Local Similarity 27.4%; Pred. No. 7,4e-45;
 Matches 151; Conservative 87; Mismatches 166; Indels 148; Gaps 9;

 QY 22 MISSEKELRAHASADLMISISGVYDVTPWLPHPHGGDLPLTLAQDATDAFAAYHPS 81
 DB 4 IISRGIEIDRIAGQAIIVIEGVLNLEKIKFPGDKAIHHMIGRDATDEMKAYHCD 63
 QY 82 ARPLARFVGR-----LSDYAVSPASAD----- 105
 DB 64 TWEIEFKMRIGRIDQEMENFLPIQGQVREFLNQOHDSITDLGSLNKMIAPISTSDQFKTK 123
 QY 106 ----- 105
 DB 124 NEKHMCGEPDVKIYPKIPQGVIPSLNLKAEYKQVYTDPAIVADNYDNELVRODLETLPD 183
 QY 106 -----YRLLAQISSAGLFE-----RVGPTPKVQLVIMAVLFYAALY 142
 DB 184 LDPKTQEWLSKEYNKNHNEIEAGLYQCVFRYKELTRIG-----LLFALSYLLVH 236
 QY 143 LVLAACASAWAHLLAGLIGFWIQSGMGGHDSGHRITGHPVLDRAVVOVLSGNCITGLSI 202
 DB 237 RQCKFSAFS-----MGCAMQQLVFIADAGHISITTHYOLDNIFGMIASWVGLSL 289
 QY 203 AWMKCHNTHHIIACNSLDHPDLDQHPMLFAVSPKLFGNISVYFQRTLAFDAASKFFISY 262
 DB 290 GMMKRNHNHHLITNDPIHDPIQHLPRFAVSTRLPDNIYSTYEKFLWFDAPAKKVPEW 349
 QY 263 QHWTFYPVNCIARINLQAQALFVL-----TEKRVPORLLEIAGVATP--WAMYPLVA 314
 DB 350 QNVLYYPMIAFGFENLYRLSMWHLVLLGDRBGKAGMFRFELGILFFNYMFFYLLVGC 409
 QY 315 SLPNMTERAVFVFSFTTIGIQHVQCLNHF---SSDVYVGPCKGDMPEKQTAGTLDTL 371
 DB 410 KIQTGWDRFOYIMVSHITLTVHVOITLSHFAMSTSDLGV---GEGFPMRQRTSMDDV 465
 QY 372 CSPMMDMFGGLQFOLEHLPRLPRCHLRKVAFAVADLCKKHGLTYSATFGANVLTW 431
 DB 466 CPMWLDPLHGLQFOVHHLPRLPRHNLRAQPVIECEKGVIXSYIGFSKGVVVL 525
 QY 432 KTLRAAALQART 443
 DB 526 TKLQEIAYOAKT 537

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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 16.051 Seconds
(without alignments)
1217.848 Million cell updates/sec

Title: US-09-857-524B-4

Perfect score: 2521

Sequence: 1 MPPSYDAMPAPGADAGADV.....TATSGAPKLVWEAVNTHG 462

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1387	55.0	448	1	US-08-366-779-5 Sequence 5, Appl1
2	1387	55.0	448	1	US-08-789-936-5 Sequence 5, Appl1
3	1387	55.0	448	4	US-08-934-254-5 Sequence 5, Appl1
4	1379	54.7	452	4	US-08-934-254-27 Sequence 27, Appl1
5	1370	54.3	446	2	US-08-833-610-5 Sequence 5, Appl1
6	1370	54.3	446	3	US-08-834-033A-15 Sequence 15, Appl1
7	881	34.9	252	2	US-08-834-033A-8 Sequence 8, Appl1
8	881	34.9	252	3	US-08-834-033A-11 Sequence 11, Appl1
9	881	34.9	252	3	US-09-363-526-7 Sequence 7, Appl1
10	881	34.9	252	4	US-09-363-526-7 Sequence 7, Appl1
11	523	20.7	457	2	US-08-834-655-2 Sequence 2, Appl1
12	523	20.7	457	3	US-08-834-033A-2 Sequence 2, Appl1
13	523	20.7	457	3	US-09-363-526-2 Sequence 2, Appl1
14	523	20.7	457	4	US-09-330-235-18 Sequence 18, Appl1
15	523	20.7	457	4	US-09-330-235-18 Sequence 18, Appl1
16	523	20.7	458	4	US-09-439-261-10 Sequence 10, Appl1
17	523	20.7	458	4	US-09-439-261-10 Sequence 10, Appl1
18	523	20.7	458	4	US-09-439-261-10 Sequence 10, Appl1
19	523	20.7	458	4	US-09-439-261-10 Sequence 10, Appl1
20	521	20.7	457	2	US-08-833-610-41 Sequence 41, Appl1
21	521	20.7	457	3	US-08-834-033A-14 Sequence 14, Appl1
22	443	17.6	125	3	US-08-834-655-8 Sequence 8, Appl1
23	443	17.6	125	3	US-08-834-033A-9 Sequence 9, Appl1
24	443	17.6	125	3	US-09-363-526-8 Sequence 8, Appl1
25	443	17.6	125	3	US-09-363-526-8 Sequence 8, Appl1
26	431.5	17.1	445	4	US-09-439-261-10 Sequence 10, Appl1
27	408.5	16.2	323	4	US-09-439-261-10 Sequence 10, Appl1

28	408.5	16.2	323	4	US-09-227-613-17 Sequence 17, Appl1
29	408.5	16.2	355	2	US-08-834-655-5 Sequence 5, Appl1
30	408.5	16.2	355	3	US-08-834-033A-6 Sequence 6, Appl1
31	408.5	16.2	355	3	US-09-363-526-5 Sequence 5, Appl1
32	408.5	16.2	355	4	US-09-363-526-5 Sequence 5, Appl1
33	406.5	16.1	444	4	US-09-227-613-42 Sequence 42, Appl1
34	406.5	16.1	444	4	US-09-227-613-42 Sequence 42, Appl1
35	406.5	16.1	444	4	US-09-439-261-11 Sequence 11, Appl1
36	404	16.0	444	4	US-09-439-261-11 Sequence 11, Appl1
37	404	16.0	444	4	US-09-227-613-12 Sequence 12, Appl1
38	404	16.0	444	4	US-09-439-261-13 Sequence 13, Appl1
39	404	16.0	444	4	US-09-439-261-13 Sequence 13, Appl1
40	390	15.5	432	4	US-09-439-261-9 Sequence 9, Appl1
41	390	15.5	432	4	US-09-227-613-9 Sequence 9, Appl1
42	390	15.5	465	4	US-09-439-261-40 Sequence 40, Appl1
43	390	15.5	465	4	US-09-227-613-38 Sequence 38, Appl1
44	390	15.5	465	4	US-08-833-610-2 Sequence 2, Appl1
45	320	12.7	446	2	US-08-834-033A-5 Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-08-366-779-5
Sequence 5, Application US/08366779
Patent No. 5614393
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Reddy, Avulu S.
APPLICANT: Nuccio, Michael
APPLICANT: Freysinet, Georges L.
APPLICANT: Numborg, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,779
FILING DATE: 30-DEC-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4366
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-366-779-5
Query Match 55.0%, Score 1387, DB 1, Length 448;
Best Local Similarity 55.5%, Pred. No. 1, 1e-134;
Matches 246; Conservative 73; Mismatches 122; Indels 2; Gaps 2;
21 RMISSEKELRAHNSADDLWISISGDVYDVTPLPHRPGDPLLTLAGDQATDAFAAHP 80

Db		7	KYITSEBKXHKDKRGDLMWISIGCKAYDSDWKDHPGGSFPLKSLAGCEVTDATFAVTHPA	66
	Y	81	SARPLLRRFFVG-RLSDYAVSPASADYRLLAQSSAGLPERVGPTRPKVOLVMAVLFYA	1399
	Y	67	STWKNIDKFETGYLLKDYDVSSEVSKDYRKLVEFESKMLYDKKGHIMPATLCFIAMLFAM	1266
	Y	140	ALVLVLACASAMHLLAGLIGFWITQSGMMCHDSGHHIRITGHFPLRDVVOVLSGNCLTG	1399
	Y	127	SVYGVLFCEGVLVHLRSGCLMGELWVQSGMICHDDGHVTVVSDSLKNNFMGIFPANCLSG	1866
	Y	200	LSIAMMKCNHNTHHIACNSLIDHPDLQHPFLPAYSRLFGNIMSYFYORTAPAAASKPF	2529
	Y	187	ISIGMKMNHNNAHHIACNSLEJYDPDLQYIFELVYSSKFFGSGTSHFYEKRLTFEJLSRFF	2466
	Y	260	ISYOHMTFYPVMCIARINLLAQSALFVLTEKEVRPRLLEIAGVATFWMAVPLVLAASLPNV	3196
	Y	247	VSYQHMTFYPVIMCAARLLNMYQSLIMLLTKRNVSRAGELLAGCLVFISWYLLVASCIPNV	3066
	Y	320	WERVAFLVESFTYCGIYOHVQFCINHESSDVYVGPXKGDWDFEKOCTAGTLIDLCSPPMWD	3799
	Y	307	GEIIMEFVIAFLSVTGMQVQVQFSINHESSSVYVGKPKGNWFEKQDGTLDLISCPMWD	3666
	Y	380	HGGLQFOIEHHLFPRPLRCHLKRKVAAYADLCKKGGLTYSATFPKANVLTWKTLRAAL	4399
	Y	367	HGGSOFIEIHLEFPKMPRCNLRKISPYVIELCKGNLPPYNAFSPKANEMTLRTLRTAL	4266
	Y	440	QARTATSGAPKXULWEAVNTHG	462
	Y	427	QARDITK-PULPKULWEALHTHG	448
Db				

RESULT 2
 US-08-789-936-5
 : Sequence 5, Application US/08789936
 : Patent No. 5789220
 : GENERAL INFORMATION:
 : APPLICANT: Thomas, Terry L.
 : APPLICANT: Reddy, Avutu S.
 : APPLICANT: Nuccio, Michael
 : APPLICANT: Freysinet, Georges L.
 : APPLICANT: Nuberger, Andrew N.
 : TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 : TITLE OF INVENTION: DELTA 6-DESATURASE
 : NUMBER OF SEQUENCES: 25
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Scully, Scott, Murphy & Presser
 : STREET: 400 Garden City Plaza
 : CITY: Garden City
 : STATE: New York
 : COUNTRY: United States
 : ZIP: 11530
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/789,936
 : FILING DATE: 28-JAN-1997
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/366,779
 : FILING DATE: 30-DEC-1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Presser, Leopold
 : REGISTRATION NUMBER: 19,827
 : REFERENCE/DOCKET NUMBER: 8383ZYXW
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (516) 742-4343
 : TELEFAX: (516) 742-4366
 : TELE: 230 901 SANS UR
 : INFORMATION FOR SEQ ID NO: 5:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
US-08-789-936-5

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Query Match	55.0%	Score 1387	DB 1	Length 448
Best Local Similarity	55.5%	Pred. No. 1.1e-134		
Matches 246	Conservative 73	Mismatches 122	Indels 2	Gaps 2

QY	21	RMISKEKEIRAAASADLTLISISGDYDVT PMLPHHPGGLPLTYLAGQDATPAFAAYHBP	80
Db	7	KYITSDELKNDKDPEDLWISIQGKAYVSDWVKDHPGGSFPLKSLAGCEVTAFAFAHRA	66
QY	81	SARPLRRFPVG-RUSDYAVSPASADYRRLLAQLSSAGLFEENVGPFPKQVLYMAVLVFA	139
Db	67	STWKULDFEFGUYLKDYSVSEVSXDYKRVFEFRKMGLYDKKHIMFATLCEFIANLFAM	126
QY	140	ALYVLACASAMHLIAGGLIGFVWIOSGMWHDSCNHRITGHPVLDRAWVUJSGCLTG	199
Db	127	SVYGVLFEEGVLYVHLPSCGLMGFWLTIOGMIHGDGHYVWSDSLRNMKGIFPANCISG	186
QY	200	LSIAWKNCHNTHHIAACNSLDHPDLQHPMLFAVSPKLFGINWSYFYORTLAFDAASKFP	259
Db	187	ISIGMKWNHNAHIAACNSLSEYDPDLOQYIPLVWSKFGGSLTSHFYERKLTNFDLSRPF	246
QY	260	ISYQWMTYTPMWCIRINULIQAOSALFVLTKEKVPORLBLEIAGVAFPMANYPLLVASLPMW	319
Db	247	VSQWMTYTPMWCARILMNYOQLIMLTLLTKRNVSYRAOELLCCLVFSIYVPLLVSCLPW	306
QY	320	WERVAVFLVFEFTICGIOHVQFCNLHFSSDDVYVGPKGNDMEFEKOTAGTLDILCSPMMDNF	379
Db	307	GERIMEFVIAISLVTCMQOVQFSLNHFSSVYVGRKKNWMEFKQTDGTLIDISCPMMDMF	366
QY	380	HGGIOFOIEHHLFPLPRCHLRKVAFAVAVRDLCKKGLTYSAAETFWGANVLTMYKTLFAALL	439
Db	367	HGGSFOIEHHLFPMPCPRCNLRKISPYVIELCKGNLPLYNVAFSKANEMETLRTLNTAL	426
QY	440	QARTSGAPRNVLWEAVNTHG	462
Db	427	QARDITK-PLPRNVLWEALNTHG	448

RESULT 3
 US-08-934-254-5
 Sequence 5, Application US/08934254
 Patent No. 635861
 General Information:
 Applicant: Thomas, Terry L.
 Title of Invention: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 TITLE OF INVENTION: DELTA 6-DESATURASE
 NUMBER OF SEQUENCES: 27
 Correspondence Address:
 Addressee: Scully, Scott, Murphy & Presser
 Street: 400 Garden City Plaza
 City: Garden City
 State: New York
 Country: United States
 Zip: 11530
 Computer Readable Form:
 Medium Type: Floppy disk
 Computer: IBM PC compatible
 Operating System: PC-DOS/MS-DOS
 Software: PatentIn Release #1.0, Version #1.25
 Current Application Data:
 Application Number: US/08/934,254
 Filing Date:
 Classification: 435
 Attorney/Agent Information:
 Name: Presser, Leopold
 Registration Number: 19,827
 Reference/Docket Number: 83832YXWVU

TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-934-254-5

Query Match	55.0%	Score 1387;	DB 4:	Length 448;
Best Local Similarity	55.5%	Pred. No. 1	1e-134;	
Matches 246;	Conservative	73;	Mismatches 122;	Indels 2;
				Gaps 2;

Qy	21	RMSSSELEBAHSAADLMISISGDVYDTVPMLEPHHGGDLPLTLTAAGDADDAFAAHP	80
Db	7	KYTSDELKNHDKPGLMISIQKAYVDSDVKHHPGSSPFLKSLAGEVTDFAVAFHPA	66
Qy	81	SARPLLRPFVG-RUSDVAVSPASADYRRLLAQSSAGLFEFVGPTPKVQVLMAVLFYA	139
Db	67	STWKNDKEFFGTGYLLKDYVSSEVSDYRKLYEFESKMLYDKKHIMPATLCFIAMLFAM	126
Qy	140	ALVLYACASAMHLLAGGLIGFWIISGSMWCHDSGHHRIIGHVYLDVRVYVLSGNLTG	139
Db	127	SVYGVLPFGCVLVHLPSSGCLMGPLMIISQWIGHDGHMTVSDSLNKKFMIIPANCLSG	166
Qy	200	LSIAMKCNHNTHILACNSLDDHDPLOJHMPLEFVAVSPKLFGNIMSYFYQRTLAAPASKEF	259
Db	187	ISIGMKMHNHNAHILACNSLEVDPLQYIPLVYSKRFSGSLTHFPEKRLTFPSSSRFF	246
Qy	260	ISVQHHTFPFWNCIARINLLAOSALFVLTKEKRVORLLIEAGVTFMAYPLVLAACPNN	319
Db	247	VSVQHHTFPFPCIAALNNYQSLITMLTLKRVNSYRAOELLGCVFSSIMYPLVASCCLPNN	306
Qy	320	MEVAVLVLSFTICGLOHYOFCILNFSSDYYGPPKGDMEFEKOTDAGTLIDCSPPMDWF	379
Db	307	GERIMVIVIASLSTYGMQVQVPSLNFSSVYVGRKXGNMWEKQTDGTLIDSCPPMDWF	366
Qy	380	HGGLQFOIEHHLFPRLLPRCHLRKVAIPAVRDLCKHGGLTYSAAITFWGANVLTWKTLRRAAL	439
Db	367	HGSSQCFQIEHHLFPPKMRCLNRKISIPUYELCKGNLLEPYNAASSFKNNEMTLRTLRATAL	426
Qy	440	QARTATSGAPKNIVLEAVNTHG 462	
Db	427	QARDITK-PLPKNLWEALHTHG 448	

RESULT 4
US-08-934-254-27
Sequence 27, Application US/08934254
Patent No. 635861
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
FILING DATE:

```

1 CLASSIFICATION: 435
2
3 ATTORNEY/AGENT INFORMATION:
4
5 NAME: Presser, Leopold
6
7 REGISTRATION NUMBER: 19, 827
8
9 REFERENCE/DOCKET NUMBER: 8383ZYXWVU
10
11 TELECOMMUNICATION INFORMATION:
12
13 TELEPHONE: (516) 742-4343
14
15 TELEFAX: (516) 742-4366
16
17 TELEX: 230 901 SANS UR
18
19 INFORMATION FOR SEQ ID NO: 27:
20
21 SEQUENCE CHARACTERISTICS:
22
23 LENGTH: 452 amino acids
24
25 TYPE: amino acid
26
27 TOPOLOGY: linear
28
29 MOLECULE TYPE: protein
30
31 US-08-934-254-27

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Query Match	54.7%	Score 1379;	DB 4;	Length 452;
Best Local Similarity	56.7%	Pred. No. 7	7e134;	
Matches 253;	Conservative	64;	Mismatches 125;	Indels 4;
				Gaps 31

[illegible]

RESULT 5
US-08-633-610-5
Sequence 5, Application US/08833610
Patent No. 5972664
GENERAL INFORMATION:
APPLICANT: KUNITZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VEENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA

RESULT 5
US-08-633-610-5
Sequence 5, Application US/06833610
Patent No. 597864
GENERAL INFORMATION:
APPLICANT: KNOTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-YENNER LAW GROUP, P.C.,
STREET: 260 SHELDON AVE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA

RESULT 7

US-08-834-655-7

; Sequence 7, Application US/08834655

; Patent No. 5968809

; GENERAL INFORMATION:

; APPLICANT: KUTTZON, DEBORAH

; APPLICANT: MUKERJI, PRADIP

; APPLICANT: HUANG, YUNG-SHENG

; APPLICANT: THURMOND, JENNIFER

; APPLICANT: CHAUDHARY, SUNITA

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.

; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039

; CITY: PALO ALTO

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/834,655

; FILING DATE: 11-APR-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: RAE-VENTER, BARBARA

; REGISTRATION NUMBER: 32,750

; REFERENCE/DOCKET NUMBER: CGNE.124.00US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 328-4400

; TELEFAX: (650) 328-4477

; TELEX: N/A

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 252 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-834-655-7

Query Match 34.9%; Score 881; DB 2; Length 252;

Best Local Similarity 59.6%; Pred. No. 8.8e-83;

Matches 149; Conservative 39; Mismatches 62; Indels 0; Gaps 0;

141 LYLVLACASAMAHLLAGLIGFVWIOSGMMGHDSGHHRTGHPVLDVVQVLSGNCITGL 200

3 LVGVLAICTSVFAHQIAAALLGLMTIOSAVYIGHDSGHVYIMSNKSYNRFAPQLLSGNCITGL 62

201 SIAMWKCNHTNHIAICNSLDHDPDLQHMLPFAVSPKLFENISYFYORTLAFDAASKFPI 260

63 SIAMWKMTNNAHLLACNSLDYDLDLQHIPFAVSTKFSLSLTSRFDRLTGTGPVAFV 122

261 SYQHTFYVPMCIARINLLAQSALFVLTEKRVQRLLEIAGVATFWAAYPLVASIPNMW 320

123 SYQHTFYVPMCIARINLLAQSALFVLTEKRVQRLLEIAGVATFWAAYPLVASIPNMW 182

321 ERVAFLVPSFTTCGIOHVOFCNLHSSDYVGPCKNDWFEKOTAGTDLILCSPPMMDWFH 380

183 ERFFVFTSFTVTAALQIOTLNHFPAADVVPPTGSDWFEKOAAGTIDISCRSYMDWFF 242

381 GGLQFOLEHH 390

243 GGLQFOLEHH 252

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

US-08-834-033A-8

; Sequence 8, Application US/08834033A

; Patent No. 6075183

; GENERAL INFORMATION:

; APPLICANT: KUTTZON, DEBORAH

; APPLICANT: MUKERJI, PRADIP

; APPLICANT: HUANG, YUNG-SHENG

; APPLICANT: THURMOND, JENNIFER

; APPLICANT: CHAUDHARY, SUNITA

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.

; STREET: 2001 PERRY BUILDING

; CITY: SAN FRANCISCO

; STATE: CA

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/834,033A

; FILING DATE: 11-APR-1997

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: WARD, MICHAEL R.

; REGISTRATION NUMBER: 38,651

; REFERENCE/DOCKET NUMBER: CGAB-300. USA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 433-4150

; TELEFAX: (415) 433-8716

; TELEX: N/A

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 252 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-834-033A-8

Query Match 34.9%; Score 881; DB 3; Length 252;

Best Local Similarity 59.6%; Pred. No. 8.8e-83;

Matches 149; Conservative 39; Mismatches 62; Indels 0; Gaps 0;

141 LYLVLACASAMAHLLAGLIGFVWIOSGMMGHDSGHHRTGHPVLDVVQVLSGNCITGL 200

3 LVGVLAICTSVFAHQIAAALLGLMTIOSAVYIGHDSGHVYIMSNKSYNRFAPQLLSGNCITGL 62

201 SIAMWKCNHTNHIAICNSLDHDPDLQHMLPFAVSPKLFENISYFYORTLAFDAASKFPI 260

63 SIAMWKMTNNAHLLACNSLDYDLDLQHIPFAVSTKFSLSLTSRFDRLTGTGPVAFV 122

261 SYQHTFYVPMCIARINLLAQSALFVLTEKRVQRLLEIAGVATFWAAYPLVASIPNMW 320

123 SYQHTFYVPMCIARINLLAQSALFVLTEKRVQRLLEIAGVATFWAAYPLVASIPNMW 182

321 ERVAFLVPSFTTCGIOHVOFCNLHSSDYVGPCKNDWFEKOTAGTDLILCSPPMMDWFH 380

183 ERFFVFTSFTVTAALQIOTLNHFPAADVVPPTGSDWFEKOAAGTIDISCRSYMDWFF 242

381 GGLQFOLEHH 390

243 GGLQFOLEHH 252

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

RESULT 8

RESULT 9

US-09-363-574-7

; Sequence 7, Application US/09363574

Patent No. 6136574
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YONG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
NUMBER OF SEQUENCES: 18
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-574-7

Query Match 34.9%; Score 881; DB 3; Length 252;
Best Local Similarity 59.6%; Pred. No. 8.8e-83;
Matches 149; Conservative 39; Mismatches 62; Indels 0; Gaps 0;

QY 141 LYLVLACASAMHLLAGLIGFWIQQSGMKGHDSGHHRTGHPVLDREVQVLSGNCITGL 200
DB 3 LYGVLACTSVFAHQIAAALLGLMIQSAVIGHDSGHVYVMSNKSYNRFAQLLSGNCITGL 62
QY 201 SIAMWKCNHNTTHIACNSLDHDPDLQMPPLFVSPKLFQINMSYFYORTLAFDAASKFTI 260
DB 63 SIAMWKCNHNTTHIACNSLDHDPDLQMPPLFVSPKLFQINMSYFYORTLAFDAASKFTI 122
QY 261 SYOHMTFYPWCJARINLQAQALFVLTETKRVORLLEIAGVATFPAWYPLVASLPMNW 320
DB 123 SYOHMTFYPWCJARINLQAQALFVLTETKRVORLLEIAGVATFPAWYPLVASLPMNW 182
QY 321 ERVAFVLFSTTCIGIHOVQCLNHFSSDYVVGPKNDWFEKOTAGTLDILCSPPMDWFH 380
DB 183 ERVAFVLFSTTCIGIHOVQCLNHFSSDYVVGPKNDWFEKOTAGTLDILCSPPMDWFH 242
QY 381 GGLQFOLEHH 390
DB 243 GGLQFOLEHH 252

RESULT 10
US-09-363-526-7
Sequence 7, Application US/09363526
Patent No. 6410288
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP

APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YONG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
NUMBER OF SEQUENCES: 18
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,526
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-201 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-526-7

Query Match 34.9%; Score 881; DB 4; Length 252;
Best Local Similarity 59.6%; Pred. No. 8.8e-83;
Matches 149; Conservative 39; Mismatches 62; Indels 0; Gaps 0;

QY 141 LYLVLACASAMHLLAGLIGFWIQQSGMKGHDSGHHRTGHPVLDREVQVLSGNCITGL 200
DB 3 LYGVLACTSVFAHQIAAALLGLMIQSAVIGHDSGHVYVMSNKSYNRFAQLLSGNCITGL 62
QY 201 SIAMWKCNHNTTHIACNSLDHDPDLQMPPLFVSPKLFQINMSYFYORTLAFDAASKFTI 260
DB 63 SIAMWKCNHNTTHIACNSLDHDPDLQMPPLFVSPKLFQINMSYFYORTLAFDAASKFTI 122
QY 261 SYOHMTFYPWCJARINLQAQALFVLTETKRVORLLEIAGVATFPAWYPLVASLPMNW 320
DB 123 SYOHMTFYPWCJARINLQAQALFVLTETKRVORLLEIAGVATFPAWYPLVASLPMNW 182
QY 321 ERVAFVLFSTTCIGIHOVQCLNHFSSDYVVGPKNDWFEKOTAGTLDILCSPPMDWFH 380
DB 183 ERVAFVLFSTTCIGIHOVQCLNHFSSDYVVGPKNDWFEKOTAGTLDILCSPPMDWFH 242
QY 381 GGLQFOLEHH 390
DB 243 GGLQFOLEHH 252

RESULT 11
US-08-834-655-2
Sequence 2, Application US/08834655
Patent No. 5968809
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP

APPLICANT: HUANG, YUNG-SHENG
 APPLICANT: THURMOND, JENNIFER
 APPLICANT: CHAUDHARY, SUNITA
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
 STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
 CITY: PALO ALTO
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/834,655
 FILING DATE: 11-Apr-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: RAE-VENTER, BARBARA
 REGISTRATION NUMBER: 32,750
 REFERENCE/DOCKET NUMBER: CGNE.124.00US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 328-4400
 TELEFAX: (650) 328-4477
 TELETYPE: N/A
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 457 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-834-655-2

Query Match 20.7%; Score 523; DB 2; Length 457;
 Best Local Similarity 30.2%; Pred. No. 2e-45;
 Matches 138; Conservative 64; Mismatches 171; Indels 84; Gaps 15;

15 AGAGDVRLMISKEL-----RAHASADLMISGVDVDTPLPHNPGGDLPLTL 65
 2 AARPSTRTTRAEVLAELNEGKDAEAPFLMT-IDNKYDVRREVPHPGGSV-ILTH 59
 66 AGQDATDAFAAYPPSARPLRLRRFVGRIS---DYAVSPASADYRRLAQLSSAGLPER 121
 60 VGKDGTDVDTFHPREAWETLANFYVGDI DESDRIKNDFAAEVAKRTLPQSLGYD- 118
 122 VGPTPVQVLMAVLFYA-----ALYVLAC---ASAMHLLAGLIGFWIQS 167
 119 -----SSKAYIAFVSVNLCIWSLSTVIYAKWGQSTLANVLSAALLGLFWQC 167
 168 GWMGDSGHRITGHPVLDRLVQVLSGNCITGLSIAMWKCNHTHIIACNSLDHDPDLOH 227
 168 GMLADFLHLYQVQDFRFGWDLFGALFGVCGQFSSSMWKDKNTHAARVNGEDPDIT 227
 228 MPLFAVSP--KLFGNI-----WSYFYQRTLAFDAASKFPISYQHTFYVPMCIARI 276
 228 HPLLTWSEHALBMFSDVPDEBLTRMW-----SRFMVLNQTWTFYFPIISFARL 274
 277 NLLAQSALFVL-----TEKRVQRLIEIAGVATFWAMY-DLVLASLPMNMMERVAFVL 327
 275 SWLQSLILFLPVGQAKHKSAGARVPISLVQLSLAMHMTWYLAETWELFIKDPVNMVLYEL 334
 328 FSTTIG-IGHVQFCNH-----FSSDYYVYGPCKDMPEKQTAAGLIDILCSMMWMPFG 381
 335 VSGAVCGNLAIATFSLNHNMGMPVYSKEAV---DMDFTKQIITGRDVHPLGLFANWFTG 390
 382 GLQFOIEHHLFRLPRCHLRKVAFAVADLCKKGLTY 418

DB 391 GUNYOIEHHLFSPMRHNFESKIQPAVETLCKKYNRY 427

RESULT 12
 US-08-834-033A-2
 Sequence 2, Application US/08834033A
 Patent No. 6075183
 GENERAL INFORMATION:
 APPLICANT: KUNTZON, DEBORAH
 APPLICANT: MIKERTI, PRADIP
 APPLICANT: HUANG, YUNG-SHENG
 APPLICANT: THURMOND, JENNIFER
 APPLICANT: CHAUDHARY, SUNITA
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
 STREET: 2001 FERRY BUILDING
 CITY: SAN FRANCISCO
 STATE: CA
 COUNTRY: USA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/834,033A
 FILING DATE: 11-Apr-1997
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: WARD, MICHAEL R.
 REGISTRATION NUMBER: 38,651
 REFERENCE/DOCKET NUMBER: CGAB-300.USA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 433-4150
 TELEFAX: (415) 433-8716
 TELETYPE: N/A
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 457 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-834-033A-2

Query Match 20.7%; Score 523; DB 3; Length 457;
 Best Local Similarity 30.2%; Pred. No. 2e-45;
 Matches 138; Conservative 64; Mismatches 171; Indels 84; Gaps 15;

15 AGAGDVRLMISKEL-----RAHASADLMISGVDVDTPLPHNPGGDLPLTL 65
 2 AARPSTRTTRAEVLAELNEGKDAEAPFLMT-IDNKYDVRREVPHPGGSV-ILTH 59
 66 AGQDATDAFAAYPPSARPLRLRRFVGRIS---DYAVSPASADYRRLAQLSSAGLPER 121
 60 VGKDGTDVDTFHPREAWETLANFYVGDI DESDRIKNDFAAEVAKRTLPQSLGYD- 118
 122 VGPTPVQVLMAVLFYA-----ALYVLAC---ASAMHLLAGLIGFWIQS 167
 119 -----SSKAYIAFVSVNLCIWSLSTVIYAKWGQSTLANVLSAALLGLFWQC 167
 168 GWMGDSGHRITGHPVLDRLVQVLSGNCITGLSIAMWKCNHTHIIACNSLDHDPDLOH 227
 168 GMLADFLHLYQVQDFRFGWDLFGALFGVCGQFSSSMWKDKNTHAARVNGEDPDIT 227
 228 MPLFAVSP--KLFGNI-----WSYFYQRTLAFDAASKFPISYQHTFYVPMCIARI 276
 228 HPLLTWSEHALBMFSDVPDEBLTRMW-----SRFMVLNQTWTFYFPIISFARL 274

QY 277 NLLQSALEFVL-----TEKRVPRRLLEIGVAFAMFY-PLVVASLEPNMWERARFVL 327

Db 275 SWCIQSILIFVLPNQAAHKRGSGARVPISLVEQSLAHMHWYLAITMPLFIKDPVNMIVYFL 334

QY 328 FSEFTICG-IQHQFCLNH-----FSSDYVVGPPKGNDFEKGQATGLTILICSPMMDMPFG 381

Db 335 VSAQACGNLALAVESLNHNGMPVISISEEAV---DMDFTFKQIITGRDVHPGLFANWFTG 390

QY 382 GLQFOIEHHLLPRRLPRCHLRKVAAPAYRDLCKKHGLTY 418

Db 391 GLNVOIEHHLLFSPMRHNPFSKIQAPAVETILCKKINNAVY 427

RESULT 13
US-09-363-574-2
; Sequence 2, Application US/09363574

? Patent No.:6136574
 ? GENERAL INFORMATION:
 ? APPLICANT: KUTUZON, DEBORAH
 ? APPLICANT: MURKERJI, PRADIP
 ? APPLICANT: HUANG, YUNG-SHENG
 ? APPLICANT: THURMOND, JENNIFER
 ? APPLICANT: CHAUDHARY, SUNITA
 ? TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ? TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 ? NUMBER OF SEQUENCES: 18
 ? CORRESPONDENCE ADDRESS:

```

1 ADDRESS: LIMBACH AND LIMBACH L.L.P.
2 STREET: 2001 FERRY BUILDING
3 CITY: SAN FRANCISCO
4 STATE: CA
5 COUNTRY: USA
6 ZIP: 94111
7
8 COMPUTER READABLE FORM:
9
10 MEDIUM TYPE: Floppy disk
11
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: PatentIn Release #1.0, Version #1.30
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/09/363,574

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? CLASSIFICATION:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: WARD, MICHAEL R.
? REGISTRATION NUMBER: 38,651
? REFERENCE/DOCKET NUMBER: CGMB-202 USA
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 433-4150
? TELEFAX: (415) 433-8716
? TELEX: N/A
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 457 amino acids
? TYPE: amino acid
? STRANDEDNESS: not relevant
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? PS-09-363-574-2
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Query Match 20.7%; Score 523; DB 3; Length 457;
 Best Local Similarity 30.2%; Pred. No. 26-45;
 Matches 138; Conservative 64; Mismatches 171; Indels 84; Gaps 15

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QY      15 AGAGDVNRISSEL-----RNASADLMISISGVVDVFWLRPHNPGGDLRLTL 65
      | | | | | : | | | | | : | | | | | : | | | | | : | |
Db      2 AAASVRFTRFAEVLNAELNEGKDAEAFIMI-IDNKYVDREVFVRPHPGSV-ILTN 59
QY      66 AGQATDTPAAIVHPSPASRPLRRFFVGRLS---DYASPSADYRRLLAQSSAGLFR 121
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D_b 60 VGRQGTDFVETFHPEAAMEITLNFYVGDDIDESDRDIKONDDFAAEVRKLTLLFQSLGYD-118
 :|||:|||||:

O_y 122 VGPRPKVQLVMAYLFYA-----ALYLVLAC---ASAMALLAGGLIGFWTIS 167
 :|||:|:|:|:|:

Db	119	-----SKRAYFAFKVSPFNLCINGSLSTVIAKKNQOSTLANVLSAALLGFWQC	167
Qy	168	GMWGDGSHHRTIGHPIVLDIVVQVLSGCLTGLSLAMWKCNHNTHHIACNSLDHPDLOH	227
Db	168	GMLHDFLHHQVPODFRFGWDLFGAFLGGVCCGFSSSMMKDKKNTHHAANVGEBDIDT	227
Qy	228	MPLEAVSP--KLEGNI-----WSYFYORTLAFDAASKFEFISYOHNTFPYVMCIARI	276
Db	228	HPLLTWSHAALEMSDVPDEELTRWM-----SRMVLNQTFEYFPIISFALT	274
Qy	277	NLLAOSALFVJ-----TEKRYDQRLLEIAGVATFWAMY-PLVABSLPMMEBVAFTL	327
Db	275	SWCLOSLIFVLPNGOAKHPSGARFPFISLVEQSLNHHMTWLYATNPLFKDVPNNLVYFL	334
Qy	328	FSFTICG-IQHVQCLNH-----FSSDYVGPBKNDWFEKQTAJTLDILCSPMWDFHG	381
Db	335	VSQAVCGGTLIAIVSLNNGMPVLSKEBAV-----DMDEFTKQIITGRDVHPLFLANWFTG	390
Qy	382	GLOFOIEHHLEFPRLPRCHLRKVAPARVRLCKKHGLTY	418
Db	391	GLANYQIEHHLEFPSPKRHNPFKIQRAVETLCKKKNIVRY	427

RESULT 14
US-09-363-526-2
; Sequence 2, Application US/09363526

Patent No. 6410288
GENERAL INFORMATION:
APPLICANT: KUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L. L. P.
STREET: 2001 PERRY BUILDING
CITY: SAN FRANCISCO

STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,526
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-201 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150

```

? TELEFAX: (415) 433-8716
? TELEX: N/A
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 457 amino acids
? TYPE: amino acid
? STRANDEDNESS: not relevant
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? OS-09-363-526-2

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Query Match	20.7%	Score 523	DB 4	Length 457
Best Local Similarity	30.2%	Pred. No. 2e-45		
Matches 138	Conservative 64	Mismatches 171	Indels 84	Gaps 15

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QY 15 AGAGDVRMISSEKLE-----RAHSAADLMWISISGDYVDYPMYHPNHGQDPLPULT 65
Db 2 AAAPSRFTFRBAEVLNAAEALNECKDKDAEPFLMT-IDNKVDYDEFEVDFHGSSV-ILTH 59
QY 66 AGODATDAFAAHPSPSARPLRRFFVYGRLS-----DYAVSPASADYRRLAQLSAGHFER 121
Db 60 VGRDGDYDFEPTFRPEAAEMETLANFVYGDIDEEDRIDKIDDFAAEVRKRLTFOGLGYD- 118
QY 122 VGRTPKQVLMAVLVA-----ALYVLAC-----ASAMHLLAGLIGFWIQS 167
Db 119 -----SKAYAAFRKVSBNLICWGLSTVIYAKKQSTLANVLASALLGLFMOQC 167
QY 168 GMMHDSGHHRIIGHVILDRVVQVLSGNCLTGLSIAMWKCNHNTIHLACSLDDPDLOH 227
Db 168 GMLAHDFLHHQVQRDFMGWDLFGAFLGVCQCGFSSSMWKDKHNTTHAARNVHGSDPIDT 227
QY 228 MPEFVSP--KLFGNI-----WSFYQRTLAFDAASKFSPSYQWHTYPRMCIAPI 276
Db 228 HPLLTWSEHALEMFSDVPDEBLTRM-----SRPMVLNQWTFEYFLISFARL 274
QY 277 NILAOSALFVL-----TEKRVPORTLEIGAVTAPMAY-PLTVASLPRMWERVAFVL 327
Db 275 SKCLQSLFLPLRPGQAHKPSGARVPLSLVEQLSLMHTWILATFLFKDPVAMLVYFL 334
QY 328 FSEFTICG-IQHWQCLNH-----FSSDYVVGPRKNDWFEKQTAGTLIDILCSPMWDFHG 381
Db 335 VSOAVCGNLLATVFSLNHGMPVISEBAV-----DMDEFTKQIITGRDVHFGLPANWFTG 390
QY 382 GLOFOIEHLHFLRLPRCHLRKVAAPNRDLCRKGGLTY 418
Db 391 GLNYQLEHHLEFSPMRHNSKIQAPAEYLCKKKYNRY 427

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RESULT 15
US-09-330-235-18
: Sequence 18 Application US/09330235
: Patent No. 6459018
: GENERAL INFORMATION:
: APPLICANT: Kuntzon, Debbie
: TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS
: FILE REFERENCE: MOCO.156.00US
: CURRENT APPLICATION NUMBER: US/09/330,235
: CURRENT FILING DATE: 1999-06-10
: PRIOR APPLICATION NUMBER: 60/089,043
: PRIOR FILING DATE: 1998-06-12
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 18
: LENGTH: 457
: TYPE: PRF
: ORGANISM: Moritella alpina
: US-09-330-235-18

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Query Match	20.7%	Score	523	DB	4	Length	457
Best Local Similarity	30.2%	Pred. NO.	2e-45				
Matches	138	Conservative	64	Mismatches	171	Indels	84
						Gaps	15

QY 15 AGAGDVRMISKKL-----RAIASADLMISIGDYYDVFWYHPHHNGGGLPLTL 65

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Db 60 VGRDGDVDFPTFRPEAAWETLANFYGDIIDSDROIKNDDFAAEVRKRLTFFQSLGYD- 118

QY 122 VGPFPKQVLVAALFYA-----ALYIVLAC---ASAAHLLAGLIGFWIQS 167

Db 119 -----SSKAYAAFKVSEFNLCIGWLSFVIAAKQGQSTLANVLAAILLGLFWQC 167

QY 168 GMMGHDGSHHRIIGHVLDRLVQVULSGNCLTGLSLAMWKCHNTHNLCSNLDHDPDQH 227

Db 168 GMLAHDFLLHHQVDFRFGWGLFGALFGVCGQFSSSMWKDKRNTTHAAPVNHGDPIDT 227

QY 226 MELFANP---LTLPGNI-----WSFFYQRTILAFDAKSEFLSYOHMFYPMWCARI 276

Db 228 HPLLTWSEHALMEFSDVPDEBLTRNM-----SREVLNQTWTFPILSLFARL 274

QY 277 NLDAQALFVL-----TEKRAYQRLLEIAGVATEFWAW--PLVLVASLPMMERVAFVL 327

Db 275 SWELQSLFVLVINGQAHKPSGARVPSLVEQLSLAMHTWLTWLTAFLEFIDPVMMLVYFL 334

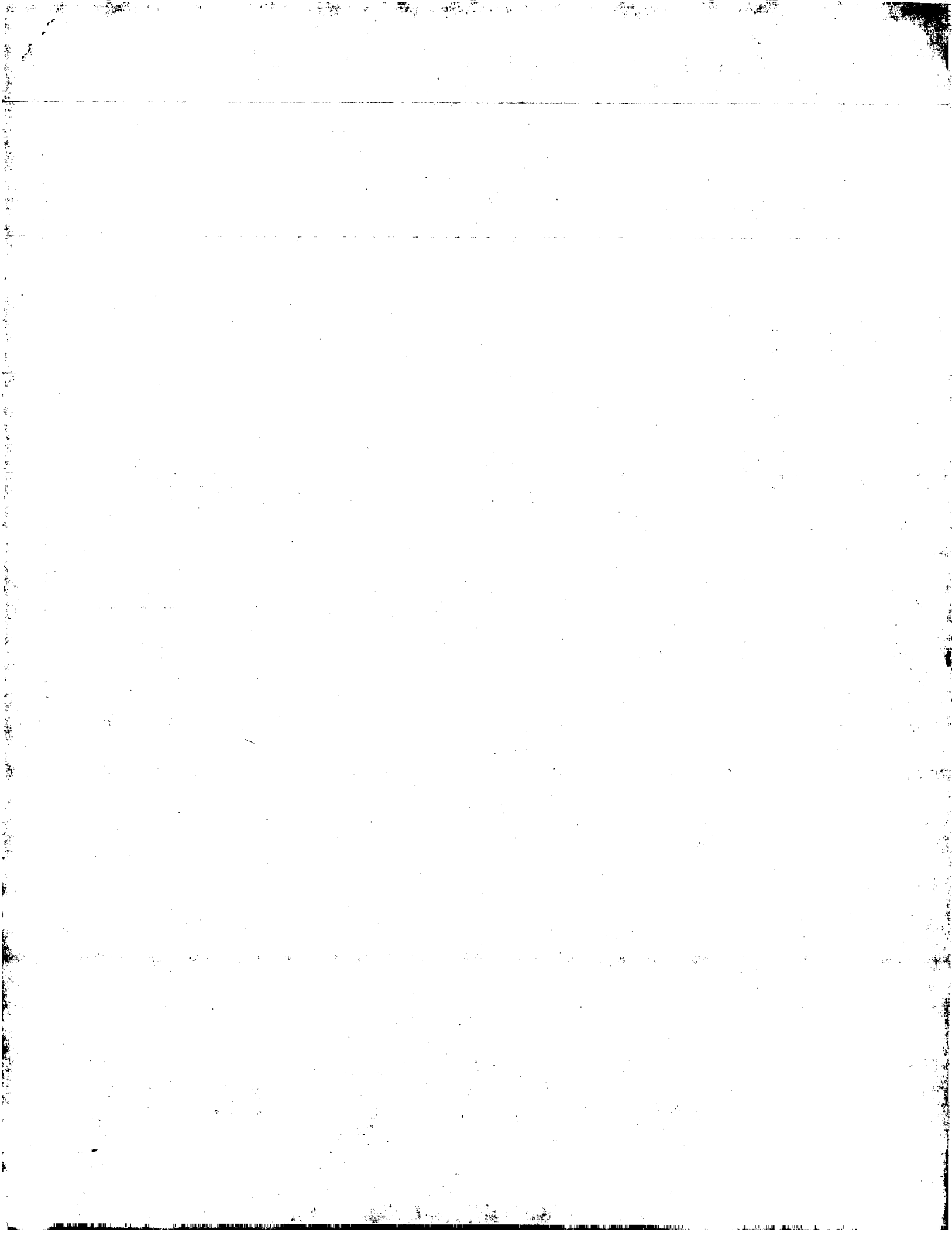
QY 328 FSTTTCG-IQHVOFCLNH-----FSSDYVVGPPKGNDFEKQNTGLTDLICSPMMDVHG 381

Db 335 VSGAVCGNLTALVFSLNHGMFVLSKEBAV---DMDFETQIITGRDVHGLFANWFG 350

QY 382 GLQFOIEHHLPRLRPRCHLRKVAAPVRDLCKKHGLTY 418

Db 391 GLNVTQLEHHLFSPSPRNHNSKIQPAVEFLCKKINRY 427

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Search completed: January 1, 2004, 06:38:13
Job time : 17.251 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:37:05 ; Search time 88.0127 Seconds
(without alignments)
1053.214 Million cell updates/sec

Title: US-09-857-524B-4
Perfect score: 2521
Sequence: 1 MPSPVDAMPAGDAAGADV.....TATSGAPKLVWEAVNTHG 462

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 733937 seqs, 200641211 residues

Total number of hits satisfying chosen parameters: 733937

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications AA:*
1: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubppa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/prodata/1/pubppa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/prodata/1/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
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11: /cgn2_6/prodata/1/pubppa/US09C_PUBCOMB.pep:*
12: /cgn2_6/prodata/1/pubppa/US09C_NEW_PUB.pep:*
13: /cgn2_6/prodata/1/pubppa/US10_PUBCOMB.pep:*
14: /cgn2_6/prodata/1/pubppa/US10_PUBCOMB.pep:*
15: /cgn2_6/prodata/1/pubppa/US10C_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1427.5	56.6	458	12	US-10-340-779A-11 Sequence 11, Appl
2	1392	55.2	448	12	US-10-340-779A-13 Sequence 13, Appl
3	1387	55.0	448	14	US-10-029-756-5 Sequence 5, Appl
4	1379	54.7	452	14	US-10-029-756-27 Sequence 27, Appl
5	612	24.3	459	10	US-09-967-477B-8 Sequence 8, Appl
6	571	22.6	453	12	US-09-769-863-14 Sequence 14, Appl
7	571	22.6	453	12	US-10-054-534B-14 Sequence 14, Appl
8	571	22.6	453	12	US-10-431-952-14 Sequence 14, Appl
9	568.5	22.6	366	12	US-10-369-493-4137 Sequence 4137, Ap
10	523	20.7	457	12	US-10-278-391-4 Sequence 4, Appl
11	523	20.7	458	15	US-10-191-513A-11 Sequence 11, Appl
12	523	20.7	458	15	US-10-191-513A-41 Sequence 41, Appl
13	455.5	18.1	443	15	US-10-340-779A-20 Sequence 20, Appl
14	454.5	18.0	473	12	US-10-369-493-6108 Sequence 6108, Ap
15	431.5	17.1	445	15	US-10-262-617-1 Sequence 1, Appl

16	413	16.4	439	12	US-09-769-863-29	Sequence 29, Appl
17	413	16.4	439	12	US-10-054-534B-29	Sequence 29, Appl
18	413	16.4	439	12	US-10-431-952-29	Sequence 29, Appl
19	408.5	16.2	323	15	US-10-191-513A-17	Sequence 17, Appl
20	408.5	16.1	444	15	US-10-191-513A-42	Sequence 42, Appl
21	406	16.1	444	15	US-10-262-617-3	Sequence 3, Appl
22	404	16.0	444	15	US-10-191-513A-12	Sequence 12, Appl
23	390	15.5	432	15	US-10-191-513A-9	Sequence 9, Appl
24	390	15.5	465	15	US-10-191-513A-38	Sequence 38, Appl
25	380	15.1	442	12	US-10-054-534B-35	Sequence 35, Appl
26	371	14.7	448	12	US-10-340-779A-4	Sequence 4, Appl
27	358	14.2	454	12	US-10-369-493-6107	Sequence 6107, Ap
28	351	13.9	439	10	US-09-967-477B-4	Sequence 4, Appl
29	348.5	13.8	470	12	US-09-769-863-20	Sequence 20, Appl
30	348.5	13.8	470	12	US-10-054-534B-20	Sequence 20, Appl
31	348.5	13.8	470	12	US-10-431-952-20	Sequence 20, Appl
32	348	13.8	453	15	US-10-156-761-9130	Sequence 9130, Ap
33	344	13.6	433	12	US-10-120-637A-69	Sequence 69, Appl
34	344	13.6	433	12	US-10-120-637A-55	Sequence 55, Appl
35	340	13.5	365	15	US-10-156-761-9835	Sequence 9835, Ap
36	330	13.1	439	12	US-10-054-534B-31	Sequence 31, Appl
37	327.5	13.0	456	10	US-09-967-477B-6	Sequence 6, Appl
38	326	12.9	513	12	US-10-120-637A-46	Sequence 46, Appl
39	323	12.8	509	12	US-10-120-637A-37	Sequence 37, Appl
40	320	12.7	446	10	US-09-903-456-30	Sequence 30, Appl
41	320	12.7	446	12	US-10-278-391-2	Sequence 2, Appl
42	320	12.7	446	12	US-10-156-761-30	Sequence 30, Appl
43	320	12.7	446	12	US-10-408-736-27	Sequence 27, Appl
44	320	12.7	447	15	US-10-191-513A-10	Sequence 10, Appl
45	314	12.5	446	12	US-10-340-779A-3	Sequence 3, Appl

ALIGNMENTS

US-10-340-779A-11	RESULT 1
Sequence 11, Application US/10340779A	
Publication No. US20030152963A1	
GENERAL INFORMATION:	
APPLICANT: Napier, Johnathan A.	
APPLICANT: Michaelson, Louise	
APPLICANT: Stobart, Keith	
TITLE OR INVENTION: Desaturase	
FILE REFERENCE: 005407.00004	
CURRENT APPLICATION NUMBER: US/10/340,779A	
CURRENT FILING DATE: 2003-03-24	
PRIOR APPLICATION NUMBER: US 09/582,034	
PRIOR FILING DATE: 2000-12-19	
PRIOR APPLICATION NUMBER: PCT/GB98/03895	
PRIOR FILING DATE: 1998-12-23	
PRIOR APPLICATION NUMBER: UK 9814034.6	
PRIOR FILING DATE: 1998-06-29	
PRIOR APPLICATION NUMBER: UK 9727256.1	
PRIOR FILING DATE: 1997-12-23	
NUMBER OF SEQ ID NOS: 23	
SOFTWARE: FaerSeq for Windows Version 4.0	
SEQ ID NO 11	
LENGTH: 458	
TYPE: PRT	
ORGANISM: Helianthus annuus	
US-10-340-779A-11	
Query Match	56.6%; Score 1427.5; DB 12; Length 458;
Best Local Similarity	55.1%; Pred. No. 4.7e-131;
Matches 254; Conservative	77; Mismatches 123; Indels 7; Gaps 3;
QY	3 PSVDAMPAGDAAGADVMSKELRAASADDLWISGVDYVTPVLPHPHGGDDL 62
DB	4 PSLEVNSIADSK-----RYITSKEIKKNNPNDLWISLIGKYVNTWEAKHPPGDA 58
QY	63 LTIAGODADAPAAVPPAPRLRRFFVG-RLSDYAVSPASADYRRLAQLSAGLFFR 121

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Db      59 INLAGODVTDAFIAFHGPTAMKHLDKLFTGYHLKDYQVSDISRHYRKLASEFAKAGMFEK 118
Qy      122 VGPTRPVQVLMVLYVLAALYVLACASMAHLIAGLIGFVWIOSGWMGDSGHHRTIG 181
Db      119 KGGVITVSLCEVSLISACVYGVLSGSEFTHMLSGALGLAMWQIAYIGHDGHYQMA 178
Qy      182 HPLADVVVQVLSGNCUTGLSIAMWKNHNTHTIACNSLDHDPDLQMPLEFVAVSPKLFNGI 241
Db      179 TRGMNPFAGIFIGNCITGISIAMWKNHNTHTIACNSLDVDPDLQHLPLMVAVSKLFNSI 238
Qy      242 WSYFYORTAFDPAASKFPISYQHTWYTPVWCARINLAQSAFLVLTERRVOPRLLEIAG 301
Db      239 TSFVYRQRLFDPLAFVSVYQHYLYPIWCVARVNLVYQITILLISKRIIPRGANIIG 298
Qy      302 VAFEMAVPLVAVSLNMMWRVAVLFEFTICIGIHOVQFCLNHFSSDVVYGPBKNDWFE 361
Db      299 TLIETWTFPLVRLPWRPRAVAVLVSFCVTGIQHIQFTLNHPSGVYVGPBKNDWFE 358
Qy      362 KOTAGTLDILCSPMWDFHGLQFOIEHHLFPLRCHLRKVAVAVDLCKKGLTYSAA 421
Db      359 KOTRGITIDACSSMDWFFGLOFQLEHHLFPLRCHLRKVAVAVDLCKKGLTYSAA 418
Qy      422 TFWGANVLTWKTIRAAALQARITATSGAPKVLWEAVNTHG 462
Db      419 SFYDANVTTLKTRTALQARLDLTN-PAPQNLAMEAFNTHG 458

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RESULT 2

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US-10-340-779A-13
; Sequence 13, Application US/10340779A
; Publication No. US20030152983A1
; GENERAL INFORMATION:
; APPLICANT: Napier, Johnathan A.
; APPLICANT: Michaelson, Louise
; APPLICANT: Stobart, Keith
; TITLE OF INVENTION: Desaturase
; FILE REFERENCE: 005407.00004
; CURRENT APPLICATION NUMBER: US/10/340, 779A
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/582, 034
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/GB98/03895
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: UK 9814034.6
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: UK 9727256.1
; PRIOR FILING DATE: 1997-12-23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Borago officinalis
; US-10-340-779A-13

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Query Match      55.2%; Score 1392; DB 12; Length 448;
Best Local Similarity 55.8%; Pred. No. 1.4e-127;
Matches 247; Conservative 73; Mismatches 121; Indels 2; Gaps 2;

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Qy      21 RMISSEKELRAHASADLMIISISGDVYDVTPWLPNHHGGLPLITLAGODATDAFAVHPP 80
Db      7 KYTSELKNDKHPGDMISIOGKAYVSDVNDHDPGSGFPLKSLAQEVTDAFVAFHFA 66
Qy      81 SARPLLRFFVVG-RLSDYAVSPASADYRRLIAQLSSAGLFEVGPPTPKVQVLMVAVLFYA 139
Db      67 STWKNDKFFFTGYLLKDYVSEVSKDYRKLVFEFSKMGGLYDKGHIMFATLCFIAMLFAM 126
Qy      140 ALVLVLAACAAMAHLAGLIGFVWIOSGWMGDSGHHRTIGHVYLDVVVQVLSGNCGLTG 139
Db      127 SVYGVLFCEGVVHLFGSGCLMGFLMIOGMIIGHAGHYMVAVSDSRINKFEGIFPANCLSG 186
Qy      200 LSLAMWKNHNTHTIACNSLDHDPDLQMPLEFVAVSPKLFNGIIPRGANIIG 259

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Db      187 ISIGWKNHNTHTIACNSLBYDPLQYIPLVVSKFEGSLTSHFEKRLTFDSLSRPF 246
Qy      260 ISYQHTWYTPVWCARINLAQSAFLVLTERRVOPRLLEIAGVATFVAVPPLVAVSLPMM 319
Db      247 VSYQHTWYTPVWCARINLAQSAFLVLTERRVOPRLLEIAGVATFVAVPPLVAVSLPMM 306
Qy      320 WERVAVLVSFTICIGIHOVQFCLNHFSSDVVYGPBKNDWFEKQTAGTLDILCSPMWDF 379
Db      307 GERIMVAVSLVSTVGQVQVSLNHFSSVYVGPBKNDWFEKQTAGTLDILCSPMWDF 366
Qy      380 HGLGLOFQIEHHLFPLRCHLRKVAVAVDLCKKGLTYSATFPGANVLTWKTIRAAAL 439
Db      367 HGLGLOFQIEHHLFPLRCHLRKVAVAVDLCKKGLTYSATFPGANVLTWKTIRAAAL 426
Qy      440 QARTATSGAPKVLWEAVNTHG 462
Db      427 QARDITK-PLPKNLWEALNTHG 448

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RESULT 3

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US-10-029-756-5
; Sequence 5, Application US/10029756
; Publication No. US20020108147A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; DELTA 6-DESATURASE

```

```

; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/029, 756
; FILING DATE: 21-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/934, 254
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 8383ZYXWVU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANG UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
; US-10-029-756-5

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Query Match      55.0%; Score 1387; DB 14; Length 448;
Best Local Similarity 55.5%; Pred. No. 4.2e-127;
Matches 246; Conservative 73; Mismatches 122; Indels 2; Gaps 2;

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Qy      21 RMISSEKELRAHASADLMIISISGDVYDVTPWLPNHHGGLPLITLAGODATDAFAVHPP 80
Db      7 KYTSELKNDKHPGDMISIOGKAYVSDVNDHDPGSGFPLKSLAQEVTDAFVAFHFA 66
Qy      81 SARPLLRFFVVG-RLSDYAVSPASADYRRLIAQLSSAGLFEVGPPTPKVQVLMVAVLFYA 139

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DB 67 STWKNDKFFETGYLLKDYVSSEVSKDYRKLVFEPFSKMGKGLDKGHIMFATLCTIAMLPAM 126
QY 140 ALVLVACASAMHLLAGLIGFWITQSGMGGHDSGHRITGHPVLDRVVOVLSGNCILG 199
DB 127 SVYGFPCBECVULVHLSGCLMGFLWQSGWIGHDAGVIVSDSRINKFGEITFANCLSG 186
QY 200 LSIAMWKCNHNTTHIACNSLDHDPDLQHMPLFAVSPKLFNGINISYFYORTLAFDAASKFP 259
DB 187 ISIGMKNMNAHNAHICNSLEVPDLOIYPLVSSKFPGLSHRYEKLTDLSRFF 246
QY 260 ISYQHTFPPVNCIARINLQSGALFVLEKRVQRLLEIAGVATFWAMYPLLVASLPMN 319
DB 247 VSYQHTFPPVNCIARINLQSGALFVLEKRVQRLLEIAGVATFWAMYPLLVASLPMN 306
QY 320 WERVAVLVSFTICGLOHVOFCNLHFSDDVYVGPCKGNDWEKOTAGTLDILCSPPMMDW 379
DB 307 GERIMFVLASLSTYGMQVQFSLNHFSDDVYVGPCKGNDWEKOTAGTLDILCSPPMMDW 366
QY 380 HGLQLOFQIEHHLFPLRCHLRKVAAPAVRDLCCKGGLTYSATFWGANVLTWKTLPRAAL 439
DB 367 HGSQOQIEHHLFPLRCHLRKVAAPAVRDLCCKGGLTYSATFWGANVLTWKTLPRAAL 426
QY 440 QARTATSGAPKXULVWEAVNTG 462
DB 427 QARDITK-PLPKXULVWEALHTHG 448

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RESULT 4

US-10-029-756-27
Sequence 27, Application US/10029756
Publication No. US20020108147A1

GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.

TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A DELTA 6-DESATURASE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza.
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/029,756
FILING DATE: 21-Dec-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,254
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Presser, Leopold

REGISTRATION NUMBER: 19,827

REFERENCE/DOCKET NUMBER: 8383EYXWVU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 452 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-029-756-27

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Query Match 54.7%; Score 1379; DB 14; Length 452;
Best Local Similarity 56.7%; Pred. No. 2,6e-126;
Matches 253; Conservative 64; Mismatches 125; Indels 4; Gaps 3;
QY 21 RMISSEKELPAHSAADLWISIGDYDVTWPLPHHFGCLPLITLAGODATDAFAAYHPP 80
DB 7 KYITAEDELRRHNSGDLWISIGKYDCSRMAAEHPGGGVPLISLAGODVTAFAIYHNG 66
QY 81 SARPLLRFFVCG-RLSDVAVSPASADYRRLAOLSSAGLFRVGVTPPVQVLMAVLFY 138
DB 67 TAMRHLDPLFTGYIYKDFEVEBISQDYRRLNENSRSGIFERKGNHIMWTFVGAVMMA 126
QY 139 AALVVLACASAMHLLAGLIGFWITQSGMGGHDSGHRITGHPVLDRVVOVLSGNCILG 198
DB 127 ALVYGVLLASESGVHMLGALLGLMLQAAVYGHDSGHVQWPTGYNKIIITDLACNII 186
QY 199 GUSIAMWKCNHNTTHIACNSLDHDPDLQHMPLFAVSPKLFNGINISYFYORTLAFDAASKF 258
DB 187 GISIAMWKCNHNTTHIACNSLDHDPDLQHMPLFAVSPKLFNGINISYFYORTLAFDAASKF 246
QY 259 FTSYQHTFPPVNCIARINLQSGALFVLEKRVQRLLEIAGVATFWAMYPLLVASLPMN 318
DB 247 LVSYQHTFPPVNCIARINLQSGALFVLEKRVQRLLEIAGVATFWAMYPLLVASLPMN 306
QY 319 WERVAVLVSFTICGLOHVOFCNLHFSDDVYVGPCKGNDWEKOTAGTLDILCSPPMMDW 378
DB 307 WERVAVLVSFTICGLOHVOFCNLHFSDDVYVGPCKGNDWEKOTAGTLDILCSPPMMDW 366
QY 379 FHGGLQFQIEHHLFPLRCHLRKVAAPAVRDLCCKGGLTYSATFWGANVLTWKTLPRAA 437
DB 367 FHGGLQFQIEHHLFPLRCHLRKVAAPAVRDLCCKGGLTYSATFWGANVLTWKTLPRAA 426
QY 438 ALQARTATSGAPKXULVWEAVNTG 462
DB 427 AVQARDLNSAPCPKXULVWEAVNTG 452

```

RESULT 5

US-09-967-477B-8
Sequence 8, Application US/09967477B
Patent No. US20020156254A1

GENERAL INFORMATION:

APPLICANT: Xiao Qiu

TITLE OF INVENTION: FAD4, FAD5, FAD6, AND FAD6, NOVEL

TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF

FILE REFERENCE: BMZ-001

CURRENT APPLICATION NUMBER: US/09/967,477B

PRIOR APPLICATION NUMBER: 60/236,303

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: 60/297,562

PRIOR FILING DATE: 2001-06-12

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FaastSeq for Windows Version 4.0

SEQ ID NO 8

LENGTH: 459

TYPE: PRT

ORGANISM: Thraustochytrium sp.

US-09-967-477B-8

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Query Match 24.3%; Score 612; DB 10; Length 459;
Best Local Similarity 32.8%; Pred. No. 3.5e-51;
Matches 154; Conservative 74; Mismatches 157; Indels 84; Gaps 15;
QY 5 VDAMPAPGADAGADVRMISSEKELPAHSAADLWISIGDYDVTWPLPHHFGCLPLIT 64
DB 2 VDLKP-----GVKRLVSKWEIREHATPAWAIYHHKIVYDISKM-DSHFGGSV-MLT 51
QY 65 LAGODATDAFAAYHPPSARPLLRFFVGLSDYAVS-----PAS-----AD 105
DB 52 QAGEDATDAFAVHPPSALKLEQGFYGVDETSKAEIGEPASDEBERARRERINEFIAS 111

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QY 106 YRLLLOLSSAGJFE-----RQPEPRKQVLTAAVLAFY---AATLVLA CASAWAHL 154
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 112 YRRLRKVVKMGMLYDASALYAMKLVSTFGIAVLSMALCFPPNSPAMTV----- 161
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 155 LAGGLGFVWIOGGMWGHDSGHHRIITGHPVLDRVVQVLSGNCITGLSIAWKKCNHNTHTI 214
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 162 -AGVINGLFQOQSGWLAHDFLHNQVCENRTLGNLIGCLVGNAMQSFQVOMKKNHNLHHA 220
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 215 ACN-----SLDHPDLQHPPLFAVSPPLFSGNISYFYQRTLAFAASKFFISYQHTWF 267
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 221 VPLNLSAKDEGFIGDIPDIDITMPLLA-----WSKEMARAFESAGPFFIRNQAFLY 271
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 268 YPIMCLARINLQAOLQSLFVLTE-----KRPQRLLIETAGVATPAWPLVLASLP---- 317
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 272 FPLLLARLSMLAQSFPEYFTEFSPFOIPDKVAFDPBEKAGLIVHWIQO---LAIPLYCN 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 318 -NMWERVAFVLFSTFIG-IOHWQPCINHFSSDYYVVGPKNDWPEKOTAGTDLIDLSPW 375
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 328 MSJFEGVAFYLMQOASGGLLALVFSIGANGMSYVERETKDPFW-QLOLVTTTRNIRASVF 366
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 376 MDWFHGOLOFOIEHNLFPRLPRCHLRKVAVPAVRDCKKHGGLTYSATPW 424
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 387 MDWFTGSLNQIDHNLFPVLVPRHNLKXNVILKSLCKEEDLPFRHETGW 435
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 6
US-09-769-863-14
: Sequence 14, Application US/09769863
: Publication No. US20030157144A1
: GENERAL INFORMATION:
: APPLICANT: Abbott Laboratories
: APPLICANT: Mukerji, Pradip
: APPLICANT: Huang, Yung-Sheng
: APPLICANT: Das, Tapas
: APPLICANT: Thurmond, Jennifer
: APPLICANT: Pereira, Suzette L.
: TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
: FILE REFERENCE: 6763.US.O1
: CURRENT APPLICATION NUMBER: US/09/769,863
: CURRENT FILING DATE: 2001-01-25
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 14
: LENGTH: 453
: TYPE: PRT
: ORGANISM: Saprolegnia diclina
US-09-769-863-14

Query Match      22.6%; Score 571; DB 12; Length 453;
Best Local Similarity 31.2%; Pred. No. 3,6e-47;
Matches 138; Conservative 77; Mismatches 163; Indels 64; Gaps 13

QY      23 ISSKELRLHAGSADDWMISGSDYVVTWPLPHNPGDDPLTLTLAGODATDAFAATHPSPA 82
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      10 ISMATIREHNRQDNAMIVIHNRVYDISAF-EDHPGG-VVMFTQAGEDADDAFAVHPSPA 67
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      83 RPLRLRFVFG-----RLSDYAVSPA$--ADYRLIAQTSAGLFE----- 120
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Db      68 LKLEGGYVGVGDOSTAAVDNISISBEVKKSGSDFLASTRKALKLEVYKRGUYSSKLYLY 127
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      121 RVGPTPKQVLYLMAVLFY--AAULYVLACASAMALLAGLIGFVMIQSGMNGHDSGH 177
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Db      128 KCASTL$IALVSA$ICLHFDSTAMTVAAV-----ILGFFYQCCGWLADHDFLH 176
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      178 RITGPRVLDYRVVQVLSGNCITGL$TAMWKKCNNTHTIACN-----SLDHDPDLOHMP 230
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Db      177 QVFENHLRGDLAGVWVGNIWQGF$VQWKNKRNTHAIPNLATBEIAFHGPDPIDTMPI 236
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      231 FAV$PKLFGNIN$YFQRTLAFDA$KFFISYQHWTFYVMVC$IARINL$QALFVL-- 287
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Db      237 LA-----WSLKGMAQHAUD$PVG$LFPMRQATLYLPIFLPAHSWIG$AMTA$FNV 287
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      288 ----TEK$PQRLLEIAGVATFWAW-YPLLVASL$PMMERVA$VLF$SFTICGI-OHVQFC 341
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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Db 288 GPGGTFPDKVQYPLLEERAGLLLLYYGNNGLGYYVAANNSSLLQAAAFLEFVSGASCGELFLAMVPS 347

QY 342 LNHSSDYVVGPPPKNDWFEKOTAGTLILCSPPMWDWTFHGGIQQFQLEHLLFRLLPRCHLR 401

Db 348 VGHNGMEVFDXDSKDFW-KLQVLSRVNTSSLIWDWFGNGLYQIDHLLFPVPRHNLPR 406

QY 402 KVARAVRDLCCKKGLTYSATF 423

Db 407 ALNVLVKSLLCKQYDLPYHETGF 428

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RESULT 7
US-10-054-534B-14
? Sequence 14, Application US/10054534B
? Publication No. US20030167525A1
? GENERAL INFORMATION:
? APPLICANT: Abbott Laboratories
? APPLICANT: Mukerji, Pradiip
? APPLICANT: Huang, Yung-Sheng
? APPLICANT: Dae, Tapas
? APPLICANT: Thurmond, Jennifer M.
? APPLICANT: Pereira, Suzette L.
? TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
? FILE REFERENCE: 6763. US. P1
? CURRENT APPLICATION NUMBER: US/10/054.534B
? CURRENT FILING DATE: 2002-01-22
? PRIOR APPLICATION NUMBER: US 09/769,863
? PRIOR FILING DATE: 2001-01-25
? NUMBER OF SEQ ID NOS: 55
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 14
? LENGTH: 453
? TYPE: PR1
? ORGANISM: Saprolegnia diclina
US-10-054-534B-14

```

Query Match	22.6%	Score 571	DB 12	Length 453
Best local similarity	31.2%	Pred. No. 3,66-47		
Matches 138	Conservative 77	Mismatches 163	Indels 64	Gaps 13
QY	23	ISSKELRAHASADDLWISIGDVYDVTWLEPHHFGDILPLITLAGQADTAPAAVHPSPA	82	
DB	10	ISMATIEHHNQDAMWIVIHKKVYDISAF-EDHEGG-VVMFTQAGEBDTDAFAVHPSSA	67	
QY	83	RPLRRFPVGG-----RLSDYAVSPA-----ADYRRLAOTSAGLAE-----	120	
DB	68	LKLIEQYVGGVDOOSTAAVDTISDEYKSSQSDPTASTRKRLREYKRGVLDSKLYLY	127	
QY	121	RVGPTPKVQVLVMAVLFFY---AALYVLACASAMAHLLAGLIGFWIIGSGMGHSGHH	177	
DB	128	KCASTLSIALVSAAIICLHFSDSTAMVMAAV-----ILGLFYQQCGMLAHDFLHH	176	
QY	178	RITGHPVLDRVVOYLSNGCLGSLIAMWKKGNHTNHIACTN-----SLHDPDLQCHPRL	230	
DB	177	QVFBNHLEGGDVGWVGNGMLQGFSEVQWKKGNKNTNHAIENLHAATPELAFHGDDPDTMPL	236	
QY	231	FAVSPKLEGNWISYFQRTLAFDAASKFPISYQHTFYPVWCICARINLLAQSALFVL---	287	
DB	237	LA-----WSLKMAQHAVDSPVGLFPMRYQAVLYFERILLFARISVIVISQAMAYAFYV	287	
QY	288	-----TEKRVPRRLLEIAGVATFFMAV-YDLVLSLPMNWERAPVLFSTTIGI-QHVOFC	341	
DB	288	GGGFGFDVQYPLLEIRAGLLIYGGNIGLVPAANNLSLQAAAFLEFVSQASGGLFLAMFVS	347	
QY	342	LNHFSSDVYVPRKGNDFEFKQETAGTLDILCSPMWDMFHGGLQFOIEIHHLEPRRLRCHLR	401	
DB	348	VGHNGMEVFDKDSKPDWF-KLQVLSTRVNTSSLIWMDFGSLNYQIDHHLFPMVPRHNLPR	406	
QY	402	KVAPAVNDLCKKHGLTYSAAIF 423		
DB	407	ALNVLVSLCKQYDI PYHETGF 428		


```

RESULT 8
US-10-431-952-14
; Sequence 14, Application US/10431952
; Publication No. US2003019073A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thummond, Jennifer
; APPLICANT: Perreira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763.US.01
; CURRENT APPLICATION NUMBER: US/10/431,952
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US/09/769,863
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Saprolegnia diclina
US-10-431-952-14

Query Match      22.6%; Score 571; DB 12; Length 453;
Best Local Similarity 31.2%; Pred. No. 3.6e-47;
Matches 138; Conservative 77; Mismatches 163; Indels 64; Gaps 13;

QY 23 ISSKEIRAAASADDELISIGDYDVTPLPHPGDLPPLTLAGODATDAFAAYHPSA 82
DB 10 ISWATIRENRQDNAMIVIHKKYDLSAF-EDHPGQ-VVMFTQAGSDATDAFAVHPSSA 67
QY 83 RPLRRFFVFG-----RLSDYAVSPAS--ADYRRLAQSSAGLFE----- 120
DB 68 LKLEQYVGVGDVQSTAAVDTISIDVKKSQSPFIASRYKRLREVRRLGLYDSSKLYLY 127
QY 121 RVGPPKQVLMAVLFY---ALYLVLCASAMAILLAGLIGFWIQSGMKGHSGNH 177
DB 128 KCASTISIALVSAIICLHPDSTIMVPAV-----ILGLFYQCGWLADHFLHH 176
QY 178 RITGHPVLDRAVQVLSGNCITGLSIAMKCNHTTHIACN-----SLDHPDLQHP 230
DB 177 QVFEHNLFGDVLGVMTGNLMQSGSVQMKKNTHTAIFNLATPEIAFHGDDITMTI 236
QY 231 FAVSPRLFGNINISYFYQRTLAFDAASKFFISYQHTFFPYMCIARINLAQSAFLVL-- 287
DB 237 LA-----WSLKMAQHAVDSPVGLFFMRVQAYLYPRLIFARISWVLSQAMVAFYNY 287
QY 288 ----TEKRPQRLLEIAGVATFWAM--YPLLVASLPMWMERVAFLPSFTTCG-QHVOFC 341
DB 288 GPGGTDFDKQVPLERAGLLYYGMNLGYUAAAMSLQAAAFLLFVSQASCGFLAMVPS 347
QY 342 LNHFSDDVYVGPFGKNDWEFKOTAGTLDLICSPMMDPFGLOFOIEHLFPRLPCHLR 401
DB 348 VGHNGHEVDKSKSPFW-KLQVLSRANTVSLMIMFGGLNYQIDHHLFPVPRHNLP 406
QY 402 KVAAPAVRDLCKKGGLTYSATF 423
DB 407 ALNVLVKSICKQYDIYHETGF 428

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; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4137
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-369-493-4137

Query Match      22.6%; Score 568.5; DB 12; Length 366;
Best Local Similarity 35.1%; Pred. No. 4.7e-47;
Matches 123; Conservative 63; Mismatches 139; Indels 25; Gaps 9;

QY 106 YRLLAQSSAGLFRVGPFPKQVLMAVLFYAALYVLACAS----AMA-HLLAGGL 160
DB 7 YRELNERIKAEGLVD-----CNVVAVAIBGFR--YTLIFGCGLLFLKMGVYVPSAFL 57
QY 161 GFVWTQSGMGGHSHHRTGHPVLDRAVQVLSGNCITGLSIAMKCNHTTHIACNSLD 220
DB 58 GSFMTQVFTAHADAGHMGIITHFHVDTVGIITADFIGLSIGMKRNHNHIIITNSPE 117
QY 221 HDPDLQHPLEFVSPKLCNINISYFYQRTLAFDAASKFFISYQHTFFPYMCIARINLA 280
DB 118 HDPDIEHLPFFAISHPFTNLSTYDRWEMEDIAKPFVSLQHLVYIIMPARNLVLR 177
QY 281 QSAFLVL---TEKRPV---QRLLEIAGVATFWAM--YPLLVASLPMWMERVAFLPSFT 332
DB 178 LSWELILKQAGAKHGRPAMHRLBELVGOVFFCWCYGYGMKAIQNMKRFPMISHAV 237
QY 333 CGIQHVQCLNHF--SDVYVGPFGKNDWEFKOTAGTLDLICSPMMDPFGLOFOIEHL 391
DB 238 TSPRLHVVQTLISHPAMSTSDIGPHE--SFPQRMILRTMTDVCPEMIDFFHGLOFOIHL 295
QY 392 FPRLRCHLRKVAAPAVRDLCKKGGLTYSATFWGNVLTWKLTLBAALQA 441
DB 296 YRIRHNRKRTQKLVQPCNDVGIYALYGVFEGNKHVIGRLADVARA 345

RESULT 10
US-10-278-391-4
; Sequence 4, Application US/10278391
; Publication No. US2003015916A1
; GENERAL INFORMATION:
; APPLICANT: KOCCHIK, JOHN J.
; KELLER, BRUCE
; HUANG, YUNG-SHENG
; KIRCHNER, STEPHEN J.
; MUKERJI, PRADIP
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM
; PRODUCTS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/278,391
; FILING DATE: 23-Oct-2002
; CLASSIFICATION: 800

```

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/087,578
 FILING DATE: 29-MAY-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: CARROLL, PETER G.
 REGISTRATION NUMBER: 32,837
 REFERENCE/DOCKET NUMBER: OHU-03348
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 457 amino acids
 TYPE: amino acid
 STRANDEDNESS: No
 TOPOLOGY: No
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-10-278-391-4

Query Match 20.7%; Score 523; DB 12; Length 457;
 Best Local Similarity 30.2%; Pred. No. 1,8e-42;
 Matches 138; Conservative 64; Mismatches 171; Indels 84; Gaps 15;

15 AGAGDVRMISSEKEL-----RAHASADLMISGVDYVTPMLPHHGGDLPLTL 65
 2 AAAPSVRTTTRAEVLAALNEGKDAEAPFLMI-IDNKYVDVREVPDHPGGSV-ILTH 59
 66 AGODATDAFAAYHPSPARPLRRFPVGRLS---DYAVSPASADYRLLAQLSSAGLPER 121
 60 VGKDGTDVDTFTPEAAMETLANFYVGDIDESDRDIKNDFAAEVRKRLTLFQSLGYD- 118
 122 VGPTRVQLVLAVALFYA-----ALYVLAC---ASAMAHLLAGLIGFWIQS 167
 119 -----SSKAYAEKVSFNLCIWGLSTVIYAKWGQSTLANVLSAALLGLFWQOC 167
 168 GNMGDSGHHRIIGHVLDREVQVLSGNCLTGLSIAMWKNHTTHIACNSLDHDPDLQ 227
 168 GMLADHFLHGVQDFRFGWDLFGAFLGVCGQSSSWMDKNTHTHAAPVHGEDDIDT 227
 228 MFLFAVSP---KLFENI-----WSYFYQRTLAFDAASKFISYQHTTFYPMCIARI 276
 228 HPLLTSEALMFSVDPEBELTRMW-----SRFVNLQTMFYFPIISFARL 274
 277 NILAAGALFVL-----TEKRVQRLLEIAGVATFWAMY-PLVASLPMNMERVAFLV 327
 275 SMCLOSLFVLDPNGQAHKPSGARVPISLVEQLSLAMHMTWYLATMFLFKDPVNMILVFL 334
 328 FSFTICG-IQHVQFCLNH-----FSSDYYVVGPPKGDWFEKQTAGTLDILCSPPMDWFG 381
 335 VGOAVCGNLATVFSLNHGMFVISKAEAV---DMDFTKQIITGRDVHPLGFANWFTG 390
 382 GLQFOIEHHLFPRLLPRCHLRKVAFAVADLCKKHGLTY 418
 391 GLNYQIEHHLFSPMRHNSKIQPAVETLCKKKNVRY 427

RESULT 11
 US-10-191-513A-11
 Sequence 11, Application US/10191513A
 Publication No. US20030104596A1
 GENERAL INFORMATION:
 APPLICANT: Abbott Laboratories
 APPLICANT: Mukerji, Pardip
 APPLICANT: Leonard, Amanda E.
 APPLICANT: Huang, Yung-Sheng
 APPLICANT: Tapas, Das
 TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
 FILE REFERENCE: 6295.US.D3
 CURRENT APPLICATION NUMBER: US/10/191,513A
 CURRENT FILING DATE: 2002-09-25
 PRIOR APPLICATION NUMBER: US 09/227,613
 PRIOR FILING DATE: 1999-01-08

PRIOR APPLICATION NUMBER: PCT/US98/07422
 PRIOR FILING DATE: 1998-04-10
 PRIOR APPLICATION NUMBER: US 08/833,610
 PRIOR FILING DATE: 1997-04-11
 NUMBER OF SEQ ID NOS: 54
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 11
 LENGTH: 458
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (458)...(458)
 OTHER INFORMATION: Xaa = Unknown or other at position 458
 US-10-191-513A-11

Query Match 20.7%; Score 523; DB 15; Length 458;
 Best Local Similarity 30.2%; Pred. No. 1,8e-42;
 Matches 138; Conservative 64; Mismatches 171; Indels 84; Gaps 15;

15 AGAGDVRMISSEKEL-----RAHASADLMISGVDYVTPMLPHHGGDLPLTL 65
 2 AAAPSVRTTTRAEVLAALNEGKDAEAPFLMI-IDNKYVDVREVPDHPGGSV-ILTH 59
 66 AGODATDAFAAYHPSPARPLRRFPVGRLS---DYAVSPASADYRLLAQLSSAGLPER 121
 60 VGKDGTDVDTFTPEAAMETLANFYVGDIDESDRDIKNDFAAEVRKRLTLFQSLGYD- 118
 122 VGPTRVQLVLAVALFYA-----ALYVLAC---ASAMAHLLAGLIGFWIQS 167
 119 -----SSKAYAEKVSFNLCIWGLSTVIYAKWGQSTLANVLSAALLGLFWQOC 167
 168 GNMGDSGHHRIIGHVLDREVQVLSGNCLTGLSIAMWKNHTTHIACNSLDHDPDLQ 227
 168 GMLADHFLHGVQDFRFGWDLFGAFLGVCGQSSSWMDKNTHTHAAPVHGEDDIDT 227
 228 MFLFAVSP---KLFENI-----WSYFYQRTLAFDAASKFISYQHTTFYPMCIARI 276
 228 HPLLTSEALMFSVDPEBELTRMW-----SRFVNLQTMFYFPIISFARL 274
 277 NILAAGALFVL-----TEKRVQRLLEIAGVATFWAMY-PLVASLPMNMERVAFLV 327
 275 SMCLOSLFVLDPNGQAHKPSGARVPISLVEQLSLAMHMTWYLATMFLFKDPVNMILVFL 334
 328 FSFTICG-IQHVQFCLNH-----FSSDYYVVGPPKGDWFEKQTAGTLDILCSPPMDWFG 381
 335 VGOAVCGNLATVFSLNHGMFVISKAEAV---DMDFTKQIITGRDVHPLGFANWFTG 390
 382 GLQFOIEHHLFPRLLPRCHLRKVAFAVADLCKKHGLTY 418
 391 GLNYQIEHHLFSPMRHNSKIQPAVETLCKKKNVRY 427

RESULT 12
 US-10-191-513A-41
 Sequence 41, Application US/10191513A
 Publication No. US20030104596A1
 GENERAL INFORMATION:
 APPLICANT: Abbott Laboratories
 APPLICANT: Mukerji, Pardip
 APPLICANT: Leonard, Amanda E.
 APPLICANT: Huang, Yung-Sheng
 APPLICANT: Tapas, Das
 TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
 FILE REFERENCE: 6295.US.D3
 CURRENT APPLICATION NUMBER: US/10/191,513A
 CURRENT FILING DATE: 2002-09-25
 PRIOR APPLICATION NUMBER: US 09/227,613
 PRIOR FILING DATE: 1999-01-08
 PRIOR APPLICATION NUMBER: PCT/US98/07422
 PRIOR FILING DATE: 1998-04-10
 PRIOR APPLICATION NUMBER: US 08/833,610
 PRIOR FILING DATE: 1997-04-11

```

; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (458) ..(458)
; OTHER INFORMATION: Xaa = Unknown or other at position 458
US-10-191-513A-41

```

```

Query Match      20.7%; Score 523; DB 15; Length 458;
Best Local Similarity 30.2%; Pred. No. 1.8e-42;
Matches 138; Conservative 64; Mismatches 171; Indels 84; Gaps 15;

```

```

QY 15 AGAGVRLMSSKEL-----RAHASADLMISIGSVYDTWLPPLPHPGGDLPLTL 65
DB 2 AAAPSVRTPTRAVLNAEALNEGKDAEAPFLMI-IDNVAVDVREFVDPHGGSV-ILTH 59
QY 66 AGODATFAAAYHPPSARPLLRFPYGRUS----DYAVSPASADYRRLAQLSSAGLPER 121
DB 60 VKKDGTDFDTHTPEAMETTLANFYGDIDESDRDIKNDFAAEVAKLTLLFQSLGXYD- 118
QY 122 VGPTKVLVLMAVLFYA-----ALYVLAC---ASAMAILLAGLIGFWIQS 167
DB 119 -----SSKAYAFKVSFNLCIMGLSTVIYAKMGOTSTLANVLSAALLGLFWQC 167
QY 168 GMMGDSGHRITGHEVLDRVVQVLSGNCLTGLSIAMWKCNHTTHIACNSLDHDPDLOH 227
DB 168 GMLADHFLHQVFODRFMGDLFGAFIGVCGFSSSMWKDKNTHHAADNVHGEDPIDT 227
QY 228 MFLFVSP---KLFGNI-----WSYVQRTIADASKEPFISQHTFFPWCIAPI 276
DB 228 HPLLTMSEHALMFSDVPDEELTRM-----SRFVNLQTFPFPILISFAL 274
QY 277 NLLAASALEFVL-----TEKRVPORLIEIAGVATFAMY--PLVASLPNMWERVAFVL 327
DB 275 SWCLOSLFVLPLNGAHRKSGARVPSILVEQSLAMHWYLAITMELFKDVNMLVYTL 334
QY 328 SFPTTCG-IQHVQCLNH-----FSSDYVYVPPKGNDFEKOCTAGTLILCSPMMDWFG 381
DB 335 VQAACVGNLAIIVFSINHGMPVISKEEAV---DMDFPTKQIIGRDVHPLFANWFTG 390
QY 382 GIQFQIEHHLFRLPRCHLRKVAAPVRDLCCKHGULT 418
DB 391 GLNYQIEHHLFSPMPHNSKIQPAVETLCKKYNRY 427

```

```

RESULT 13
US-10-340-779A-20
; Sequence 20, Application US/10340779A
; Publication No. US20030152983A1
; GENERAL INFORMATION:
; APPLICANT: Napier, Jonathan A.
; APPLICANT: Michaelson, Louise
; APPLICANT: Stobart, Keith
; TITLE OF INVENTION: Desaturase
; FILE REFERENCE: 005407.00004
; CURRENT APPLICATION NUMBER: US/10/340,779A
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/582,034
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/GB98/03895
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: UK 9814034.6
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: UK 9727256.1
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 443

```

```

; TYPE: PRT
; ORGANISM: C. elegans
; US-10-340-779A-20

```

```

Query Match      18.1%; Score 455.5; DB 12; Length 443;
Best Local Similarity 29.0%; Pred. No. 7.2e-36;
Matches 134; Conservative 70; Mismatches 173; Indels 85; Gaps 18;

```

```

QY 35 DDLWISIGDYDVTPWLPPLPHPGGDLPLTLAODATDAFAAYHPPSAR-----PLLRBF 69
DB 15 DCKMLYLSEEL-----VKGHPGAV-IBQYNSDATHIFHAFHGGSSQAYQDLCLKG 67
QY 90 -----FVGR-----LSDYAVSPAS-----ADYRRLAQLSSAG-----L 118
DB 68 GEHDFLEKQLEKRLDKYDINSAIDVSAQCKRNVSEKLRQLKHDGGLKANETVYL 127
QY 119 FERVPTKVLVLMAVLF--YAALYVLACASAMAILLAGLIGFWIQSGMNGHDSG 175
DB 128 FVAIS-----TLISAFAPFQYLQWLYTSAC-----LLALAQCFGMLTHERC 171
QY 176 HHRITGHPVLDRVVQVLSGNCLTGLSIAMWKCNHTTHIACNSLDHDPDLOHPLFVSP 235
DB 172 HQQPKRNPPLNDTISLFGNPLQGFSSRDWKKDKNTHHAATVVIDDGDIDLAPLPAFLP 231
QY 236 KLFGNIWSFYQRTIAPDAASKFISYQHTFFPWCIAPIMLAQSALFVLTEKRVPR 295
DB 232 ---GDLCY---KAFKALIKVYQHLVYTMPLRFSWTGOSVQVWVKEKQMEYK 284
QY 286 IL-----EIAGVATFAMYPLVLVASLPNMWERVAFLSFPTTCG--IQHVQCLNHFS 347
DB 285 VQRNAFWQOATIVGHMAMVVFQFLPLPLRVAVYFISQGGGLLIANH-VTFVHNSV 343
QY 348 DTVVPPKGG---NDMEKQCTAGTLILCSPMMDWFGGIQFQIEHHLFRLPRCHLRKA 404
DB 344 DKY--PANSRLINNPALQILITRMWTPSPFIDWLMGGIANTQIEHHLFPTMRCMLNACV 401
QY 405 PAVRDLCKKGIGLYTSAATFGANVLTWKTLR--AAALQRTA 444
DB 402 KYVKEMCKENLPYLVDDYFDGGMNLQQLKMAHIIQAKA 443

```

```

RESULT 14
US-10-369-493-6108
; Sequence 6108, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiandeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6108
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6108

```

```

Query Match      18.0%; Score 454.5; DB 12; Length 473;
Best Local Similarity 28.1%; Pred. No. 9.8e-36;
Matches 138; Conservative 71; Mismatches 163; Indels 113; Gaps 20;

```

```

QY 35 DDLWISIGDYDVTPWLPPLPHPGG-----DLF-----LLTLAG----- 67
DB 15 DCKMLYLSEEL-----VKKHPGAVIQVSIPLANKNIETRRGITTRGSSNALDILVFX 68

```

QY 68 --ODATDAFAAHPPEAR-----PLLR-----FVGR-----LSDYAVSPAS 103
 DB 69 RNSDATHIFPAFEGSSQAYKQDLKKGHEDEPLEKQLEKRLDKVDIVASVDVSAQ 128
 QY 104 -----ADYRRLAQLSSAG-----LFEVGPFPKVOVLMAVLF---YAAIYVLA 146
 DB 129 EKKVSEFEBELRKLHDDGIMKANETVFLPKAIS-----TLSIMAFAYLYQYIGWYITSA 183
 QY 147 CASAMAMHLLAGLIGFVWISGMMGHDSCGHRITGHPVLDIVVQVLSGNCITGLSIAMMK 206
 DB 184 C-----LALAMQOPGWLTHFECHQOPFKNPLNDTISLFGANLQSPSDMMK 232
 QY 207 CNHNTHHIACNSLDHPDLOHMPDFAVSPFLFGNIMSYFYQRTLAFDAASKFEISYQHW 266
 DB 233 DKNTHTAAITNVVDHGDIDLALFAFIP---GDLCY---KASPEKALIKVIPPQHLX 285
 QY 267 FIVVPCIRINLLAQSALFVLTKEKRVQRL-----ELGVATFMAWYPLVASLPMNW 320
 DB 286 FTMLPMLRFSWGTGOSQVWFKENOMEYKYQRNAFEQATIVGHMAWVYQULFPTWP 345
 QY 321 ERVAFVLFSTIG--IGHVQFCLNHFSSDYYVGPFGK---NDMEKQTAGTLDICSPW 375
 DB 346 LRVAFTIISQMGGLIAHV-VTFNHSVDKY--PANSRLNPFALQIITTNMTPSPF 402
 QY 376 MDMFHGLOFQIEHHLFPLRCHLRKVAFAVRLCKHGLTYSAAATFGANVLTWKTJR 435
 DB 403 IDLWGLNLYQIEHHLFPTMPCRLNACMKYVEMCKENLPLVLDYDFDGYAMNIQQLK 462
 QY 436 --AAAIQART 444
 DB 463 NMAEHIOAKXA 473

RESULT 15

US-10-262-617-1
 ; Sequence 1, Application US/10262617
 ; Publication No. US2003007747A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Corley, Neil C.
 ; TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS
 ; FILE REFERENCE: PF-0494-1 DIV
 ; CURRENT APPLICATION NUMBER: US/10/262,617
 ; PRIOR FILING DATE: 2002-09-30
 ; PRIOR FILING DATE: 1998-03-26
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1
 ; LENGTH: 445
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US2003007747A1 2451043CD1
 US-10-262-617-1

Query Match 17.1%; Score 431.5; DB 15; Length 445;
 Best Local Similarity 28.6%; Pred. No. 1.6e-33;
 Matches 129; Conservative 72; Mismatches 199; Indels 51; Gaps 17;

QY 9 PARGDAAAGADVMMISKELRAHASADDLWISGVDYDTPWLPHHFGDDLPLTLTAQ 68
 DB 9 PRGGPQPGAPLPTFCWEQIRAHDOGDKWLVERRVYDISRWAQRHFGGSRLLIGHGAE 68
 QY 69 DATDAFAAHP--SARPLRRFFVGRLSDYAVS---PASA---DYRRLAQLSSAGLF 119
 DB 69 DATDAFAAHPQDLNFPVAKFLQPLLIGLAPESQDGPLNAQULVEDFRALQAEDMKLF 128
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 DB 402 PLVKSICAHGHSYEVKPFLLVLDIVRSK 432

Search completed: January 1, 2004, 06:58:35
 Job time : 89.0127 secs

TITLE Identification of Primula fatty acid Delta(6)-desaturases with n-3 substrate preferences (1)
 JOURNAL FEBS Lett. 542 (1-3), 100-104 (2003)
 MEDLINE 22615586
 PUBMED 12729906
 REFERENCE 2 (bases 1 to 1385)
 AUTHORS Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and Napier,J.A.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton Research Station, Long Ashton, Bristol BS41 9AF, UK
 FEATURES
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 184 TCTGGCGGCT 243
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 DB 901 GATAGCGCTGTTCTGGGTTTGTATCCCTCTGCTTTCTTCTCTTACTGCGG-GA 959
 QY 722 GATAGCGGTAATGTTTNGCTGCTGCTTGTGCTGCTTGTGCTGCTGCTGCTGCTGCT 781
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 DB 1019 TTGTTGAACATTTCTCGCGGAGGTCTTACTTGCTC 1056
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 AY234124
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
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 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots;
 Asterales; Ericales; Primulaceae; Primula.
 1 (bases 1 to 1681)
 Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and Napier,J.A.
 TITLE Identification of Primula fatty acid Delta(6)-desaturases with n-3 substrate preferences (1)
 JOURNAL FEBS Lett. 542 (1-3), 100-104 (2003)
 MEDLINE 22615586
 PUBMED 12729906
 REFERENCE 2 (bases 1 to 1681)
 AUTHORS Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and Napier,J.A.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton Research Station, Long Ashton, Bristol BS41 9AF, UK
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 53. 1411
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Db	920	TCAGCTACCAACACTGACATTTTATCCGGTGATGGAGTTTGCAGAGTAATATCTTCTTG	979
QY	601	TGCAGACAAATCTGCTATTGTTTTCGAGAGNAAAAGTCAGATGAG-AGCTTGAACATPA	659
Db	980	TGCAGTCATAGTGTCTGTCATCAACAAAAGAAAGAGTCCGGAGGCTGGCTGAGATCG	1039
QY	660	TGGGATCCTGTGTGTTTTGGACTTGGTCCATCTTTAGTGNCTTGCCTGCCAAATTTGGGC	719
Db	1040	CCGGTGTCTGCCTTCTGAGGTTTGGTAAACCTTGTGTGTGTCTTGCCTCCGAATTTGAT	1099
QY	720	CTGATAGGGGNAATGTTTNGCTGCTGTACCTTGTGCTTTGTTNCCNATCCAGACACTTGAG	779
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QY	838	NTGANAATCAGACAAAGGGGTCAATTGGAATATCTTTGTGNCCC	879
Db	1219	TTTGAGAGGCAAAACCGCAGGCACACTTGATATCAAGTCTCC	1260

RESULT 4	
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LOCUS	1410 bp mRNA linear PLN 04-MAY-2003
DEFINITION	Pirula farinosa fatty acid delta-6 desaturase mRNA, complete cds.
ACCESSION	U78442

VERSION	AY234125.1	GI:30350276
KEYWORDS		
SOURCE	Primula farinosa	
ORGANISM	Primula farinosa	

REFERENCE
1 (bases 1 to 1410)

REVIEWED	OGUNGBAYE, O. V., DEACON, E. J., MICHAELSON, D. V., SENEY, F. R. and NAPIER, J. A.
TITLE	Identification of <i>Prunella</i> fatty acid Delta(6)-desaturases with n-3 substrate preferences (1)
JOURNAL	FEBS Lett. 542 (1-3), 100-104 (2003)

MEDLINE	22613586
PUBMED	12729906
REFERENCE	2 (bases 1 to 1410)
AUTHORS	Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and Nanier,J.A.

FEATURES	Direct Submission
JOURNAL	Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton Research Station, Long Ashton, Bristol BS41 9AF, UK
1	Location/Qualifiers
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Query Match	33.24;	Score 292.2;	DB 8;	Length 1410;
Best Local Similarity	60.94;	Pred. No. 2.7e-58;		
Matches 499; Conservative	0;	Mismatches 319;	Indels 2;	Gaps 2;

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VERSION      AF005096.1 GI:4101625
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SOURCE       Ricinus communis
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
REFERENCE    1 (bases 1 to 1856)
AUTHORS      Sayanova, O., Smith, M.A., Lapinskas, P., Stebarta, A.K., Dobson, G.,
              Christie, W.W., Shewry, P.R. and Napier, J.A.
TITLE        Expression of a borage desaturase cDNA containing an N-terminal
              cytochrome b5 domain results in the accumulation of high levels of
              delta6-desaturated fatty acids in transgenic tobacco
              Proc. Natl. Acad. Sci. U.S.A. 94 (8), 4211-4216 (1997)
JOURNAL      97268723
MEDLINE      9108131
PUBMED       2 (bases 1 to 1856)
REFERENCE    Napier, J.A. and Shewry, P.R.
AUTHORS      Direct Submission
TITLE        Submitted (22-MAY-1997) Cell Biology, IACR-Long Ashton Research
              Station, Long Ashton, Bristol BS18 9AF, UK
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BASE COUNT   493 a      326 c      388 g      648 t      1 others
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Query Match 31.9%; Score 280.8; DB 8; Length 1856;
Best Local Similarity 63.8%; Pred. No. 1.4e-55;
Matches 445; Conservative 0; Mismatches 250; Indels 2; Gaps 2;

QY 126 AAGGGCCACAAACCTCCATCTCTCTCTCTATTTCTACCTTTTCTCTCTCTGTC 185
DB 460 AAGGGCCACAAACCTCCATCTCTCTCTCTATTTCTATGCTATGCTACTGCTTTGAGTGT 519
QY 186 TGGCGGCTCCTCTTCCGACAGCAGCTTTCGACAGTGGCTTCCGCTGATGATAGGC 245
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QY 246 TTTCTCTGATTCAGAGCGGCTGATAGGCAAGCTCCGCGCATTAACAAGTATGCTC 305
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QY 306 AGCGCGCGCTCAACCGCGCAATTCAGATTCTCTCGGCAACATTTCTCGCGGATACGC 365
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QY 426 GACCTGATCTGAGACATGCGGCTCTTTCAGATTGCTGCGGCTTCTTCATTCATCA 485
DB 760 GATCCAGATCTGAGCATATGCTCTTTCTTGGCGTATCCCAAAATTTTTCAGTTCAATT 819

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QY 486 ACCCTCATTTNCTATGAGGAGAGTTNGAGTTGATTCATTTGATNGTTTGAATCTGC 545
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QY 665 ATCTTGTGTTTGGACCTGCTGCTCTTATAGTNCCTGCTGCAATTTGGGCTGAT 724
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DB 1119 TTTGATCATTTCTGCTCAGATGTTATCTTGGCCTC 1155

RESULT 5
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LOCUS       AX007239 1594 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 1 from Patent WO0000593.
ACCESSION   AX007239
VERSION     AX007239.1 GI:9995105
KEYWORDS    BRAESSICA napus (rape)
ORGANISM   Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1
AUTHORS     Zaehring, U., Heinz, E., Schmidt, H. and Sperling, P.
TITLE       Sphingolipid-desaturase
JOURNAL     Patent: WO 0000593-A 1 06-JAN-2000;
            ZAEHRINGER ULRICH (DE); HEINZ ERNST (DE); SCHMIDT HERMANN (DE);
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Query Match 31.7%; Score 279; DB 6; Length 1594;
Best Local Similarity 61.4%; Pred. No. 3.6e-55;
Matches 518; Conservative 0; Mismatches 319; Indels 6; Gaps 5;

QY 1 CGGCTCCCTCTCTCTCCCGCTTCTCCACCTCCACCTGTTTTCGACACACAGCTT 60
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 QY 121 ACCGCAAGGCGCACACAACCTCCATCTCTCTCTCTTATTTTCACTCTTCTCT 180
 DB 373 ATAAAAAGGTCAAGTCACTCTTATACAGCTCAAGTCCGCTGCTGCTGCTGCTG 432
 QY 181 CTGCTGCGGCGGCTCTCTCTCCGACAGCACTTTCGTCAGCTTTCGCTTCCGCTG 240
 DB 433 TTGTATACGCTGTTTGTTCATGACGAGCATATGGGCCCTTATATATCCGCGCTT 492
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 DB 553 CGTCAACGAAGCCGTGATTAATTAATCTGTCAGCTTCTGCTGTAATCTGCATCA 612
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 DB 613 TATGATCGGCTGTGGAAGTGAACCAACAGCCTCAATCTCTTATATAGTCTTG 672
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 DB 1091 GTT 1093

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 ACCESSION delta-8 sphingolipid desaturase; fusion protein; sld1 gene.
 VERSION AJ224160.1 GI:3819707
 KEYWORDS Brassica napus (rape)
 SOURCE Brassica napus
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 REFERENCE 1 Sperling, P., Zahringer, U. and Heinz, E.
 A sphingolipid desaturase from higher plants. Identification of a
 new cytochrome b5 fusion protein

JOURNAL J. Biol. Chem. 273 (44), 28590-28596 (1998)
 MEDLINE 9903197
 PUBMED 9786850
 REFERENCE 2 (bases 1 to 1610)
 AUTHORS Sperling, P.
 TITLE Direct Submision
 JOURNAL Submitted (13-FEB-1998) Sperling P., Physiologie, Institut fuer
 Allgemeine Botanik der Universitaet Hamburg, Ohnhorststrasse 18,
 D-22609 Hamburg, GERMANY
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 Best Local Similarity 61.4%; Pred. No. 3,6e-55;
 Matches 518; Conservative 0; Mismatches 319; Indels 6; Gaps 5;
 QY 1 CCGCTCTCCCTCTCTCTCCCGGCTCTCCACCTCCACCGCTCTTCCGACCAACCGCT 60
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 QY 61 CCGCGCTCTCTCTCGACTACCGCAAGCTTCTCGACACTCTCCGCGCTCAACTCTTCA 120
 DB 313 CCGACGCTGCGCGGATACCTGCAAGAGCTGTTAGCCGAGATTTCCAAACCGGACTCTCG 372
 QY 121 ACCGCAAGGCGCACACAACCTCCATCTCTCTCTTATTTTCACTCTTCTCT 180
 DB 373 ATAAAAAGGTCAAGTCACTCTTATACAGCTCAAGTCCGCTGCTGCTGCTGCTG 432
 QY 181 CTGCTGCGGCGGCTCTCTCTCCGACAGCACTTTCGTCAGCTTTCGCTTCCGCTG 240
 DB 433 TTGTATACGCTGTTTGTTCATGACGAGCATATGGGCCCTTATATATCCGCGCTT 492
 QY 241 TAGGCTTTCTGAGATTACAGAGCGGCTGATAGGCGCAAGCTCCGCGCATTAACA 300
 DB 493 TGGGCGCTTCTGATACAGAGGCTTACGTTGGAATGATCTGCTGATTAACAAGT 552
 QY 301 TGTCTACGCGCGCTCAACCGCGCAATTGATTTCTCCGCAACATTTCCGCGGAA 360
 DB 553 CGTCAACGAAGCCGTGATTAATTAATCTGTCAGCTTCTGCTGTAATCTGCATCA 612
 QY 361 TCAGCATCGGCTGTGGAAGTGAACCAACAGCCCAACATTCGATGACAGCCTCG 420

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Db      613  TATCGATCGGATGGTGGAAATGAGCAGCATTAACGCTCAACATATCTCTTGAATAGCTTG 672
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Db      673  ACCACAGATCTGATCTCCACACATCCCTGTCTTAAAGGCTCCAAAGTTCTTAAAGT 732
Qy      481  CCATTAACCTCTCAATNTCTATGAGAGAAAGTTAGTTGATTCATTCATGCTTANGTTCTGA 540
Db      733  CGATGACGTACGCTTCTATGAGGAGAAAGTTGACGTTTCGATTCACATGCTCGATTTCTTGA 792
Qy      541  TCTGCTACACGACACTTACTTCTTTTACCCGGTAAATGCTGTGTCAGAGGCTCACTTGTATC 600
Db      793  TCAGTACCAACACTGCTGCTGTTTATTCATCATCATGCTGTGGGAGAAATCAATCTCTTAA 852
Qy      601  TCGAGCAATCTGCTATCTTTTTCGAGAGGAAAGCGAGCATAGAG-CTTGAACATTA 659
Db      853  TCCAAAGTTACTTGTGCTATCTCGAGACGTTACGTTCTGTATCGAGCCTTGAAACATAG 912
Qy      660  TGGGATCCCTTGTGTTTGGACTTGG-TTCCTCTTTAGTGNCTTGCTGCCCAATTGGG 718
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Qy      719  CCGTATAGGGGAAATGTTTNGCTTGTGCTGCTGTTGTTGTCNATCCAGACATTCATCA 778
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Qy      779  GTTCTGCTGATACCTTCTGTAATAATTATATGCGGCG--ACNANTGGATGACTG 836
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RESULT 8
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 complete sequence.
 AC005397
 AC005397.3 GI:20197371
 HTG.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 110149)
 Rounsley, S.D., Lin, X., Kaul, S., Shea, T.P., Fujii, C.Y., Mason, T.M.,
 Shen, M., Rongning, C.M., Fraser, C.M., Somerville, C.R. and Venter, J.C.
 Unpublished
 2 (bases 1 to 110149)
 Lin, X.
 JOURNAL Direct Submission
 TITLE Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
 JOURNAL Medical Center Dr., Rockville, MD 20850, USA
 REFERENCE 3 (bases 1 to 110149)
 TOWN, C.D. and KAUL, S.
 JOURNAL Direct Submission
 TITLE Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
 JOURNAL Medical Center Dr., Rockville, MD 20850, USA, cdrom@tigr.org
 COMMENT On Apr 18, 2002 this sequence version replaced gi:5598465.
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PTTEVLPETPVLDLETGSCDARSQSILCPTSLVRSNDETEYRTEPEQWPF  

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VKLIQSGGAILSPGVSANSPWOSLAWPETWQNEBELREKRKOSNRSSARS
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CDS
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Best Local Similarity 61.1%; Pred. No. 1.6e-54;
Matches 472; Conservative 0; Mismatches 299; Indels 2; Gaps 2;

QY 48 GACACACGCTCTCCGCGCTCTCCGACTACCGAGCTCTTCCGACTCTCCGCG 107
DB 45777 GACACACGCTCTCCGCGCTCTCCGACTACCGAGCTCTTCCGACTCTCCGCG 45718
QY 108 CTCACCTCTTCAACGCCAAGGCCACACAACTTCATCTCTCTCTTATTCAC 167
DB 45717 CGCGGCTCTTCAACAAAAGGCTACGACTCTTCAACACTCACTGCGCGCGCTC 45658
QY 168 CTTTTCCT 227
DB 45657 ATCTCTCGCGGCT 45598
QY 228 TCCGCTGCAATGATAGGCTTCTCTGATTCAGAGCGCGTGTAGTACGACACTCCGCG 287
DB 45597 TCCGCGGCTTCT 45538
QY 288 CATTACAGGTGATGCTCAGCGCGCGCTCAACCGCGCAATTCATCTCTCCGCAAC 347
DB 45537 CACTACAGGTGATGCTCAGCAACCAACCGGTCAACATTCAGCTCTCTCCGCAAC 45478
QY 348 ATTCCTCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 407
DB 45477 TGTCTACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 45418
QY 408 TGCACAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 467
DB 45417 TGTACAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 45358
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DB 45357 AATTCCTTCAATTCATTAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 45298
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DB 45297 GCTTCT 45238
QY 588 GTCACTTCT 647
DB 45237 ATCACT 45178
QY 648 G-CTTGACATATAGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 706
DB 45177 GCTTGAATATAGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 45118
QY 707 TGCACATAGGCT 766
DB 45117 CTTCGAAATTTGCAAGAGATTCATCTCTCTCTCTCTCTCTCTCTCTCT 45059
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RESULT 9
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LOCUS AP005554
DEFINITION Oryza sativa (japonica cultivar-group) chromosome 9 clone
OJ1118 A10, *** SEQUENCING IN PROGRESS ***.
ACCESSION AP005554
VERSION AP005554.1 GI:21952292
KEYWORDS HTG; HTGS_PHASE2.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriatoidae; Oryzae; Oryza.

REFERENCE
1 Sasaki, T., Matsumoto, T., Hattori, M., Sasaki, Y. and Katayose, Y.
Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, BAC
clone: OJ1118 A10
Published only in Database (2002)
2 (bases 1 to 96312)
Sasaki, T., Matsumoto, T., Hattori, M., Sasaki, Y. and Katayose, Y.
Direct Submission
Submitted (23-JUL-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program, Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/
Tel: 81-298-38-7441, Fax: 81-298-38-7468)
The nucleotide sequence of this BAC clone was generated by
combining Monsanto and RGP-Japan sequencing data.

COMMENT
NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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BASE COUNT 26463 a 21050 c 21350 g 27309 t 100 others

ORIGIN

Query Match 31.5%; Score 276.8; DB 2; Length 96312;
Best Local Similarity 60.8%; Pred. No. 2e-54;
Matches 508; Conservative 0; Mismatches 321; Indels 7; Gaps 4;

QY 7 CCTCTCTCTCCCGCCTTCTCCACCTCCACCGTCTTTCCGACCAACCGTCTCCGCG 66
DB 88376 CCGGCCCGCTCCGCGGAGGTTCTCTGCGGCGCGCTCGAGACTACACGGTCTCCCGG 88435

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QY 247 TTCCTGATTCAGAGCGGCTGATAGGCCAGACTCCGCGCATTAACAGTATGCTCA 306
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QY 427 ACCGTGATTCGACAGCAATGCGGCTTCTTGACATTTCGCGGCTTCTCAATTCATPA 486
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RESULT 10
AR200409 1702 bp DNA linear PAT 20-APR-2002
LOCUS AR200409
DEFINITION Sequence 26 from patent US 6355861.
ACCESSION AR200409
VERSION AR200409.1 GI:20250483
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1702)
AUTHORS Thomas, T.L.
TITLES Production of gamma linolenic acid by a .DELTA.6-desaturase
JOURNAL Patent: US 6355861-A 26 12-MAR-2002;
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Location/Qualifiers

BASE COUNT 358 a 471 c 446 g 427 t

ORIGIN

Query Match 31.2%; Score 274.2; DB 6; Length 1702;
Best Local Similarity 59.6%; Pred. No. 5e-54;
Matches 484; Conservative 0; Mismatches 326; Indels 2; Gaps 2;

QY 18 CCGGCTTCTCCACCTCCACCGTCTTTCGACGACAGCGTCTCGCGCGCTCTCTCCGAC 77
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QY 78 TACCGAAGCTTCTTCCGACCTCTCCGCGCTCAACCTTTTCACCGAAGGCGACACA 137
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QY		198	TTCCTCCGACAGCACATTCTGTGACAGCTGCTTTCCTGCTGATTAAGCTTTCTCTGAAT	257
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QY		258	CAGAGCGGCTGGATTAAGGCACAGACTCCGGCCATTACACGTGATGCTCAGCCGCGCTC	317
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QY		438	CAGACATGCGGCTTGTTCAGATTTCGTGCGGCTTCTCAATTCCATACTCTATTNC	497
Db		687	CAGACATGCCCGGTATTCGCCGTCCACCCGACTTTCAATCCATCACCCTCGTCTTC	746
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QY		558	ACTTTTTACCCGGTAAATGTGTGTGGCCAGGGTCAACTTGATCTGCACACAATTTCTGTA	617
Db		807	ACCTACTACCGGGTCAATGATCTTGGCGCGAATCAACCTTTCATCCAACTTTTATGG	866
QY		618	TTGTTTTCGACGNAAAAGTCAGAGATAGAAT-TGAAATPATGGGATCTGTGTTT	676
Db		867	CTCTCTACAGAGCCGACAGTCCCTGACCGCGCTCTAAACTTAATGGGTATGCGCGTTTTC	926
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QY		737	GNCGTTGTACCTTGTGCTGTGTGTCNCATCCAGACAGATTGAGTCTGGTGAATCACT	796
Db		987	GTCCTCATCAGCTTTGC-GTTCACGGCGCATCCAGACGCTCCAGTTCACGCTCAACCACTT	1046
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Db		1046	CTCCGGCGACACATPACGTGGGCCCCCAAGG	1077
RESULT 11				
AY055117		1478 bp	DNA	linear
LOCUS	Echium gentianoides delta-6-desaturase (D6DS) gene, complete cds.			PLN 01-DEC-2001
DEFINITION	Echium gentianoides delta-6-desaturase (D6DS) gene, complete cds.			
ACCESSION	AY055117			
VERSION	AY055117.1			
KEYWORDS	GI:17223794			
SOURCE				
ORGANISM	Echium gentianoides			
	Echium gentianoides			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;			
	Asteridae; lamids; Boraginaceae; Echium.			
REFERENCE	1 (bases 1 to 1478)			
AUTHORS	Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R.			
TITLE	Cloning and Molecular Characterization of the D6-Desaturase from			
JOURNAL	Echium: Functional Expression in Yeast and Tobacco			
REFERENCE	Unpublished			
AUTHORS	2 (bases 1 to 1478)			
	Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R.			
TITLE	Direct Submission			
JOURNAL	Submitted (10-SEP-2001) Biochemistry, Universidad de Almeria,			
	Campus Universitario, la Canada s.n., Almeria 04120, Spain			

FEATURES		Location/Qualifiers	
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BASE COUNT	364 a	258 c	365 g
ORIGIN	491 t		
Query Match	28.9%	Score 254.2	DB 8
Best Local Similarity	58.5%	Pred. No. 2.6e-49	
Matches	467	Conservative	0
		Mismatches	329
		Indels	2
		Gaps	2
24	TTCTCACTCCCAACCGCTCTTCCGACACACCGCTCCGCGCTCTCCGACATCCGC	83	
259	TTCTTCACTGGCTATATATCTTAAGATTAATCTGTTCTGAGGTGTCGAAAGATTACAGG	318	
84	AAGCTCTTCCGACCTCTCCGCGCTCAACTCTTCAACGCGAAGGCGACACACACTTC	143	
319	AAGCTGTGTTGAGTTAATAAATAGGGGTGTTTGACAAAGGGCTCATATTGTGCTT	378	
144	ATCTCTCTCCCTTATTTCTACACCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC	203	
379	GTGACTGTGTTTAAAGCTATGATGTTTCTATGAGTGTATTAAGGGATTTGTTTGT	438	
204	GACAGCACTTTCGTGACAGTCTTTCGCTGCATGATGAGGCTTCTCTGATTCAGAGC	263	
439	GAGGTGTTTGTGATCATTTTGTCTTGACAGGGGGGTGATGGGTTTGTCTGATTCAGAGT	498	
264	GGCTGATAGGCAACGACTCCGCGCCATTACAACGTGATGCTCAGCGCGCGCTCAACGCG	323	
499	GGGTGATTTGGGACATGATGCTGGGATTAATTAAGTTATGCTTAATCCAAAGGCTTAATAG	558	
324	GCAATTGATTTCTCTCCGCAACATTTCTCCCGGAATCAGCATGGGCTGGTGGAAATGG	383	
559	CTTATGGGATATGTTGCTGATTAATGCTTTCAGGAATTAACATGTTGGTGGAAATGG	618	
384	AACACCAACGCGCCACACATGATGATGCAACAGCCCTGATTAATGACCTGATTCGACAGC	443	
619	AACCATTAATGACATCATATGCTCTGTAAATAGCTCCGATTAATGACCCGGAATTAACAAATAC	678	
444	ATGCCGCTCTTGGAGTTTGTGCGGGTCTTCTTCAATTCACATCACTCATATTCTATGGG	503	
679	ATACCGTTTCTTGTGTGTGTGTCCCAAGTTGTTTGTAGCTGGCTCACTCATTTCTATGAA	738	
504	AGGAAATGAGTTGATTAATGATGCTAATGTTCTTGAATCTGACACGACTTAACTTT	563	
739	AAGAACTGACATTTGACTCGTTATCGAGATTTCTTGTAAACCATCAATTTGACGTTT	798	
564	TACCCGGTAATGTGTGTGTCGAGGCTCAACTTGAATCTGACAGAAATCTGTGATATGTT	623	
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 Db 919 TGGTACCAATGCTGTTCTTCTGCTTCCCAATTTGGGAGAAATATATGTTGTGTT 978
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 Db 979 GCTAGCTCTCGGTGCTG-CAATGCAACAAGTGCATTTCTTTGAACCATTTCTCGGC 1037
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RESULT 12
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 DEFINITION complete cds.
 ACCESSION AY055118
 VERSION AY055118.1 GI:17223796
 KEYWORDS
 SOURCE Echium pitardii var. pitardii
 ORGANISM Echium pitardii var. pitardii
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; lamids; Boraginaceae; Echium.
 1 (bases 1 to 1450)
 Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and
 Ruiz,J.R.
 Cloning and Molecular Characterization of the D6-Desaturase from
 Echium: Functional Expression in Yeast and Tobacco
 Unpublished
 2 (bases 1 to 1450)
 Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and
 Ruiz,J.R.
 Direct Submission
 Submitted (10-SEP-2001) Biochemistry, Universidad de Almeria,
 Campus Universitario, La Canada s.n., Almeria 04120, Spain
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 RNVFYSQELGLVFWIWPILVSLCPMWEIRIMFVASLSTGLQVQFSLNHFAL
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BASE COUNT 355 a 252 c 358 g 485 t

ORIGIN

Query Match 28.7%; Score 252.6; DB 8; Length 1450;
 Best Local Similarity 58.4%; Pred No. 6.1e-49;
 Matches 466; Conservative 0; Mismatches 330; Indels 2; Gaps 2;

QY 24 TTCTCCACCTCCACCGCTTTCGACACACCGTCTCGCGCTCTCCGACTACCGC 83
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 QY 84 AAGCTCTCTCCGACCTCCGCGCTCAACTCTTCAACCGCAAGGCCACAACTCC 143
 Db 290 AAGCTGTGTTGAGTTTAATTAATTAATGAGGCTGTTTGAACAAAGGTCATATGTGCTT 349
 QY 144 ATCCCTCCCTCCCTAATTCACCTTTTCTCTCTGCTGCGGCGCTCTCTCC 203
 Db 350 GTACTGTGTTTATTAAGTATGATGTTGCTATGAGTGTATAGGGTGTGTTTGT 409
 QY 204 GACAGCACTTTCGTGACGCTTTCGCTGATGATTAAGCTTCTCTGATTCAGAGC 263
 Db 410 GAGGGTGTGTTGATACATTTACTTCAGAGGGGTTGATGGGTTGTCTGATTCAGAGT 469
 QY 264 GCGTGGATGAGCCAGCACTCCGCGCATTAACAAGTATGCTCAGCCGCGCTCAACGC 323
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 QY 324 GCAATTCAGATTCCTCCGCGCAACATTCCTCCGCGCAATGAGATGCGGCTGGAAGTG 383
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RESULT 13
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 ACCESSION AR076814
 VERSION AR076814.1 GI:10003560
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1684)

AUTHORS Thomas, T.L., Nunberg, A.N. and Beremand, P.D.
TITLE Sunflower albumin 5' regulatory region for the modification of
plant seed lipid composition

JOURNAL Patent: US 5959175-A 1 28-SEP-1999;

FEATURES Location/Qualifiers
source 1..1684

BASE COUNT 430 a 277 c 358 g 619 t
ORIGIN /organism="unknown"

Query Match 27.9%; Score 245.2; DB 6; Length 1684;

Best Local Similarity 57.7%; Pred. No. 3.5e-47;
Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

24 TTCTCCACCTCCACCGCTCTTCCGACCAACGCTCCGCGCTCTCCGACTACCGC 83
265 TTTTTCACCTGGGTTTATCTTAAAGATTACTCTGTCTGAGTTTCTTAAAGATTATAG 324
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LOCUS AR084177 1684 bp DNA linear PAT 01-SEP-2000

DEFINITION Sequence 1 from patent US 5977436.

AR084177

AR084177.1

GI:10010948

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 1684)

AUTHORS

TITLE

Thomas, T.L. and L.N.

Olsepin 5' regulatory region for the modification of plant seed

lipid composition

Patent: US 5977436-A 1 02-NOV-1999;

LOCATION/Qualifiers

source 1..1684

/organism="unknown"

BASE COUNT 430 a 277 c 358 g 619 t

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Query Match 27.9%; Score 245.2; DB 6; Length 1684;

Best Local Similarity 57.7%; Pred. No. 3.5e-47;

Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

24 TTCTCCACCTCCACCGCTCTTCCGACCAACGCTCTCCGCGCTCTCCGACTACCGC 83
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84 AAGCTCTTCCGACCTCCGCGCTCAACCTCTTCAACGCAAGGCAACACACCTCC 143
325 AAGCTGTGTTGAGTTTCTTAAATGGGTTGTATGACAAAAAGCTATATATGTTT 364
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 DEFINITION A sunflower albumin 5' regulatory region for the modification of
 plant seed lipid composition.
 ACCESSION BD062571
 VERSION BD062571.1 GI:22608174
 KEYWORDS JP 2001518795-A/1.
 SOURCE Homo sapiens (human)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1684)
 Thomas, T.L., Beremand, P.D. and Nunberg, A.N.
 A sunflower albumin 5' regulatory region for the modification of
 plant seed lipid composition
 Patent: JP 2001518795-A 1 16-OCT-2001;
 JOURNAL RHOHE POULENC AGRO
 COMMENT PN JP 2001518795-A/1
 PD 16-OCT-2001
 PF 09-APR-1998 JP 1998543140
 PR 09-APR-1997 US 08/831570
 PI TERRY L. THOMAS, PHILLIP D. BEREMAND, ANDREW N. NUNBERG PC
 C12N15/82, C12N15/29, C12N15/53, A01H5/00, A01H5/10 CC Strandedness:
 Double;
 CC Topology: Linear;
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 Best Local Similarity 57.7%; Pred. No. 3.5e-47;
 Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;
 Qy 24 TTCTCACTCCACCGCTTTTCCGACACACCGCTCTCCGCGCTCTCCGACTACCGC 83
 Db 265 TTTTCTACGCGGTATATCTTAAAGATTAATCTGTTCTGAGGTTTCTAAGATTATAGG 324
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Search completed: December 31, 2003, 21:04:27
 Job time : 2210.2 secs

PN WO200032790-A2.
 XX 08-JUN-2000.
 XX 02-DEC-1999; 99WO-US28589.
 XX 03-DEC-1998; 98US-0110784.
 XX (DUPO) DU PONT DE NEMOURS & CO E. I.
 XX Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;
 XX WPI; 2000-412336/35.
 XX P-PSDB; AAY71553.
 XX
 PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries
 XX
 PS Claim 2; Page 44-45; 57pp; English.
 XX
 CC The present sequence is a cDNA encoding sphingolipid desaturase
 CC derived from a contig of clones sfil.pk0012.c5 and sfil.pk0031.d11
 CC isolated from soybean immature flower cDNA library, sfil.
 CC The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is also useful as a primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
 XX
 SQ Sequence 880 BP; 162 A; 267 C; 184 G; 251 T; 16 other;
 Query Match 98.2%; Score 864; DB 21; Length 880;
 Best Local Similarity 100.0%; Pred. No. 1e-208;
 Matches 880; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGGCGCTCCCTCCCTCCCGGCTCTCCAGCACTCCGACGCTTTCCGACACACCGCT 60
 Db 1 CGGCGCTCCCTCCCTCCCGGCTCTCCAGCACTCCGACGCTTTCCGACACACCGCT 60
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 Db 121 ACCGCAAGGGCCACACACCTCTCTCTCTCCCTTATTCACCTCTTTCTCTCT 180
 QY 181 CTGTGCGGCGCTCTCTCTCCGACAGCACTTCCGACGCTTTCCGACATTTGA 240
 Db 181 CTGTGCGGCGCTCTCTCTCCGACAGCACTTCCGACGCTTTCCGACATTTGA 240
 QY 241 TAGGCTTTCTCTGATTCAGAGCGCTGATAGAGCCAGCTCCGCGCATTAAGGTGA 300
 Db 241 TAGGCTTTCTCTGATTCAGAGCGCTGATAGAGCCAGCTCCGCGCATTAAGGTGA 300
 QY 301 TGTCTACCGCGCGCTCTACCGCGCAATTGATTTCTTCGCGCAATTTCTGCGGAA 360
 Db 301 TGTCTACCGCGCGCTCTACCGCGCAATTGATTTCTTCGCGCAATTTCTGCGGAA 360
 QY 361 TCAGCATTCGCGTGTGAGTGAACGACCAAGCCCAACCATTTGACATGCAAGCTCG 420
 Db 361 TCAGCATTCGCGTGTGAGTGAACGACCAAGCCCAACCATTTGACATGCAAGCTCG 420
 QY 421 ACTATGACCTGATTCAGACACATGCGGCTTTTGAGATTTGCTGCGGTTCTTCAT 480
 Db 421 ACTATGACCTGATTCAGACACATGCGGCTTTTGAGATTTGCTGCGGTTCTTCAT 480
 QY 481 CCAATACCTCTCATTTCTATGAGAGGAAGTTGATTTGATTCATGCTTANGTTCTTGA 540
 Db 481 CCAATACCTCTCATTTCTATGAGAGGAAGTTGATTTGATTCATGCTTANGTTCTTGA 540

QY 541 TCTGTACAGACACTTACTTTTACCCGGTATGTTGTTGCCAGGTCACCTTGTATC 600
 Db 541 TCTGTACAGACACTTACTTTTACCCGGTATGTTGTTGCCAGGTCACCTTGTATC 600
 QY 601 TGCAGCAATTTGCTATTGTTTTCGAGGAGGAAAAGTGCAGATGAGCTTGAACATTA 660
 Db 601 TGCAGCAATTTGCTATTGTTTTCGAGGAGGAAAAGTGCAGATGAGCTTGAACATTA 660
 QY 661 GGGGATCCTTGTGTTTGGACTTGTCTCTTTTATGATGCTTGGCTGCAATTTGGGCC 720
 Db 661 GGGGATCCTTGTGTTTGGACTTGTCTCTTTTATGATGCTTGGCTGCAATTTGGGCC 720
 QY 721 TGATAGGGGATGTTGATGCTTGTAGCTTGTCTGTTTTCGATGACATTCAGT 780
 Db 721 TGATAGGGGATGTTGATGCTTGTAGCTTGTCTGTTTTCGATGACATTCAGT 780
 QY 781 TCTGTTGATACCTTGTCTGTAATAATTATGTCGGGACAAATGGAATGACTGATG 840
 Db 781 TCTGTTGATACCTTGTCTGTAATAATTATGTCGGGACAAATGGAATGACTGATG 840
 QY 841 AATATCAGACAGGGGTCTATGATATCTCTTGTGCTCCT 880
 Db 841 AATATCAGACAGGGGTCTATGATATCTCTTGTGCTCCT 880
 RESULT 2
 AAD01352
 ID AAD01352 standard; cDNA, 1934 BP.
 AC AAD01352;
 XX
 DT 12-OCT-2000 (first entry)
 XX
 DE Soybean sphingolipid desaturase cDNA #2.
 XX
 KW Soybean; sphingolipid desaturase; membrane-bound desaturase;
 KM transgenic plant; fatty acid; ss.
 XX
 OS Glycine max.
 XX
 FH Key Location/Qualifiers
 FT CDS 305..1657
 FT /*tag a
 FT /product= "sphingolipid desaturase"
 XX
 PN WO200032790-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 02-DEC-1999; 99WO-US28589.
 XX
 PR 03-DEC-1998; 98US-0110784.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 XX
 PI Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;
 XX
 DR WPI; 2000-412336/35.
 XX
 DR P-PSDB; AAY71554.
 XX
 PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries
 XX
 PS Claim 2; Page 46; 57pp; English.
 XX
 CC The present sequence is a cDNA encoding sphingolipid desaturase
 CC from clone sfil.pk0017.b4.f15 isolated from soybean seedling cDNA
 CC library, sfil. The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is also useful as primer or probe for screening cDNA libraries to

CC isolate desired full-length cDNA clones.

XX Sequence 1934 BP; 505 A; 367 C; 448 G; 614 T; 0 other;

Query Match 53.1%; Score 467.6; DB 21; Length 1934;
Best Local Similarity 76.0%; Pred. No. 2.5e-108;
Matches 656; Conservative 0; Mismatches 199; Indels 8; Gaps 7;

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24 TTCTCCACCTCCGCGCTCTTCCGACCAACCGCTCCGCGCTCCGACCTACCGC 83
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
533 TTCTTACCTGGCTACCACTCAGTACTTCAAGCTCTGAGGTGTCACAAAGCTACAA 592
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
84 AAGCTCTTCCGACCTCTCCGCTCAACCTTCAACCGCAAGGCGCAACAACCTCC 143
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
593 AAGCTTGCATCTGAGTTCACAAATGGGCTTTTGAACACCAAGGAGCATGCACTTA 652
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
144 ATCTCTCTCTCCCTTATCTCAACCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCC 203
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
653 TGCACCTTGCATCTGCTGCTTATGTTCTCATTTGTACTATGATGTTGAGGTGC 712
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
204 GACAGACCTTGTGACGCTGCTTCCGCTGATGATGAGGCTTCTGATTCAGAGC 263
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
713 ACTAGTGTGTGGCTATTTGGTTGAGGATGCTTTAGGCTTTGATGACAAAGT 772
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
264 GCGTGTATAGGCGACACTCCGCGCATTAACAGTATGCTCAGCGCGCTCAACCGC 323
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
773 GCTTATGTGGCCATATTTCTGCGCACTATGTGTTATGACAAACATGTTCAACAG 832
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
324 GCATTTCAATTCCTCTCCGCGCAACATTTCTGCGCGAATGACATCGGCTGTGGAAGTG 383
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
833 GTTGACACATCTCTCTGCGAATCTGTTGACCGGATTAAGCATTTGTTGGAAGTG 892
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
384 AACCAAAAGCCCAACCAATGATGACAAACAGCTGATATACCTTATCTGACGAC 443
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
893 ACTCAAAATGCTCACCAATGCTGCAACAGCTTGAACATGACCTTATCTGACGAC 952
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
444 ATGCCGCTCTTGCATCTGCTGCGGCTTCTCAATTCCTATTCATTAATGAGG 503
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
953 ATGCCGCTCTTGCATCTGCTGCGGCTTCTCAATTCCTATTCATTAATGAGG 1012
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
504 AGGAAGTTGAGTTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 563
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1013 AGGAAGTTGAGTTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 1072
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
564 TACCCGCTATGCTGTGCTGCGAGGCTCACTTATTCGACACATTCCTGATTTGTT 623
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1073 TACCCGCTATGCTGTGCTGCGAGGCTCACTTATTCGACACATTCCTGATTTGTT 1132
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
624 TCGAGNGAAGAGTGCAGATAGAG-CTTGAACATATGAGGAGTCTTGTGTTGAGCT 682
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1133 TCGAGGCGAAGAGTGCAGATAGAGCTTGAACATATGAGGAGTCTTGTGTTGAGCT 1192
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
683 TGGTT-CTCTTTTATGCTGCTGCTGCGCAATTTGGGCTGATAGGAGGATTTNGCT 741
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1193 TGGTTCTCTTTTATGCTGCTGCTGCGCAATTT-GGCTGAGAGGATATGTTTGTCT 1251
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
742 TGTACTTCTGCTGTTTTCNCAATCAGACATTCATTCATTCATTCATTCATTCATTC 801
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1252 TGTACTTCTGCTGTTTTCNCAATCAGACATTCATTCATTCATTCATTCATTCATTC 1310
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
802 AAAATTTATATGCGGGC--ACNANTGGGAATGACTG--NTGNANTCAGACAAAGGGT- 857
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1311 CAATTTATATGCTGCGGCGACGAGTGGAGATAGCTGTTGAGAGCAGACAAAGGTGA 1370
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
858 CATTGATATCTCTTGTGNCCT 880
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1371 CATTGATATCTCTTGTGNCCT 1393

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RESULT 3
AAD01353
ID AAD01353 standard; cDNA; 1972 BP.
XX

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AC AAD01353;
XX
DT 12-OCT-2000 (first entry)
XX
DE Wheat sphingolipid desaturase cDNA #1.
XX
KW Wheat; sphingolipid desaturase; membrane-bound desaturase;
XX transgenic plant; fatty acid; ss.
XX
OS Triticum aestivum.
XX
FH Key Location/Qualifiers
FT CDS 124..1533
FT /tag= a
FT /product= "sphingolipid desaturase"
XX
PN WO200032790-A2.
XX
PD 08-JUN-2000.
XX
PF 02-DEC-1999; 99MO-US28589.
XX
PR 03-DEC-1998; 98US-0110784.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E. I.
XX
PI Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;
XX
XX WPI; 2000-412336/35.
XX DR P-PSDB; AAY71555.
XX
PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
PT transgenic plants and for producing antibodies specific to which is
PT useful for screening cDNA expression libraries
XX
PS Disclosure; Page 48-49; 57pp; English.
XX
CC The present sequence is a cDNA encoding sphingolipid desaturase
CC from clone wrel.pk0004.c7:fls isolated from wheat etiolated
CC seedling root cDNA library, wrel.
CC The present sequence is useful for producing
CC transgenic plants having altered levels of sphingolipid desaturase which
CC in turn would alter the fatty acid composition. The enzyme is useful
CC for producing polyclonal or monoclonal antibodies. The polynucleotide
CC is also useful as primer or probe for screening cDNA libraries to
CC isolate desired full-length cDNA clones.
XX
SQ Sequence 1972 BP; 382 A; 616 C; 490 G; 484 T; 0 other;

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Query Match 36.5%; Score 320.8; DB 21; Length 1972;
Best Local Similarity 61.8%; Pred. No. 3.5e-71;
Matches 545; Conservative 0; Mismatches 333; Indels 4; Gaps 3;

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1 CCGCCTCCCTCTCTCTCCCGGCTTCTCCACCTCCACCGTCTTCCGACACACCGTCT 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
383 CTTCCGTGCGCGGCTCTCTCCCGGCTTCTGTTGGCGCGCTCTCCACCTACCGTTC 442
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 CCGCGGCTCTCTCGAGTACCGCAAGCTTCTGCGACTCTCGCGCTCAACCTCTTCA 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
443 CCGCGGCTCTCGCGAGTCTCGCGGCTCTCTGCGAGCTCTCTCGCGGCGCTCTTGG 502
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 ACCGCAAGGCGCAACACCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
503 AGCGGCTGCGCGACACCCCAAGTCTGCTGTCGCAATGTGGGTCTTCTGCAATG 562
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
181 CTGTCTGCGGCGCTCTCTCTCTCTCGACAGACATTTGTGACGCTTTCGCTGATGA 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
563 CCTTACTGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 622
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
241 TAGGCTTCTCTGATTCAGAGCGGCTGATAGGCGACGACTCGGCGCATTAACGTTGA 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
623 TTGGCTTATCTGATTCAGTGTGGGCTGATTTGGCCATGACTCGGCGCGCACCAATCA 682

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QY 301 TGGTCAGCCGCGCTCAACCGGCAATTCATCTCCGGCAACATTCGCGGAA 360
 DB 683 CAGGACACCGCGGCTCAACCGCTCTCTGAGGAGGCTCCGGGAATGCTCAACGCGC 742
 QY 361 TCAGCATCGGCTGTGAGAGTGAACCAACGCGCCACCAATTCATGCAACAGCTCG 420
 DB 743 TCGGCAATCGCTGTGAGAGTGAACCAACGCGCCACCAATTCATGCAACAGCTCG 802
 QY 421 ACTATACCGCTGATTCGACAGATTCGCGGCTTTGAGATTCGCGGCTTTCAAT 480
 DB 803 ACCATGACCGGACCTTCACAGCTTCGCGCTTCGCGGCTTCACCAACCTCTTCAACA 862
 QY 481 CCATTAACCTCTCATTTCTATGAGAGAGTGAATGATTCATTCATGATTCATGATTCGA 540
 DB 863 ACCTTTGCTGTGCTGTGATGAGAGAGCTTCGCGGCTTCATGCAATTCATGATTCGA 922
 QY 541 TCTGCTACCAAGCACTTACTTTTACCGGTAATGATGTTGTCAGAGGTCACCTGTATC 600
 DB 923 TCAGCTACCAAGCACTGACATTCATCCGCTGATGAGATTCGCAAGGATTAATCTCTTG 982
 QY 601 TCGAGCAATTCGCTATTCCTTTTCGAGGAGAAAGCGAGATAG-AGCTTGAACATA 659
 DB 983 TCGAGCAATTCGCTATTCCTTTTCGAGGAGAAAGCGAGATAG-AGCTTGAACATA 1042
 QY 660 TGGGATTCCTTGTGTTTGGACTTGTTCCTCTTTTATGATTCGCTGCAATTCGAG 719
 DB 1043 CCGGAGTTGAGAGGTTCTGAGGTTTGGATCCCTTCTGCTGTCTGCTGCGAATTCGT 1102
 QY 720 CTGATAGGGGATGTTTGGCTTGTGATGCTTGTGCTGTTTGTGCTGATTCAG 779
 DB 1103 GGGAGAGGTTGTTTGTGCTTGTGCAAGCTTTG-TGATTCAGGGGATTCAGATGTTTCA 1161
 QY 780 TTTGCTGATGATCAGCTTGTGAAATTTATATGAGGAGG-ACNANTGGGATTCAG 837
 DB 1162 TTTGCTGATGATCAGCTTGTGAAATTTATATGAGGAGG-ACNANTGGGATTCAG 1221
 QY 838 NTGANAATCAGACAGGAGTTCATTCATCTCTTGTGAGCC 879
 DB 1222 TTGAGAGGCAACAGGAGGAGTTCATTCATCTCTTGTGAGCC 1263

RESULT 4
 AAD01350
 ID AAD01350 standard; cDNA; 1764 BP.
 XX AAD01350;
 AC
 XX 12-OCT-2000 (first entry)
 DT
 XX
 DE Corn sphingolipid desaturase cDNA.
 XX
 KW Corn; sphingolipid desaturase; membrane-bound desaturase;
 XX transgenic plant; fatty acid; ss.
 KW
 XX Zea mays.
 OS
 XX
 FH Key location/Qualifiers
 FT CDS 89..1477
 FT /tag= a
 FT /product= "Sphingolipid desaturase"
 PN MO200032790-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 02-DEC-1999; 99MO-US28589.
 XX
 PR 03-DEC-1998; 98US-0110784.
 XX
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA
 PI Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;
 XX

DR WPI; 2000-412336/35.
 DR P-PDB; AAY71552.
 XX
 PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries
 XX
 PS Claim 2; Page 41-42; 57pp; English.
 CC The present sequence is a cDNA encoding sphingolipid desaturase
 CC from clone cdelc.pX001.08:15 isolated from corn developing
 CC embryo cDNA library, cdelc. The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is also useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
 XX
 SQ Sequence 1764 BP; 310 A; 602 C; 456 G; 396 T; 0 other;

Query Match 34.3%; Score 302; DB 21; Length 1764;
 Best Local Similarity 61.6%; Pred. No. 1,9e-66;
 Matches 519; Conservative 0; Mismatches 319; Indels 4; Gaps 3;

QY 1 CCGCTCCCTCTCTCTCCCGCTTCCACCTCCACCGCTTTCGACCAACCGCTCT 60
 DB 327 CTTCCGCGCGCGCGCTCTCTCCCGCTTCTTCTGTTGCGCGCTCTCTGATACGCGCT 386
 QY 61 CCGCGCTCTCTCTCTCTCCCGCTTTCGACCTTTCGACCTTTCGCGCTCAACCTTTCA 120
 DB 387 CCGCGCTCTCTCTCTCTCCCGCTTTCGACCTTTCGACCTTTCGCGCTCTCTG 446
 QY 121 ACCGAGAGGAGCAACAACCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
 DB 447 AAGCGCTGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 506
 QY 181 CTGTCTGCGCGCGCT 240
 DB 507 CGCTGATCT 566
 QY 241 TAGCTTTCT 300
 DB 567 TTGGCTTCT 626
 QY 301 TGGTCAGCCGCGCTCAACCGGCAATTCATCTCTCCGCAACATTCGCGGAA 360
 DB 627 CCGGCAATCCGCTCTCAACCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 686
 QY 361 TCAGCATCGGCTGTGAGAGTGAACCAACGCGCCACCAATTCATGCAACAGCTCG 420
 DB 687 TCAGCATCGGCTGTGAGAGTGAACCAACGCGCCACCAATTCATGCAACAGCTCG 746
 QY 421 ACTATACCGCTGATTCGACAGATTCGCGGCTTTGAGATTCGCGGCTTTCAAT 480
 DB 747 ACCATGACCGGACCTTCACAGCTTCGCGCTTCGCGGCTTCACCAACCTCTTCAACA 806
 QY 481 CCATTAACCTCTCATTTCTATGAGAGAGTGAATGATTCATTCATGATTCATGATTCGA 540
 DB 807 ACATATGATTCATCTTCAACCAACGAGACCTTCGCGCTTCATGCGCTGCAATTCAT 866
 QY 541 TCTGCTACCAAGCACTTACTTTTACCGGTAATGATGTTGTCAGAGGTCACCTTATC 600
 DB 867 TCAGCTACCAAGCACTTACTTCTACCGGTAATGATGATTCAGAGGATTAATCTCTCG 926
 QY 601 TCGAGCAATTCGCTATTCCTTTTCGAGGAGAAAGCGAGATAG-1TAGACTTGAACATA 659
 DB 927 CCGAGTCCGCGCTGTCTCTCTCAACGAGAGGAGGTCGCGAGCGGTTGCTGAGATCG 986
 QY 660 TGGGATTCCTTGTGTTTGGACTTGTTCCTCTTTTATGATTCGCTGCAATTCGAG 719
 DB 987 CCGGAGTTCACCAATTCGAGGAGTGTGATCCGCTGTGATGCTTCTCTGCGAATTCGT 1046
 QY 720 CTGATAGGGGATGTTTGGCTTGTGATGCTTGTGCTGTTTGTGCTGATTCAG 779

Dd		1047	GCGAGAGGGTCGCGCTTTGTCTGCTTTTACGACTTCACCATTGC--CGGATTCACACGTC	CA 1105
Qy		780	TTCTGCTTGAAATCACCTTGCTGAAAATTATATGCGGGC--ACNANTGGGAATGACTGG	837
Dd		1106	TTTGCGCTGAACCACTTCTGTCGCCAGCTGATGCGGGCCACCAAGGGCAATGACTGG	1165
Qy		838 NT 839		
Dd		1166 TT 1167		
 RESULT 5 ID AAZ44832 standard; DNA; 1594 BP. XX AC AAZ44832; XX DT 27-APR-2000 (first entry) XX DE B. napus sld1 DNA. XX Km Spingolipid desaturase; sld1; sphingosase; ceramide; capnoid; Km transgenic plant; crop plant; delta-8-unsaturated long-chain base; Km tolerance; resistance; soil salinity; ion stress; toxicity; drought; Km cold; frost; phytopathogenic microorganism; flowering time; cosmetic; Km pharmaceutical; food; chemical raw material; de. XX OS Brassica napus. XX Key Location/Qualifiers FT CDS 51..1400 FT FT /tag= a FT FT /product= "sld1" XX PN DEL9828850-A1. XX PD 30-DEC-1999. XX PF 27-JUN-1998; 98DE-1028850. XX PR 27-JUN-1998; 98DE-1028850. XX PA (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH. XX PI Heinz E, Zaehrlinger U, Schmidt H, Sperling P; XX DR WPI; 2000-127549/12. XX DR P-PSDB; AAY51333. XX PT New sphingolipid desaturase that selectively introduces double bond PT into sphingolipids and capnoids - XX TS Claim 11; Fig 1; 62pp; German.				
XX	This invention describes a novel sphingolipid desaturase that selectively introduces a double bond into the sphingosine of the ceramide residue of sphingolipids and capnoids. A DNA sequence encoding the sphingolipid desaturase, or a vector containing the DNA sequence, can be used to produce transgenic plants, especially crop plants, with an increased or decreased delta-8-unsaturated long-chain base content or an altered delta-8-unsaturated long-chain base cis/trans ratio, especially to compensate for a delta-8-unsaturated long-chain base deficiency, to exclude production of delta-8-unsaturated bases, to increase tolerance or resistance to soil salinity, ion stresses or toxicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms, or to alter size growth and flowering time. Cells, transgenic organisms or plants containing the DNA sequence can be used to produce sphingolipids and capnoids with unsaturated sphingosines. The sphingolipids or capnoids can be used in cosmetics, pharmaceuticals and foods and as chemical raw materials. This sequence encodes the Brassica napus sphingolipid desaturase sld1 protein described in the method of the invention.			

SQ	Sequence	1594 BP;	382 A;	369 C;	375 G;	468 T;	0 other;
	Query Match	31.7%;	Score 279;	DB 21;	Length 1594;		
	Best Local Similarity	61.4%;	Pred.	No. 1.2e-60;			
	Matches	518;	Conservative	0;	Mismatches	319;	Indels 6; Gaps 5;
QY	1	CCGCGCTCCCCTCCTCCGCCGCTTCTCCACCTCCACCGCTCTTTCCGACCAACAGCTCT	60				
DB	253	CCGCATATGGCCCACTTGAAAACCTTCACACGGCTTACCAGTGAAGACCAACAGCTGT	312				
QY	61	CCGCGCGCTCTCTCCGACTACCGCAAGCTCTTCTCCGACCTCTCCGCGCTCAACCTTTCA	120				
DB	313	CCGACGTGTGGCGTACGCTACGCTCGTGTATTACCGGGAGTTTCCAAACGGGAGCTCTTCG	372				
QY	121	ACCGCAAGGGCCACACAACCTCATCTCTCTCTCCCTTAATTCACCCCTTTTCTCTCT	180				
DB	373	ATAAAAAAGGTCAACGTGACTCTTTAACACGCTCACGTGCGTGCATCATCTCGCGCGG	432				
QY	181	CTGTCTCGGCGCTCTCTCTCTCCGACGACCTTTCGACAGCTTCCGCTGCGATTTGA	240				
DB	433	TGTATAACGGTGTGTGTTCANVACGACGACVATAGGCCCACTTAATACCGCGCTCTTGC	492				
QY	241	TAGGCTTTCTCTGGAATTCAGAGCGGCTGTGATAGGCCACGACTCGGCGCATTAACAGTGA	300				
DB	493	TGGGCCCTTCTCTGGATACAGAGCGCTTAGCGTGGGACATGACTCTGTGATTAACAAGTGA	552				
QY	301	TGCTACGCGCGCGCTCTCAACCGCGCAATTGAGATTCTCTCCGCGCAATTCCTCGCGGAA	360				
DB	553	CGRCAACGAAGCGGTGTAATAACTCGTCAGCTTCTGTCTGGTAATGCAATCACCGGGA	612				
QY	361	TCAGCATCGGCTGTGGAATGGAACCAACAACGCCACCAATTGATGCAACAGCCTCG	420				
DB	613	TATCGATCGGCTGTGGAATGGAACGATACGCTACCAATATCTCTGTAATATGCTTGG	672				
QY	421	ACTATGACCTGTATCTGACGACATGCGCGCTCTTTCGAGTTTTGTCGCGGTTCTTCATT	480				
DB	673	ACCAAGATCTGTATCTTCAGACATCCCTGTCTTAGCGGCTCTCCAAACAAGTTCTTTAAGT	732				
QY	481	CCAATACTCTCATTTNCTATGGAGAAGATTNGAGTTGATTGCATTNAGTTCTTGA	540				
DB	733	CGATGACGTACCGTTTCTATGGGAGGAAGTTGACGTTGCATCCACTGCTGATTTTGA	792				
QY	541	TTGTCTACCAAGCACTTTTAAACCGGTAATGTGTGTCGAGGCTCAACTGTATC	600				
DB	793	TCAGCTACCAACACTGCTCGTTTATCCAAATCATGTGTGCGGAGAAATCATCTCTTTA	852				
QY	601	TGAGACAATTCTGCTATGTCTTTTCGAGGAGAAAGTGCAGGATAGAG - CTGNAACATA	659				
DB	853	TCCAAAGTTACTTTTGTCTATCTTCGAGCGTTACGTTCCGTATCGAGCCTTGAACATAG	912				
QY	660	TGGGAGATCTTGTGTTTGGACTTTGG - TTCTCTTTTAGTGNCTTGCCTGCCAATTGGG	718				
DB	913	CTGGGATTTCTTGTCTTTCGACGCTGTTCTCTTTTAGTATCCTTCTTACCAACT - GG	971				
QY	719	CTGATAGGGGMAATGTTTNGCTTGTAGCTTGTGCTGTTGTGNCNATCCAGCAATTTCA	778				
DB	972	CAAGAGAGGATTCATCTTGTCTTTTAAAGATGGCG - TCACGGCGAATTCAGCAGTTCA	1030				
QY	779	GTTCTGTGTAATCACTTGTCTGAAAATTTATATGNGGGG -- ACNANTGGGAATGACTG	836				
DB	1031	GTTCTGTTTAAACCATTTTTCGGCAGATGTTTACACCGGTCCGCTTAATGGGAACGATTG	1090				
QY	837	GNT 839					
DB	1091	GTT 1093					
RESULT 6							
AAC42244							
ID AAC42244	standard;	DNA; 1465 BP.					
XX AAC42244;							

DT 17-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 34823.
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX
XX 06-SEP-2000.
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126784.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
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PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139453.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.

PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
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PR 23-JUN-1999; 99US-0140353.
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PR 30-JUN-1999; 99US-0141287.
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PR 02-JUL-1999; 99US-0142055.
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PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
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PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148541.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.


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PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
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PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160788.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160880.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match 31.5%; Score 277.2; DB 21; Length 1465;
 Best Local Similarity 61.1%; Pred. No. 3.4e-60;
 Matches 472; Conservative 0; Mismatches 299; Indels 2; Gaps 2;

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QY 48 GACCAACACGCTCTCCGCCCTCTCTCCGACTACCGAAGCTCTTCTCCGACTCTCCGCG 107
DB 365 GACCAACACGCTCTCCGCCCTCTCTCCGACTACCGGCTTTCGCCGCCGACTCTCCCAA 424
QY 108 CTCAACCTCTTCAACCGGACGACACACACCTCATCTCTCTCTCTCTCTCTCTCTCTCT 167
DB 425 CCGCGGCTCTTTCGACAAAAGGTCAAGTCACTCTTTCACACTCACTGCGTCCGCGCTC 484
QY 168 CTTTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 227
DB 485 ATGCTCGCGGCGGCTTCTTACGCGGCTTTGGCGTGTACAGAGATCTGGGCTCACTCATC 544
QY 228 TCCGCTGCACTGATAGGCTTTCTCTGATTCAGAGGCGCTGATAGGCGACGACTCCGCG 287
DB 545 TCCGCGGCTTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 604
QY 288 CATTACACGATGCTCAGCGCGCGCTCAACCGGCAATTGATCTCTCCGCGAAC 347

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DB 605 CACTACACGCTGACGCTCAACCAACCGGTGTAACAACATTCACACTTCTCTCCGTAAC 664
QY 348 ATTCTCGCGGAATGAGATCGGCTGTGTGAAGTGAACCAACAGCCACACATTCGA 407
DB 665 TGTCTACCGGATCTTCAATCGCTGTGTGAAGTGAACCAACAGCTTACACATTCGCT 724
QY 408 TGCAACGCTCTGACTATGACCTGTGATCTGACAGACATGCGGCTTGTTCAGTTTCGTG 467
DB 725 TGTACACGCTTGAACAGATCGGATCTTACACACATTCGCGATCTTCCGCTCTCTACA 784
QY 468 CGGTTCTTCAATTCATACCTCTCTCATTCATGAGAGAGAGATTGAGTTGATTTCATT 527
DB 785 AAATCTTCAATTCGATACGCTCAAGTTCATGTCAGAGAAATTAACATTCGATCTCTCA 844
QY 528 GCTAGTCTTGTATGATGATGATACAGACTTTCCTTTTACCGGTAATGTTGTCACAG 587
DB 845 GCTGATTTCTTAATGATGATGATACAGACTTTCATTCACAGATTCATTCGATGCTGAAGA 904
QY 588 GTCACTGTATCTGACAGACAAATTCGCTATTTTCGAGGMAAAGTGCAGAGATAGA 647
DB 905 ATCAACCTCTTCATTCACAAATTCCTATTCATTCGAAAGCGACGTCACATCGG 964
QY 648 G-CTTGAACATPANGGAGATCCCTGTGTTTGGACTTGCTCTCTTTCATGATGCTGCC 706
DB 965 GCTTGAACATGCGCGGAATTTTGTGATGTTTTCGACATGTTCCCTCTTATGTCGTTTC 1024
QY 707 TGCCAAATTTGGCCCGATAGGAGNATGTTTNGCTTGTAGTTTGTCTTGTTCNAT 766
DB 1025 CTTCCGAATTTGGCAAGAGATTCATCTTCCTTCGAGATGTCGCG-TCACGCGAT 1083
QY 767 CCAGACATTCAGTCTGTTGATCACCTTGCTGTAATTAATTAATGAGGCG 819
DB 1084 TCACATGTTCAATTCGTTTAAACATTCGACAGATGTTATACCGGTC 1136

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RESULT 7
ABK49503
ID ABK49503 standard; DNA; 1702 BP.
XX AC ABK49503;
XX 15-JUL-2002 (first entry)
XX DE DNA encoding Evening primrose delta6-desaturase.
XX KW delta6-desaturase; sunflower; soybean; maize; tobacco;
XX KW peanut; carrot; oil seed rape; gamma linolenic acid; GLA;
XX KW chilling tolerance; gene; ds; evening primrose.
XX OS Oenothera biennis.
XX FH
XX FT Key Location/Qualifiers
XX FT CDS 48..1406
XX FT /*tag= a
XX FT /product= "delta6-desaturase"
XX PN US6355861-B1.
XX PD 12-MAR-2002.
XX PF 19-SEP-1997; 97US-0934254.
XX PR 13-OCT-1992; 92US-0959952.
XX PR 10-OCT-1991; 91US-0774475.
XX PR 08-JAN-1992; 92US-0817919.
XX PR 14-SEP-1994; 94US-0307382.
XX PR 28-JAN-1997; 97US-0789936.
XX PA (RHON ) RHONE-POULENC AGROCHIMIE.
XX PI Thomas TL;
XX WPI; 2002-380944/41.

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DR P-PSDB; AAU79851.
 XX Novel nucleic acid encoding evening primrose delta6-desaturase which
 PT converts linoleic acid to gamma linolenic acid useful for producing
 PT gamma linolenic acid in transgenic plant or bacteria
 XX
 PS Claim 2; Column 41-46; 53pp; English.
 XX
 CC The invention describes an isolated nucleic acid encoding an evening
 CC primrose delta6-desaturase. The nucleic acid and a vector expressing the
 CC nucleic acid are useful for producing a plant such as sunflower, soybean,
 CC maize, tobacco, peanut, carrot or oil seed rape plant, with increased
 CC gamma linolenic acid (GLA) content, and also for inducing or increased
 CC production of GLA in a bacteria or plant deficient, lacking in or
 CC producing low levels of GLA. The nucleic acid is also useful for inducing
 CC chilling tolerance in plants. This sequence encodes the evening primrose
 CC delta6 desaturase involved in the production of gamma linolenic acid.
 XX
 SQ Sequence 1702 BP; 358 A; 471 C; 446 G; 427 T; 0 other;
 Query Match 31.2%; Score 274.2; DB 24; Length 1702;
 Best Local Similarity 59.6%; Pred. No. 2e-59;
 Matches 484; Conservative 0; Mismatches 326; Indels 2; Gaps 2;
 QY 18 CCGCGCTTCTCCACCTCCACCGCTTCTCCGACACACCGCTCCGCGCTCCGAC 77
 DB 267 CCGCTCTTACCGGCTACTACTACTCTCAAGGACTTGAAGTCCGAGATCCAGAGAC 326
 QY 78 TACCGCAAGCTTCTTCCGACCTTCGCGCTCAACTCTTCAACCGCAAGGCGCACACA 137
 DB 327 TACCGGAGGCTTTGAAACGAGATGCGCGGATCTTTCGAGAAAGAGGCGCACAC 386
 QY 138 ACCTTCATCTCTCCCTTATTTCTCACCTTTTCTCTCTCTCTCTCTCTCTCTCTCT 197
 DB 387 ATATATGTGACGTTCTGTCGCGCTTCCGCTATGATGCGGCAATCGTCTACGCGTCTG 446
 QY 198 TTCTCCGACGACCTTCTGTCAGCTTCTTCCGCTGACATTTAGGAGCTTCTCTGAT 257
 DB 447 GCGTCCGAGTCCGTCGCGAGTTCAATGCTGTGGGCGCACTGCTGGCTTGTGTGATC 506
 QY 258 CAGAGCGGCTGATAGGCGCACGCTCCGCAATTAACAAGTATGCTACGCGCGCTC 317
 DB 507 CAGCGCGCTATGTGGGCTCATGACTCCGCGCATTAACGAGTGAATGCGCAACCGCTGATAC 586
 QY 318 AACCGGCAATGAGATTTCTCCGCAATTTCTGCGGAGATTCAGCACTCGGCTGTG 377
 DB 567 AACAGATACGCAACTCATAGAGGCAACATCTTAACGGAATCAGCACTCGGCTGTG 626
 QY 378 AAGTGAACCAACAGCGCCACCATTTGATGCAAGAGCTCGATATGACCTGATCTG 437
 DB 627 AACTGAGCCCAACAGCGCCACCATTTGATGCAAGAGCTCGATATGACCTGATCTG 686
 QY 438 CAGACATGCGGCTTCTTGAAGTTGCTGCGGCTTCTTCAATTCATACCTCTCAT 497
 DB 687 CAGCAGATCCCGCTATGTGCGGCTCTCACCGCACTCTTCAATTCATACCTCTCTCT 746
 QY 498 TATGGGAGAGATTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 557
 DB 747 TATGGCGAGATCTCTGAATTCAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 806
 QY 558 ACTTTTACCCGGTAATGTTGTTGTCAGAGGATCAACTTGTATGTCAGAGAAATTTGCTA 617
 DB 807 ACCTACTACCCGGTATGATCTTGTGCGGAGTCAACTCTTCACTCAGACCTTTTAT 866
 QY 618 TTGTTTTCAGAGGAAAGTGAAGATAGCTTGAACATTAATGGGATCTTTGTTT 676
 DB 867 CTCTCAACAGGCGCGAGCTCCCTGACCGGCTCTAAACTTAATGAGGATCTGCGGTTTTC 926
 QY 677 TGAAGTTGTTCTCTTTTATGATGCTGCTGCAATTTGGGCTGATAGGAGATCTT 736
 DB 927 TGAACGTTGTTCTCTTTGATCTTGTCTCCGAACTGGAACGTTTGGGTTTC 986
 QY 737 GAGCTTGCTAGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 796

DB 987 GTCTCATGACGCTTTC-GGTACCGCGATCCAGCACGCTCATGACCTCAACCACTT 1045
 QY 797 TGCTGAATTTATATNGCGGACGACANTGG 828
 DB 1046 CTCGCGGACACATGATGCGGCCCGCCCAAG 1077
 RESULT 8
 ABX15367
 ID ABX15367 standard; cDNA; 1702 BP.
 XX
 AC ABX15367;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Evening primrose delta-6-desaturase #1 cDNA.
 XX
 KM Delta-6-desaturase; gene; ss; delta-12-desaturase; sunflower; soybean;
 KM maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
 KM octadecatetraenoic acid; alpha-linolenic acid; delta-15-desaturase;
 XX evening primrose.
 XX
 OS Oenothera biennis.
 XX
 FH Key Location/Qualifiers
 FT CDS 48..1406
 FT /tag= a
 FT /product= "Evening primrose delta-6-desaturase #1"
 XX
 PN US2002108147-A1.
 XX
 PD 08-AUG-2002.
 XX
 PF 21-DEC-2001; 2001US-0029756.
 XX
 PR 13-OCT-1992; 92US-0959952.
 PR 19-SEP-1997; 97US-0934454.
 PR 10-OCT-1991; 91US-0774475.
 PR 08-JUN-1992; 92US-0817919.
 PR 14-SEP-1994; 94US-0307382.
 PR 28-JAN-1997; 97US-0789936.
 XX
 PA (THOM/) THOMAS T L.
 XX
 PI Thomas TL;
 XX
 XX WPI; 2003-066659/06.
 DR P-PSDB; ABG73416.
 XX
 PT Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
 PT for producing plant with increased gamma linolenic acid content, and
 PT for inducing octadecatetraenoic acid production in plant
 XX
 PS Claim 2; Fig 10; 55pp; English.
 XX
 CC The invention relates to a nucleic acid encoding an evening primrose
 CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
 CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
 CC for producing a plant (such as sunflower, soybean, maize, tobacco,
 CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
 CC acid (GLA) content by transforming a plant cell with the nucleic acid or
 CC vector and regenerating a plant with increased GLA content from the plant
 CC cell, for inducing or increasing production of GLA in an organism lacking
 CC in or producing low levels of GLA and for inducing production of
 CC octadecatetraenoic acid in at least one of a plant deficient or lacking
 CC in or producing low levels of octadecatetraenoic acid, a bacterium which
 CC produces alpha-linolenic acid or a bacterium which exhibits a
 CC delta-15-desaturase activity on a GLA substrate. This sequence represents
 CC cDNA encoding an evening primrose delta-6-desaturase polypeptide.
 XX
 SQ Sequence 1702 BP; 358 A; 471 C; 446 G; 427 T; 0 other;

Query Match 31.2%; Score 274.2; DB 25; Length 1702;
 Best Local Similarity 59.6%; Pred. No. 2e-59;
 Matches 484; Conservative 0; Mismatches 326; Indels 2; Gaps 2;

QY 18 CCGGCTTCTCCACCTCCCAACCGTCTTCCGACCAACCGTCTCCGCGCTCTCCGAC 77
 DB 267 CCGCTTTCACCGGCTACTACTCAAGAGATTGAAGTGTGGAGATCTCCAGAGAC 326
 QY 78 TACCGAAGCTCTTCCGACCTCTCCGCGCTCAACCTTCAACCGAGGAGCCACACA 137
 DB 327 TACCGAAGCTTTCAGACGATGTGCGGTCCGGATCTTCAAGAGAGGAGCCACAC 386
 QY 138 ACCCTCATCTCTCTCCCTTAATCTCAACCTTTTCTCTCTCTCTCTCTCTCTCTC 197
 DB 387 ATCATGTGACGTTGTCGCGGTGCGGTGATGATGCGGCAATGCTTACCGCGGTG 446
 QY 198 TTCTCCGACAGACTTGTGACGCTGCTTCCGCTGCAATTGATAGGCTTTCTTGAT 257
 DB 447 GCGTGGAGTCCGTGGAGTTCAATGCTCTGCGGCGCATGCTGGGCTTGTGTGATC 506
 QY 258 CAGAGCGGTGATAGGACGACCTCGGCAATTCAAGTATGCTGACCGCGCTC 317
 DB 507 CAGCGCGTATGTGGCCATGATCTCGGCAATACAGGTGATGCAACCGGTGATAC 566
 QY 318 AACCGGCAATTCAATCTCTCCGCAACATTTCTCGCGAATCAGATCGGCTGTG 377
 DB 567 AACGATACCACTCATAGAGAGCAATCTCTAACCGAATCAGATCTCGGTGTG 626
 QY 378 AAGTGAACCAACCGCCACCAATGATGATGACAGCTGATGATGATGATGATGATG 437
 DB 627 AAGTGAACCAACCGCCACCACTGCTGCAACGCTGATGATGATGATGATGATG 686
 QY 438 CAGCAATCGGCTCTTCCGATGCTGCGCTTCAATCTCAATCTCAATCTCAATCT 497
 DB 687 CAGCAATCGGCTCTTCCGATGCTGCGCTTCAATCTCAATCTCAATCTCAATCT 746
 QY 498 TATGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 557
 DB 747 TATGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 806
 QY 558 ACTTTTACCGGATATGATGATGATGATGATGATGATGATGATGATGATGATG 617
 DB 807 ACTTACTACCGGATATGATGATGATGATGATGATGATGATGATGATGATGATG 866
 QY 618 TTGTTTTCAGAGNAGAAATGAGATGAGATGAGATGAGATGAGATGAGATGAG 676
 DB 867 CTCTCACCAGGCGGACGCTCTGACCGGCTTAATGATGATGATGATGATGATG 926
 QY 677 TGGACTTGGTCTCTTTTATGATGATGATGATGATGATGATGATGATGATGATG 736
 DB 927 TGGAGTGTGCTCGCTCTTCTGATGATGATGATGATGATGATGATGATGATGATG 986
 QY 737 GAGCTTGTAGCTTGTGCTGATGATGATGATGATGATGATGATGATGATGATG 796
 DB 987 GTCTCATAGCTTGTGCTGATGATGATGATGATGATGATGATGATGATGATG 1045
 QY 797 TGTCTGAATTTATATGAGGAGCAATGAGG 828
 DB 1046 CTCTCGGCGACATATGATGATGATGATGATGATGATGATGATGATGATG 1077

RESULT 9
 AAV34398
 ID AAV34398 standard; DNA; 1684 BP.
 XX AAV34398;
 AC
 XX
 DT 02-MAR-1999 (first entry).
 XX
 XX Borage delta-6 desaturase gene.
 DE
 XX
 XX Upstream region; regulatory region; sunflower; albumin; seed; expression;
 KW lipid metabolism; delta-6 desaturase; transgenic plant; de.

XX Borage officinalis.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 43..1389
 FT /*tag= a
 FT /product= "delta-6 desaturase"
 FT primer_bind complement (616..632)
 FT /*tag= b
 FT primer_bind 1165..1181
 FT /*tag= c

PN W09845460-A1.
 XX
 PD 15-OCT-1998.
 XX
 PF 09-APR-1998; 98WO-US07178.
 XX
 PR 09-APR-1997; 97US-0831570.
 XX
 PA (RHON) RHONE-POULENC AGROCHIMIE.
 PI Beremand PD, Nunberg AN, Thomas TL;
 XX
 DR WPI; 1998-583201/49.
 DR P-PSDB; AAM67471.
 XX
 PT New sunflower albumin 5' regulatory region - useful for directing
 PT altered lipid metabolism in plant seeds
 XX
 PS Example 2; Fig 1; 38pp; English.
 XX

CC This sequence is the gene encoding the borage (Borage officinalis)
 CC delta-6 desaturase enzyme. The lipid metabolism gene is an example
 CC of a heterologous gene which can be expressed at high levels in a
 CC seed-specific manner in transgenic plants, when placed under control
 CC of the sunflower albumin gene 5' regulatory region (AAV34397).
 XX

SQ Sequence 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 other;

Query Match 27.9%; Score 245.2; DB 19; Length 1684;
 Best Local Similarity 57.7%; Pred. No. 4.4e-52;
 Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

QY 24 TTCTCAGCTCCACCGCTTTCCGACCAACCGTCTCCGCGCTCTCCGACTACCGC 83
 DB 265 TTTTTCATGGGATATATCTAAAGATTAATCTGTTCTGAGTTCTAAAGATTAATG 324
 QY 84 AAGCTTCTCCGACCTCTCCGCGCTCAACCTTCAACCGGAGGAGCAACACTCC 143
 DB 325 AAGCTTGTGTGAGTTTCTAAAGATTAATCTGTTCTGAGTTCTAAAGATTAATG 384
 QY 144 ATCTCTCTCCCTTATTTCTCAACCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCC 203
 DB 385 GCAATTTGTGTTATATGCAATGCTGTTGCTATGATGATGATGATGATGATGATG 444
 QY 204 GACAGACTTGTGACGCTCTTCCGCTGATGATGATGATGATGATGATGATGATG 263
 DB 445 GAGGCTGTTTGTGATATTTCTGAGTTTCTGAGTTTCTGAGTTTCTGAGTTTCTG 504
 QY 264 GCGTGGATGAGCAACGATCCGCGCATTAACAGGATGATGATGATGATGATGATG 323
 DB 505 GGTGATGATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 564
 QY 324 GCAATTCAGATTTCTCCGCAACATTTCTCCGCGGATCAGATGATGATGATGATG 383
 DB 565 TTTATGGGTATTTTGTGCGCAATTTGTTCTTCAAGATTAATGATGATGATGATG 624
 QY 384 AACCAAGCGCCACCACTGATGATGATGATGATGATGATGATGATGATGATGATG 443
 DB 625 AACCATATGACATCACTGATGATGATGATGATGATGATGATGATGATGATGATG 684
 QY 444 ATGCGGCTTGTGAGTTTCTGCGGCTTCTTCAATTCATTAACCTCATTTNCTATGG 503

```

Db      685 ATACCAATCTGTGTGCTCTTCAAGTTTGTGTTCACTCACTCTCATTTCTATGAG 744
Qy      504 AGAAGTTNAGTTTATGATTCATTCGTGTGATCTGCTACCGACACTTACTTT 563
Db      745 AAAAGTTGACTTTTGTCTTTTATCAAGATCTTTGTAGTTATCAACATTTGACATTT 804
Qy      564 TACCCGTAATGTGTGTGTCAGGGTCACTGTATCTGACGACAAATTCGTATTGTT 623
Db      805 TACCTATTATGTGTGTGCTAGGCTCAATATGATGATACAACTCTCATTAATGTTGTT 864
Qy      624 TCAGAGNAAAAGTGCAGATTAAGCT-TGAACATTAATGGGATCCTTGTGTTGACT 682
Db      865 ACCAAGAGAAATGTCTCTATTCAGCTCAGAACTCTTGGAGATGCCATGTTCTCAT 924
Qy      683 TGGTTCCTCTTTAGTGNCTTGCCTGCAATTTGGCCTGATGAGGATGTTGNCCT 742
Db      925 TGGTACCCGTTGCTTTGTTCTTTGCTTATTTGGGCTGAAGAAATTAATGTTTAT 984
Qy      743 GCTAGCTTGTCTGTGTGTCNATCCAGACATTCAGTTCTGTTGATCACCCTGCTGA 802
Db      985 GCAAGTTTATCAGTGAAGT-GAATGCAACAAGTTTCTCTTGAACACATTTCTTTC 1043
Qy      803 AAATTTATATGCGGCA--CNATGGAAATGACTGNT--GANAATCAGACAAGGGGTC 858
Db      1044 AAGTGTATATGTGAAAGCTTAAGGGAATTAATGTTGAGAAACAACGATGGAG 1103
Qy      859 ATTGATATCTCTGTGNCCT 880
Db      1104 ACTTGACATTTCTTGTCTCT 1125

```

RESULT 10

AAK24917
ID AAK24917 standard; cDNA; 1684 BP.

AC AAK24917;

DT 21-JUN-1999 (first entry)

DE Borage delta-6 desaturase cDNA.

KW Delta-6 desaturase; borage; oleosin; AtS21; promoter;
KM transgenic plant; seed; lipid; fatty acid; oilseed; vegetable oil;
KM Gamma-linolenic acid; octadecatetraenoic acid; de.

OS Borage officinalis.

Key Location/Qualifiers
CDS 43..1389
FT /*tag= a

PN MO9845461-A1.

PD 15-OCT-1998.

PF 09-APR-1998; 98MO-US07179.

PR 09-APR-1997; 97US-0831575.

PA (RHON) RHONE-POULENC AGROCHIMIE.

PI L4 Z, Thomas TL;

DR WPI; 1999-180333/15.

DR P-PSDB; AAW98130.

PT Nucleic acid containing oleosin 5'-regulatory region - useful for
modulating fatty acid synthesis and lipid metabolism in plants,
particularly to increase content of gamma-linolenic acid

PS Example 2; Page 59-61; 101bp; English.

CC The present sequence encodes borage delta-6 desaturase (see
CC AAW98130), an enzyme that catalyses the conversion of linoleic acid
CC to gamma-linolenic acid (GLA). Delta-6 desaturase cDNA was
CC isolated from a borage membrane-bound polysomal cDNA library
CC using a partial clone, obtained from an EST database search, as
CC probe. The borage delta-6 desaturase nucleic acid can be
CC operably linked to the seed-specific 5' regulatory region (see
CC AAK24916) of the Arabidopsis thaliana oleosin AtS21 gene in claimed
CC expression cassettes of the invention. Transgenic plants, e.g.
CC sunflower, soybean, maize, tobacco, cotton, peanut, oilseed of
CC rape or Arabidopsis are obtained that show increased levels of
CC GLA or octadecatetraenoic acid. The levels of desirable fatty
CC acids in oilseed crops can be manipulated to provide seed
CC oils of use in human health and industrial applications.

CC Sequence 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 other;

Query Match 27.9%; Score 245.2; DB 20; Length 1684;

Best Local Similarity 57.7%; Pred. No. 4,4e-52;
Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

```

Qy      24 TTCTCCACCTCCACCGTCTTCCGACACACCGTCCGCGCCCTCCGACTACCGC 83
Db      265 TTTTTCACGCGGTATTATCTTAAAGTTACTCTGTTTGAAGTTTCAAGATTATAG 324
Qy      84 AAGCTTCTTCGACCTCTCCGCGCTCAACTCTTTCACACGGAAGGCCACAACTCC 143
Db      325 AAGCTTGTGTGATGTTTCTAAATGGGTTGTATGACAAAAGATCATATATGTT 384
Qy      144 ATCTCTCTCTCCCTTATCTCACTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 203
Db      385 GCAACTTGTGCTTATTAACAATGCTGTGCTATAGTGTATAGGGCTTTGTTTGT 444
Qy      204 GACAGCACTTGTGTGACGCTTCCGCTGATGATAGCTTCTCTGATTCAGAC 263
Db      445 GAGGCTGTTTGTATCAATTTGTTCTGTGAGTGTGATGAGGTTTGTGATTCAGAT 504
Qy      264 GGCTGATAGGCGACAGCTCCGCGCATTAACAAGTATCTGACCGCCCTCAACCGC 323
Db      505 GGTGTGATGACATATATGCTGGCATTTATATGATGATGATTCAGAGCTTATTAAG 564
Qy      324 GCAATTCAGATTTCTCCGCAACATTTCTCCGGAATCAGATCGGCTGTGGAAGTG 383
Db      565 TTATAGGATATTTTCTCCAAATTTCTTTCAGGAATTAATGTTGTTGGAATG 624
Qy      384 AACCAAGGCCACACATTCATGATCAGAGCTGATGATGATGATGATGATGATGAT 443
Db      625 AACCATTAATGACATACATGCTGTATATAGCTTGAATATGATGATGATGATGAT 684
Qy      444 ATCCGCTCTTTCGATTCGTGCGGTTCTTCAATTCATTAACCTCTATTTGAGG 503
Db      685 ATACCAATCTCTTGTGTGCTTCCAGTTTGTGTTGTTGTTGTTGTTGTTGTTG 744
Qy      504 AGAAGTTNAGTTTATGATTCATTCGTGTGATCTGCTACGACGACTTACTTT 563
Db      745 AAAAGTTGACTTTTGTACTTTTATCAAGATCTTTGTAAGTTATCAATGAGACATTT 804
Qy      564 TACCCGTAATGTGTGTGTCAGGGTCACTGTATCTGACGACAAATTCGTATGTT 623
Db      805 TACCTATTATGTGTGTCTAGGCTCAATATGATGATGATGATGATGATGATG 864
Qy      624 TCAGAGNAAAAGTGCAGATTAAGCT-TGAACATTAATGGGATCCTTGTGTTGACT 682
Db      865 ACCAAGAGAAATGTCTCTATTCAGCTCAGAACTTTGGATGCTTATGTTCTGATT 924
Qy      683 TGGTTCCTCTTTAGTGNCTTGCCTGCAATTTGGCCTGATGAGGATGTTTNGCTT 742
Db      925 TGGTACCCGTTGTTTCTTTGTTTGTGCTTATTTGGGCTGAAGAAATTAATGTTTAT 984
Qy      743 GCTAGCTTGTCTGTGTGTCNATCCAGACATTCAGTTCTGTTTAAATCACCCTGCTGA 802
Db      985 GCAAGTTTATCAGTGAAGT-GAATGCAACAAGTTTCTCTTGAACACATTTCTTTC 1043

```

QY 803 AATTATATGNCGGCA--CNANTGGAAATGACTGNT--GANAATCAGACAAAGGGTC 858
 Db 1044 AAGTGTATATGTTGAAAGCCTAAAGGAAATATGTTTGAGAAACAAACGATGGAC 1103
 QY 859 ATTGATATCTCTTGNCCT 880
 Db 1104 ACTTGACATTTCTTGCTCTCT 1125

RESULT 11
 AAT30395
 ID AAT30395 standard; DNA; 1685 BP.
 AC AAT30395;
 XX
 XX 15-SEP-1996 (first entry)
 DT
 XX Borage delta-6-desaturase gene.
 DE
 XX Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;
 KM polyunsaturated fatty acid; octadecatetraenoic acid;
 KM chilling resistance; oilseed; ss; ds.
 XX
 OS Borage officinalis.
 XX
 FH Key Location/Qualifiers
 FT CDS 44..1390
 FT /tag= a
 XX
 XX W09621022-A2.
 XX
 XX 11-JUL-1996.
 XX
 XX 28-DEC-1995; 95WO-IB01167.
 XX
 XX 30-DEC-1994; 94US-0366779.
 XX
 XX (RHON) RHONE POULENC AGROCHIMIE.
 XX
 XX Freyresinet GL, Nuccio M, Numberg AN, Reddy AS, Thomas TL;
 DR WPI, 1996-333997/33.
 DR P-PSDB; AAR98455.
 XX
 PT Transgenic plants comprising the borage delta-6-desaturase gene
 PT show increased production of gamma linolenic acid and having
 PT increased resistance to chilling
 PT
 PS Claim 2; Page 51-52; 75p; English.
 XX
 XX A DNA clone (AAT30395) codes for borage delta-6-desaturase (AAR98455),
 CC which catalyses the conversion of linoleic acid to gamma-linolenic
 CC acid (GLA). It was isolated from a borage membrane-bound polysomal
 CC library using probes based on abundantly expressed seed storage
 CC protein cDNAs and with an isolated partial cDNA clone. The gene
 CC can be incorporated into a vector, pref. incorporating a
 CC tissue-specific promoter, for the expression of delta-6-desaturase
 CC in transgenic plants, esp. sunflower, soybean, maize, tobacco,
 CC peanut, carrot or oilseed rape, resulting in increased GLA prodn.
 CC Alteration of plant lipids may also lead to improved chilling
 CC resistance.
 CC
 XX Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 other;

Query Match 27.9%; Score 245.2; DB 17; Length 1685;
 Best Local Similarity 57.7%; Pred. No. 4.4e-52;
 Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

QY 24 TTCTCCACTCCACCGCTCTTCCGACACACCGTCTCCGCCCTCTCCGACTACCGC 83
 Db 266 TTTTTCACGTGGGTATATATCTCTGTTCTGAGGTTTCTAAGATTATAG 325
 QY 84 AAGCTCTCTCCGACCTCTCCGGCTCAACCTCTTCAACCGCAAGGCGACACAACTCTCC 143

Db 326 AAGCTGTGTGAGTTTCTAATAATGGGTTGTATGACAAAAGGATATATATGTTT 385
 QY 144 ATCTCCCTCTCCCTTATTTCTACACCTTTTCTCTCTGTGCGGCGCTCTCTCC 203
 Db 386 GCAACTTGTGTGCTTATAGCAATGCTGTGTGCTATAGAGTGTATAGGGGTTTGT 445
 QY 204 GACAGCACTTGTGTCAGCGTCTTCCGCTGATGATGATGAGCTTCTCGATTCAGAC 263
 Db 446 GAGGCTTTTGTGATCATTTGTTTCTGTGGGTGTGATGGGTTTCTTGGATTCAGAGT 505
 QY 264 GGCCTGATAGGCGACAGACTCCGCGCATTAACAAGTATGCTGACCGCGCTCAACCGC 323
 Db 506 GGTGGATTGACATGATGCTGGCATTTATATGATGTCTGATTCAGAGCTTAATAG 565
 QY 324 GCAATTCAGATTTCTCCGGCAACATTCGCGCGGAATAGACATGCGTGTGAGAGTGG 383
 Db 566 TTTATGGATATTTTGTGCGCAATGTCTTTCAGGAATAGATGTTGTGGAATAG 625
 QY 384 AACCAACAGCGCCACACATGTCATGCAACAGCTCGACTATGACCTGATCGACAGAC 443
 Db 626 AACCATATGACATACATTCCTCTGTATACCTTGAATATGACCTGATTTACATAT 685
 QY 444 ATGCGGCTTTTGCAATTGCTGCGGCTTCTTCAATTCATACCTCTCATTTCTATGAG 503
 Db 686 ATACCATCTCTGTTGTGTCTTCAAGTTTGTGTTGCTACCTCATTTCTATGAG 745
 QY 504 AGGAAGTTGAGTTGATTTCAATGCTANGTTCTTGATCTGCTACAGACATTTACTTTT 563
 Db 746 AAAAGGTGACTTTTGACTCTTATCAAGATTCCTTGTATGATTCATACATTTGACATTT 805
 QY 564 TACCGGTATAGTGTGTCGACGGGCAACTGTATTCGACAGACAACTGCTATGTTT 623
 Db 806 TACCTATATATGTGTGCTGATGCTCAATATATATGATCAATCTCAATATGTTGTG 865
 QY 624 TCGAGGNGAAGATGACAGATAGACT-TGAACATATGAGGATCTGTGTTTGAGACT 682
 Db 866 ACCAAGAGAAATGTGCTCATGAGCTCAGAACTTGTGATGCTGATGTTCTGATTT 925
 QY 683 TGGTCTCTTTTATGATGCTGCTGCAATTTGGGCTGATAGGGGATGTTGNGCTT 742
 Db 926 TGGTACCCGCTGCTTGTCTTCTTGTGCTTAATTTGGGGAAGATTAATGTTTAT 985
 QY 743 GCTAGCTTGTCTGTGTTGNCNAATCCAGACATTCAGTTCTGTGAAACACTTGTCTGA 802
 Db 986 GCAAGTTATATGATGATCTG-GAATGCAACAGTCAATCTTGTGAACTCTCTTTC 1044
 QY 803 AATTATATGNCGGCA--CNANTGGAAATGACTGNT--GANAATCAGACAAAGGGTC 858
 Db 1045 AAGTGTATATGTTGAAAGCCTAAAGGAAATATGTTTGAGAAACAAACGATGGAC 1104
 QY 859 ATTGATATCTCTTGNCCT 880
 Db 1105 ACTTGACATTTCTTGCTCTCT 1126

RESULT 12
 ABK49502
 ID ABK49502 standard; DNA; 1685 BP.
 AC ABK49502;
 XX
 XX 15-JUL-2002 (first entry)
 DT
 XX
 XX DNA encoding Borage officinalis delta6-desaturase.
 DE
 XX delta6-desaturase; sunflower; soybean; maize; tobacco;
 KM peanut; carrot; oil seed rape; gamma linolenic acid; GLA;
 KM chilling tolerance; gene; ds; borage.
 XX
 OS Borage officinalis.
 FH Key Location/Qualifiers

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FT CDS 44..1390
FT /*tag= a
FT /product= "delta6-desaturase"
FT /transl_except= (pos:1151..1153, aa:Ser)
XX
XX US6355861-B1.
XX
XX 12-MAR-2002.
XX
XX 19-SEP-1997; 97US-0934254.
XX
XX 13-OCT-1992; 92US-0959952.
XX 10-OCT-1991; 91US-0774475.
XX 08-JAN-1992; 92US-0817919.
XX 14-SEP-1994; 94US-0307382.
XX 28-JAN-1997; 97US-0789936.
XX
XX (RHON ) RHONE-POULENC AGROCHIMIE.
XX
XX Thomas TL;
XX
XX WPI: 2002-380944/41.
XX P-PSDB; AAU79830.
XX
XX Novel nucleic acid encoding evening primrose delta6-desaturase which
XX converts linoleic acid to gamma linolenic acid useful for producing
XX gamma linolenic acid in transgenic plant or bacteria
XX
XX Example 9; Column 29-32; 53pp; English.
XX
XX The invention describes an isolated nucleic acid encoding an evening
XX primrose Delta6-desaturase. The nucleic acid and a vector expressing the
XX nucleic acid are useful for producing a plant such as sunflower, soybean,
XX maize, tobacco, peanut, carrot or oil seed rape plant, with increased
XX gamma linolenic acid (GLA) content, and also for inducing or increasing
XX production of GLA in a bacteria or plant deficient, lacking in or
XX producing low levels of GLA. The nucleic acid is also useful for inducing
XX chilling tolerance in plants. This sequence encodes the borage delta6
XX desaturase involved in the production of gamma linolenic acid.
XX
XX Sequence 1685 BP, 431 A, 277 C, 357 G, 620 T, 0 other;
XX
XX Query Match 27.9%; Score 245.2; DB 24; Length 1685;
XX Best Local Similarity 57.7%; Pred. No. 4,4e-52;
XX Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;
XX
XX 24 TTCTCCACCTCCACCGCTTTTCCGACACACCGCTTCGCCCTCTCCGACTACCGC 83
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 266 TTTTCACTGGGTATATCTTAAAGATTACTGTTTCTGAGTTTCTTAAAGATTATAGG 325
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 84 AAGCTCTTCGACGCTCCGCGCTCAACCTTCAACGCGAAGGCGCACACACTCC 143
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 326 AAGCTGTGTTGATTTTCTTAAATGGTTTGTATGACAAAAGGCTCATATTATGTTT 385
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 144 ATCTCTCTCTCCCTTATTCACCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 203
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 386 GCAACTTGTGCTTATAGCAATGCTGTTTGTATAGATTTTATAGGGTTTGTTTGT 445
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 204 GACAGCACTTCTGACAGTGTCTTCCGCTGCATTTGATAGGCTTTCTTGATTCAGAGC 263
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 446 GAGGGTGTGTTGATATTTGTTTCTGGGTGTTTGTATGGGGTTTCTTGATTCAGAGT 505
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 264 GGCTGATAGGCGACGCTCCGCGCATTTCAAGTGATGCTCAGCGCGCCCTCAACCGC 323
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 506 GGTGATTTGATATATGCTGGGCATTTATATGATGCTGATTCAAAGCTTTAATAG 565
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 324 GCAATTCAATTTCTCCGCGCAATTTCTGCGGAATGCAATCGCGTGTGGAAGTGG 383
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 566 TTTATGGGATTTTGTGCTGCAATTTGTCTTTCAGGAATAGATTTGTTGTGGAATGG 625
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 384 AACCAACAGCCGACACATTTGATGCAACAGGCTTGACTATGACCTTGATTCAGAC 443
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 626 AACCAATATGACATCATTTGCTGTAATATAGCTTGAATATATACCTGATTTACATAT 685
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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XX 444 ATCCGATCTTTGACATTTGCTGCGGCTTCTTCAATTCATACCTCTCATTTCTATGG 503
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 686 ATACCAATCTTTGTGTGCTTCCAGTTTGTGTTCACTACCTCTCATTTCTATAGAG 745
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 504 AGGAAGTTAGATTGATTCATGCTGATGCTTGTATCTGTACACGACTTACTTTT 563
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 746 AAAAGTTGACTTTTACTCTTTATCAAGATCTTTGTAAGTTATCAACATTTGACATTT 805
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 564 TACCGGATATGCTGTGCGACGCTCACTTGTATCTGACGACAAATTCGATTTT 623
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 806 TACCTATTTATGCTGCTGCTAGCTCAATATATGATACAAATCTCATTAATGTTGTTG 865
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 624 TCGAGNGAAAATGAGGATAGAGCT-TGAACATAATGGGATCTTGTGTTTGACT 682
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 866 ACCAAGAAATATGTCTCATGAGCTCAGCAACTCTGGGATGCTTCAAGTTCTCATTT 925
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 683 TGGTTCCTCTTTTATGATGCTTGCCTGCCAAATTTGGCCTGATAGGGGATGTTGNCCTT 742
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 926 TGGTACCCGTTGCTGTTTCTTGTTCCTTAATTTGGGGTGAAGAAATATGTTTATTT 985
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 743 GCTAGCTTTGCTGTTTGTGNCNATTCAGACATTCAGTTCTGTTGAATACCTTGCTGA 802
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 986 GCAAGTTTATCAAGTCACTG-GAATGCAACAGTTCTCTTGAACCATTTCTCTTC 1044
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 803 AAATTATATGNCGGGCA--CNANTGGATGACTGANT--GANAAATCAGACAAAGGCTC 858
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 1045 AAGTGTATGTTGGAAGAGCTTAAAGGAATATTTGTTTGAGAAACAAACGATGGAC 1104
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 859 ATTGATATCTCTTGTGNCCTT 880
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 1105 ACTTGACATTTCTTGTCTCTCT 1126
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX
XX RESULT 13
XX ABX15366
XX ID ABX15366 standard; cDNA; 1685 BP.
XX XX
XX ABX15366;
XX
XX 17-APR-2003 (first entry)
XX
XX Borage delta-6-desaturase #1 cDNA.
XX
XX Delta-6-desaturase; gene: sr; delta-12-desaturase; sunflower; soybean;
XX maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
XX octadecatrienoic acid; alpha-linolenic acid; delta-15-desaturase;
XX Borage.
XX
XX Borage officinalis.
XX
XX Key Location/Qualifiers
XX CDS 44..1390
XX FT /*tag= a
XX FT /product= "Borage delta-6-desaturase #1"
XX FT /transl_except= (pos:1151..1153, aa:Ser)
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XX US2002108147-A1.
XX
XX 08-AUG-2002.
XX
XX 21-DEC-2001; 2001US-0029756.
XX
XX 13-OCT-1992; 92US-0959952.
XX 19-SEP-1997; 97US-0934254.
XX 10-OCT-1991; 91US-0774475.
XX 08-JAN-1992; 92US-0817919.
XX 14-SEP-1994; 94US-0307382.
XX 28-JAN-1997; 97US-0789936.
XX
XX (THOM/) THOMAS T L.
XX
XX Thomas TL;
XX

```

XX WPI: 2003-06659/06.
 DR P-PSDB; AB673095.
 XX
 XX Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
 PT for producing plant with increased gamma linolenic acid content, and
 PT for inducing octadecatrienoic acid production in plant
 XX
 PS Example 9; Fig 5A; 55pp; English.
 XX
 CC The invention relates to a nucleic acid encoding an evening primrose
 CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
 CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
 CC for producing a plant (such as sunflower, soybean, maize, tobacco,
 CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
 CC acid (GLA) content by transforming a plant cell with the nucleic acid or
 CC vector and regenerating a plant with increased GLA content from the plant
 CC cell, for inducing or increasing production of GLA in an organism lacking
 CC in or producing low levels of GLA and for inducing production of
 CC octadecatrienoic acid in at least one of a plant deficient or lacking
 CC in or producing low levels of octadecatrienoic acid, a bacterium which
 CC produces alpha-linolenic acid or a bacterium which exhibits a
 CC delta-15-desaturase activity on a GLA substrate. This sequence represents
 CC cDNA encoding a borage delta-6-desaturase polypeptide.
 XX
 SQ Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 other;

Query Match 27.9%; Score 245.2; DB 25; Length 1685;

Best Local Similarity 57.7%; Pred. No. 4.4e-52; Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

24 TTCTCCACCTCCACCGCTTTCCGACACACCGTCTCCGCGCTCTCCGACTACCGC 83
 266 TTTTTCACCGGGTATATCTTAAAGATTCTCTGTTTTCAGAGTTTCTAAAGATTATAG 325
 84 AAGCTTCTCTCCGACCTCTCCGCGCTCAACCTTTCAACGCGACGACCAACCTCC 143
 326 AAGCTTGTTGTTGAGTTTCTTAAATGGGTTTGTATGACAAAGATCATATATGTTT 385
 144 ATCTCTCTCTCCCTTATCTCAACCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 203
 386 GCACTTGTGTGTTTATAGCAATGCTGTTGTATGAGTTTATGAGGTTTGTGTTTGT 445
 204 GACAGACTTCTGTGAGCGTCTCCGCTGATGATAGGCTTCTCTGATTCAGAGC 263
 446 GAGGTTGTTTGTATCTTGTCTGCGGTGTTGATGGGTTCTTGTGATTCAGAGT 505
 264 GGCTGGATGAGCGACGACTCCGCGCATTTACAACTGATGCTCAGCGCGCTCAACGC 323
 506 GGTGGATTGACATGATGCTGGGCAATTATATGATGATGCTGATTCAGAGCTTAAATAG 565
 324 GCAATTCAGATTCTCTCCGCAACATTCGCGCGAATCAGATGGCTGTGGAAGTGG 383
 566 TTATAGGATATTTTCTGCAATTTGTCTTCAAGATTAAGTATGTTGTTGGAATGG 625
 384 AACCAACAGCCACACATTCATGATGACAGCTGATGATGATGATGATGATGATGATG 443
 626 AACCAATTAAGCATACATGCTGTAATGATGATGATGATGATGATGATGATGATGAT 685
 444 ATGCGGCTTTTGCAGTTTCTGCGGTTCTTCAATTCATTAACCTCTGATTTCTATGG 503
 666 ATACATTTCTGTTGTGTTCTTCAAGTTTGTGTTCTCACTCACTCTCATTTCTATAG 745
 504 AGGAAGTTGAGTTGATTCATGTTGATGTTCTGATGCTGATCCAGACATTTACTTTT 563
 746 AAAAGGTTGACTTTGACTTTTATCAAGATTTCTTGTATGATTAATCAATTCAGACAT 805
 564 TACCGGTAATGTTGTTGCGAGGCTGATGATGATGATGATGATGATGATGATGATG 623
 806 TACCTATTATGTTGTTGCTGATGATGATGATGATGATGATGATGATGATGATG 865
 624 TCGAGGNGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 862

DB 866 ACCAAGAAATGTCCTTCTATGAGCTGAGAACTCTTGGATGCTGATGCTGAT 925
 QY TGGTCTCTTTTATGATGCTGCTGCGAAATGGGCGCTGATGAGGATGTTTNGCTT 742
 DB 926 TGGTACCGGTTGCTGTTTCTTGTGTTGCTTATTTGGGTTGAAGATTAATGTTTAT 985
 QY 743 GCTACCTTTGCTGTTTGTGTCGATGATGATGATGATGATGATGATGATGATGATG 802
 DB 986 GCAAGTTTATCAGTACGCTGATGCAACAGTTGATGATGATGATGATGATGATGATG 1044
 QY 803 AAATTATATGCGGCGCA--CNATGGGAATGATGATGATGATGATGATGATGATG 858
 DB 1045 AAGTGTATGTTGGAAGGCTTAAAGGAAATGATGATGATGATGATGATGATGATG 1104
 QY 859 AATGATATCTCTGTCGCTCT 880
 DB 1105 ACTGACATTTCTGCTCTCT 1126

RESULT 14

AB212753 standard; DNA; 1350 BP.

AB212753;

21-JAN-2003 (first entry)

Arabidopsis thaliana stress regulated gene SEQ ID NO 558.

Arabidopsis thaliana; plant; gene; stress; transgenic; de.

Arabidopsis thaliana.

MO200216555-A2.

28-FEB-2002.

24-AUG-2001; 2001WO-US26685.

24-AUG-2000; 2000US-227866P.

26-JUN-2001; 2001US-264647P.

22-JUN-2001; 2001US-300111P.

(SCRI) SCRIPPS RES INST.

(SYGN) SYNGENTA PARTICIPATIONS AG.

Harper JF, Krepe J, Wang X, Zhu T;

WPI: 2002-304127/34.

Claim 6; SEQ ID NO 558; 577bp + Sequence Listing; English.

The invention relates to identifying a stress condition to which a plant

cell has been exposed, comprising:

(a) contacting nucleic acid representative of expressed polynucleotides

in the plant cell with an array or probes representative of the plant

cell genome; and

(b) detecting a profile of expressed polynucleotides in the plant cell

characteristic of a stress response. The method is useful in the

production of transgenic plants, cells and seeds and in producing plants

with increased tolerance to abiotic stresses. The present sequence is that

of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used

in methods of the invention.

Note: The sequence data for this patent is not represented in the printed

specification but is based on sequence information supplied to Derwent by

the European Patent Office.

Sequence 1350 BP; 325 A; 359 C; 274 G; 392 T; 0 other;


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PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 20-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
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PR 22-JUL-1999; 99US-0145085.
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PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147392.
PR 05-AUG-1999; 99US-0147260.
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PR 09-AUG-1999; 99US-0147493.
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PR 13-AUG-1999; 99US-0148684.
PR 15-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
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PR 25-AUG-1999; 99US-0150566.
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PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.

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PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 06-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
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PR 13-OCT-1999; 99US-0159295.
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PR 21-OCT-1999; 99US-0160741.
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PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match 27.7%; Score 244.2; DB 21; Length 1650;
 Best Local Similarity 57.2%; Pred. No. 7, 8e-52;
 Matches 469; Conservative 0; Mismatches 349; Indels 2; Gaps 2;

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QY 1 CCGCCTCCCTCTCTCCCGGCTTCCACCTCCACCGTCTTCCGACACACCGTCT 60
DB 409 CCGCTTGGCACCATCTCGACCACTCTTCTACCGGTTACCAATCAGAGATTTCAGAGTCT 468
QY 61 CCGCGCCTCTCTCGACCTACCGCAAGCTCTTCTCCGACCTCTCCGCTCAACTCTTCA 120
DB 469 CCGAGTCTCAGGCATTACCGCTCGTAGGCTGCGGAGTTTGTAATCGGCTCTTGG 528
QY 121 ACCGCAAGGCGCACCAACCTCCATCTCTCTCTCTTATTTCAACCTTTTCTCTCT 180
DB 529 AAAACAAAGATCAGCTTACTCTACACTCTAGCCTTGCCTGCCGCAATGTCCTGAG 588
QY 181 CTGTCTGCGGCTCTCTCTTCTCCGACAGACTTTGTGACAGTCTTCCGCTGATTTA 240
DB 589 TTCTCTACGGTATTTGGCTTTTACCTCGTCTGCTTACCAAAATGCGCGGCTTC 648
QY 241 TAGGCTTCTGTGATTGAGAGCGGCTGAGTGGCCAGACTCCGCACTTACAAAGTGA 300
DB 649 TGGGTCTCTCTGATCCAGAGCGCTTACATAGTACAGATTCTGTATTAAGTTATTA 708
QY 301 TGCTAGCGCGCGCTCAACCGCGCAATTGAGATTCTCTCGGCAACATTTCTGCGGAA 360
DB 709 TGTGAAACAATCTTATTAACAGATTGCTCAGCTTCTCTCGGTAATGTCACCGGAA 768

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Oy	361	CCAGATCGCGTGGGGAAGGGAACCAACAGGCCACACATGGCATGCAAGAACGCTCG	420
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Dp	829	ATTAGATTCAGATCTACACACATCCCTGCTTCCTGGCGGTCCACCAAAATTTCTTCCT	888
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Dp	1009	TTCAAAACCTTTCTCTGCTCTCTCCAAACGTGAAGTACAGATCGTGTCTTAAACTTCG	1068
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Oy	720	CTGATAGGGGNAATGTTNGCTCTGCTAGCTTTGCTGTTTGTNCCNATCAGACACATTCAG	779
Dp	1129	CTGAGAGATCTCTCTTCGCTTTCACAACTTCACCG-TCAGCGGCGCTTCAACACATTC	1187
Oy	780	TTCTGCTGATNCACTTCGGAATTTATATAGCGGC	819
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:48:07 ; Search time 1341.13 seconds
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Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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28: gb_gse1:*
29: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	402.4	45.7	579	9	A1748200 A1748200 BD49d11.Y
3	341.6	38.8	592	10	BE347857 BE347857 sp06h07.Y
4	318	36.1	414	12	B1316528 B1316528 saf04e03.

5	307.4	34.9	538	12	BG682278 sae98b11.
6	302	34.3	1764	11	AY103762
7	281	31.9	823	28	BH687867 BOH5094TF
8	276.4	31.4	588	12	BM143768
9	265	30.1	449	14	CA935212
10	261	29.7	766	13	BQ402431 GA_Ed004
11	256.8	29.2	503	13	BUS48907 GM880016B
12	254.8	29.0	783	10	BG647198 EST508817
13	254.2	28.9	494	12	BG682077 sae95g06.
14	251.8	28.6	585	14	CB829088 LjNEST93h
15	247.4	28.1	673	10	BF003445
16	243.4	27.7	702	28	BH968200 odhs5g04.
17	241.2	27.4	607	14	CD037696 UPLC005.
18	241	27.4	498	12	BM878829 P4-B04 SW
19	240.4	27.3	494	12	BI127714 G664P71Y
20	239.6	27.2	691	12	BJ465389 BJ465389
21	236.2	26.8	585	13	B0811579 UL867B02
22	236.2	26.8	674	14	CB002504 VVB017E10
23	235.2	26.7	607	14	CB002410 VVB016E06
24	232.2	26.4	607	14	CB087946 hK10c10.9
25	230.8	26.2	669	12	A1729325 BHLG1131
26	230	26.1	599	28	BH521804 BOH043TR
27	229.4	26.1	819	28	BH236433 AUCCA35TF
28	226.8	25.8	546	28	BH574553 BOHCU73R
29	225.8	25.7	468	9	A1736850 BD34d09.Y
30	223.6	25.4	498	12	BI921760 EST541663
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33	220.6	25.1	602	10	BG097852 EST462371
34	220.6	25.1	652	14	CD005403 VVB047G10
35	219.4	24.9	569	14	CB086053 hJ79d03.Y
36	219.2	24.9	744	13	BO281359 WHE31020.D
37	217.8	24.8	748	13	BQ976973 CH12104.
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41	214	24.3	765	13	BU024179 QHP16J21.
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44	210	23.9	756	13	BU025934 QHG12E03.
45	208.4	23.7	723	13	BU023873 QHP14H08.

ALIGNMENTS

RESULT 1
CA785300 726 bp mRNA linear EST 04-DEC-2002
LOCUS sau27h03.y1 Gm-cl062 Glycine max cDNA clone SOYBEAN CLONE ID:
DEFINITION Gm-cl062-9581 5' similar to TR:Q92TY9 Q92TY9 DESATURASE/CYTOCHROME
B5 PROTEIN. ; mRNA sequence.

ACCESSION CA785300
VERSION CA785300.1 GI:26048847
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max

REFERENCE 1 (bases 1 to 726)
Shoemaker,R., Kelm,P., Vodkin,L., Erpelting,J., Corryell,V., Khanna
A., Bolla,B., Macra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schuck
R., Ritzer,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished

TITLE JOURNAL COMMENT
Washingon University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130
 South Memorial Parkway Huntville, AL 35801 For further information
 call: (800)-533-4363 or contact: cdu@resgen.com web site:
 www.resgen.com

Seq primer: -40RP from Gibco
 High quality sequence stop: 434.
 Location/Qualifiers

FEATURES

source

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 /clone_lib="Gm-c1062"
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 XhoI; The cDNA library was constructed from mRNA isolated
 from stem tissue of 1 month old greenhouse grown plants
 for the cultivar Raiden. Complementary DNA was
 synthesized from mRNA using a primer consisting of a
 poly(dT) sequence with a XhoI restriction site. EcoRI
 adapters were ligated to the blunt-ended cDNA fragments
 followed by XhoI digestion. The cDNA fragments were
 directionally cloned into the EcoRI-XhoI restriction site
 of the pBluescript vector. The ligated cDNA fragments were
 transformed into DH10B host cells (GibcoBRL). This library
 was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT

121 a 216 c 158 g 231 t

ORIGIN

Query Match 57.1%; Score 502.8; DB 14; Length 726;
 Best Local Similarity 82.8%; Pred. No. 1e-110;
 Matches 581; Conservative 0; Mismatches 120; Indels 1; Gaps 1;

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 Qy 177 CTCTCTGTGCGGCGCTCTCTCTCTCGACAGCACTTTCGTGACGCTTTCGGCTGCA 236
 Db 121 CTCTCTGTGCGGCGCTCTCTCTCTCGACAGCACTTTCGTGACGCTTTCGGCTGCA 180
 Qy 237 TTGATAGGCTTTCTCTGATTCAGAGCGGCTGATAGGCAAGCACTCGGCGCATTAAC 296
 Db 181 TTGATAGGCTTTCTCTGATTCAGAGCGGCTGATAGGCAAGCACTCGGCGCATTAAC 240
 Qy 297 GTATAGTCAAGCGCGGCTCAACCGGCAATTCAGATTCTCTCCGCAATTCCTCGCC 356
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 Qy 537 TTGATCTGACAGCACTTACTTTTACCCGCTAATGTTGTCAGAGGTCACATTCG 596

Db 481 TTGTTAGTTACCAAGCACTGACTTTTACCCCTGATGATGTTCCGTAGGGTTAATCTG 540
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 Qy 656 ATATAGGAGATCTTGTGTTTGGAGCTGTTCTCTTTAGTGNCTTCCGCCAAATT 715
 Db 601 CTTTGGGGTGTGTTGATTCCTGAGTTTGATACCTTTGTGTTTCTCTTCCCAAT 660
 Qy 716 GGGCTGATAGGGGAGATGTTTNGCTTGTAGCTTCTGTT 757
 Db 661 TGGTGGAGAGGCTTTGTTGTTTCTGAGTTCTCTGTT 702

RESULT 2
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 LOCUS sb49411.y1 Gm-c1011 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 DEFINITION Gm-c1011-238 5' similar to TR:082348 082348 PUTATIVE CYTOCHROME B5.
 mRNA sequence.

ACCESSION A1748200
 VERSION A1748200.1 GI:5126464
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max

REFERENCE 1 (bases 1 to 579)
 Shoemaker R., Keim P., Vodkin L., Erpelting J., Corvett V., Khanna
 A., Bolla B., Maria M., Hillier L., Kucaba T., Martin J., Beck C.,
 Wylie T., Underwood K., Steptoe M., Theising B., Allen M., Bowers
 Y., Person B., Swaller T., Gibbons M., Page D., Harvey N., Schurk
 R., Richter E., Kohn S., Shin T., Jackson Y., Cardenas M., McCann
 R., Waterson R. and Wilson R.
 Public Soybean EST Project

TITLE Unpublished
 JOURNAL
 COMMENT Contact: Shoemaker R./Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 Possible reversed clone: similarity on wrong strand This clone is
 available through: ResGen, Invitrogen Corp. 2130 South Memorial
 Parkway Huntville, AL 35801 For further information call: (800)
 -533-4363 or contact via email: cdu@resgen.com
 Insert Length: 1134 Std Error: 0.00
 High quality sequence stop: 412.
 Location/Qualifiers

FEATURES

source

1. 579
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 plants"
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 /note="Vector: pBluescript II SK+, Site 1: EcoRI, Site 2:
 XhoI; This cDNA library was constructed from mRNA isolated
 from immature cotyledons (100-200mg) of greenhouse grown
 plants. The cDNA library was prepared using the Life
 Technologies SuperScript cDNA library construction kit.
 Complementary DNA was synthesized from mRNA using a poly
 (dT) sequence with a Not I restriction site. Sal I
 linkers adapters were ligated to the blunt-ended cDNA
 fragments followed by Not I digestion. The cDNA fragments
 were directionally cloned into the NotI-Sal I restriction
 site of the pSPORT 1 vector. The ligated cDNA fragments

were transformed into E. coli Electromax DH10B host cells.
This library was constructed by Dr. Lila Vodkin and Dr.

BASE COUNT 119 a 126 c 143 g 187 t 4 others
ORIGIN

Query Match 45.7%; Score 402.4; DB 9; Length 579;

Best Local Similarity 89.6%; Pred. No. 1.6e-86;
Matches 499; Conservative 0; Mismatches 50; Indels 8; Gaps 7;

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QY 390 AAGCCACCACTTCATTCAGCAACCTCGATAGACCTCGATTCGACGACCAACCGC 449
DB 76 AATGTCACCACTTCATTCAGCAACCTCGATAGACCTCGATTCGACGACCAACCGC 135
QY 450 GTCTTTGCAATTCGTCGCGGTTCTTCAATTCATTAACCTGATTCATTCATTCATTC 509
DB 136 GTCTTTGCAATTCGTCGCGGTTCTTCAATTCATTAACCTGATTCATTCATTCATTC 195
QY 510 TTNGAGTTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 569
DB 196 TTGAGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 255
QY 570 GTAAATGTCGCGCGGTTCTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTC 629
DB 256 GTAAATGTCGCGCGGTTCTTCAATTCATTCATTCATTCATTCATTCATTCATTCATTC 315
QY 630 NGAAGAATCAGATTCAG-CTTGAACATTAATGGGATCCTTGTGTTTGAATTCGTT- 687
DB 316 CGAAAGATCAGATTCAG-CTTGAACATTAATGGGATCCTTGTGTTTGAATTCGTT- 375
QY 688 CCTTTTGAATTCGTCGCGGTTCTTCAATTCATTCATTCATTCATTCATTCATTCATTC 747
DB 376 CCTTTTGAATTCGTCGCGGTTCTTCAATTCATTCATTCATTCATTCATTCATTCATTC 434
QY 748 CTTTGTCTTTTTCNATTCAGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 807
DB 435 CTTTGTCTTTTTCNATTCAGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 493
QY 808 TATATNCGGCG--ACNANTGGATGACTG-NTGNATTCAGACAGAGGCT-CATTCG 863
DB 494 TATATNCGGCG--ACNANTGGATGACTG-NTGNATTCAGACAGAGGCT-CATTCG 553
QY 864 ATATCTCTTGTGNCCT 880
DB 554 ATATCTCTTGTGNCCT 570

RESULT 3
BE347857 592 bp mRNA linear EST 04-DEC-2001
LOCUS sp06107.Y1 Gm-cl041 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION Gm-cl041-2102 5' similar to TR:082348 082348 PUTATIVE CYTOCHROME
BE-1, mRNA sequence.
ACCESSION BE347857
VERSION BE347857
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max

REFERENCE
AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Matra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE Public Soybean EST Project
JOURNAL Unpublished
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

Trace considered overall poor quality This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact via email: cu@resgen.com
Insert Length: 149 Std Error: 0.00
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source

1..592
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl041-2102"
/issue_type="Senescing leaves, mature plant, greenhouse grown"
/lab_host="DH10B"
/clone_1lb="Gm-cl041"
/note="Vector: pT733Pac (Pharmacia); Site 1: EcoRI; Site 2: HindIII. This library was constructed from mRNA isolated from senescing leaf tissue of mature greenhouse grown plants of the cultivar Williams. Complementary DNA was synthesized from mRNA using a 3' anchored poly(dT) primer. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and HindIII. The cDNA fragments were directionally cloned into the EcoRI-HindIII restriction site of the pT73-Pac vector. The ligated cDNA fragments were transformed into DH10B host cells. This library was constructed by Dr. Randy Shoemaker."

BASE COUNT 132 a 124 c 139 g 197 t
ORIGIN

Query Match 38.8%; Score 341.6; DB 10; Length 592;
Best Local Similarity 83.7%; Pred. No. 7.8e-72;
Matches 427; Conservative 0; Mismatches 79; Indels 4; Gaps 4;

QY 312 CCGCTCAACCGCGCAATTCATTCCTCCGCAACATTCGCGGATCGATCGGC 371
DB 2 CCGCTCAACCGCGCAATTCATTCCTCCGCAACATTCGCGGATCGATCGGC 61
QY 372 TGATGAGTGGACACACAGCCACCACTTCGATGACAGAGCTGATGACCT 431
DB 62 TGATGAGTGGACACACAGCTCTCACACATTCGCTGACACATTCGATGACCT 121
QY 432 GATTCGACACATCGCGCTCTTTCAGATTCGTCGCGGTTCTTCAATTCATTCATTC 491
DB 122 GATTCGACACATCGCGCTCTTTCAGATTCGTCGCGGTTCTTCAATTCATTCATTC 181
QY 492 CATTCATTCGAGAGAGATTCGATTCATTCATTCATTCATTCATTCATTCATTCATTC 551
DB 182 CATTCATTCGAGAGAGATTCGATTCATTCATTCATTCATTCATTCATTCATTCATTC 241
QY 552 CACTTACTTTTACCCGTAATGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 611
DB 242 CACTTACTTTTACCCGTAATGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 301
QY 612 CTGCTATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 670
DB 302 CTGCTATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 361
QY 671 GGTGTTGACATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 729
DB 362 GGTGTTGACATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 420
QY 730 NATGTTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 789

/clone="GENOME SYSTEMS CLONE ID: Gm-cl065-3910"
 /issue_type="germinating shoots"
 /lab_host="DH10B"
 /clone_lib="Gm-cl065"
 /note=Vector: pBluescript II SK+; Site 1: EcoRI, Site 2: XhoI; The cDNA library was constructed from mRNA isolated from germinating shoots of the cultivar Williams. The seeds were allowed to germinate for 24 hours prior to being cold stressed for 2 days at 4C. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(AT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT 101 a 134 c 127 g 176 t
 ORIGIN

Query Match 34.9%; Score 307.4; DB 12; Length 538;
 Best Local Similarity 73.9%; Pred. No. 1.4e-63;
 Matches 397; Conservative 0; Mismatches 139; Indels 1; Gaps 1;

222 GTGCTTCGCGCATGATGAGGCTTCTGTGATTCAGAGGCGCGATGAGCCACGAC 281
 2 GTGCTTCGCGCATGATGAGGCTTCTGTGATTCAGAGGCGCGATGAGCCACGAC 61
 282 TCGGCGCATTAACAAGTGTCTGACGCGCGCGCATTAACAAGTGTCTCTCC 341
 62 TCGGCGCATTAACAAGTGTCTGACGCGCGCGCATTAACAAGTGTCTCTCC 121
 342 GCGACATTTCTGCGCGCATTAACAAGTGTCTGACGCGCGCATTAACAAGTGTCTCTCC 401
 122 GCGACATTTCTGCGCGCATTAACAAGTGTCTGACGCGCGCATTAACAAGTGTCTCTCC 181
 402 ATTGATGACAGCGCGCATTAACAAGTGTCTGACGCGCGCATTAACAAGTGTCTCTCC 461
 182 ATTGATGACAGCGCGCATTAACAAGTGTCTGACGCGCGCATTAACAAGTGTCTCTCC 241
 462 TCGTCCGCGTCTTCAATTCATTAACCTGATTCATTAACAAGTGTCTCTCC 521
 242 TCGTCCGCGTCTTCAATTCATTAACCTGATTCATTAACAAGTGTCTCTCC 301
 522 TNCATTGCTAAGTCTTGAATCTGCTACAGACCTTACTTTTACCCTGATGTGTCT 581
 302 TCGTCCGCGTCTTCAATTCATTAACCTGATTCATTAACAAGTGTCTCTCC 361
 582 GCGAGGCTAAGTCTTGAATCTGCTACAGACCTTACTTTTACCCTGATGTGTCT 641
 362 GCGAGGCTAAGTCTTGAATCTGCTACAGACCTTACTTTTACCCTGATGTGTCT 421
 642 GATAGA-GCTTGAACAATAAGGAGTCTTGTGATTCATTAACAAGTGTCTCTCC 700
 422 AACAGATGAGTGTGATTTGGGGCTGCTGCTTGGGCTTGGTACCTTTTGTGTGT 481
 701 CTTCCTGCGCAATTGGGCTGATAGGGGATTTGAGTGTGATTTGTGTGTGT 757
 482 TCTTCTGCGCAATTGGGCTGATAGGGGATTTGAGTGTGATTTGTGTGTGT 538

RESULT 6
 AY103762 1764 bp mRNA linear HTC 16-OCT-2002
 LOCUS Zea mays
 DEFINITION Zea mays PC0087385 mRNA sequence.
 ACCESSION AY103762
 VERSION AY103762.1 GI:21206840
 KEYWORDS HTC.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCB

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
 If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES
 source
 1..1764
 /organism="Zea mays"
 /mol_type="mRNA"
 /db_xref="MaizeDB:634923"
 /db_xref="taxon:4577"
 /clone_lib="Maize Mapping Project/Dupont Consensus Library"
 /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

BASE COUNT 310 a 602 c 456 g 396 t
 ORIGIN

Query Match 34.3%; Score 302; DB 11; Length 1764;
 Best Local Similarity 61.6%; Pred. No. 4.3e-62;
 Matches 519; Conservative 0; Mismatches 319; Indels 4; Gaps 3;

1 CGGCTTCCTCTCTCTCCCGCTTCTCCACCTCCACCGTCTTTCGACACACCTCT 60
 327 CTTGCGCGCGCGCTCTCTCCCGCTTCTCTGTTGCGCGCTCTGACTAGCGCTCT 386
 61 CGGCGCTCTCTCTCTCCCGCTTCTCCACCTCTTTCGACCTCTCCGCTCAACTT 120
 387 CCGCGCGCTCTCTCTCTCCCGCTTCTCCACCTCTTTCGACCTCTCTCTCTCT 446
 121 ACCGAGGCGCGACACACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
 447 AACGCGTGGCG 506
 181 CTGCTGCGCGCGCT 240
 507 CGCTGACCTGCT 566
 241 TAGGCTTCT 300
 567 TTGGCTTCT 626
 301 TGCTAGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
 627 CCGGCGCGCGCGCT 686
 361 TCAGCATGCGCTGTGAGTGAAGTGAACAACAGCGCCACACATTCATGCAACAGCT 420
 687 TCAGCATGCGCTGTGAGTGAAGTGAACAACAGCGCCACACATTCATGCAACAGCT 746
 421 ACTATGACCTGTATGACGACATGCGCGCTTCTCTCTCTCTCTCTCTCTCTCT 480
 747 ACCATGACCTGTATGACGACATGCGCGCTTCTCTCTCTCTCTCTCTCTCTCT 806
 481 CCATTAACCTGTATTCATGAGGAGGAGTTCGATTCATTCATTCATTCATTCAT 540

Db 807 ACATATGCTCTTCTTACCAACGAGCCCTGGGCTTCGATGCGCCTCGAAATTCCTCA 866
 Qy 541 TCGCTACAGCACTTACTTTTACCCGGTAATGTGTGTCAGAGGTGAACCTGTATC 600
 Db 867 TCGACTACAGCACTGACCTTCTACCCGGTAATGTGTGTCAGAGGTGAACCTGTATC 926
 Qy 601 TGCAGCAATTCCTGCTAATGTTTTCGAGGAAAGTGCAGGA-TAGAGCTTGAAACATA 659
 Db 927 CGCAGTCCGCTGTGTCTTCACGGAAGAGGGTCCGACAGCGTGTCTGAGATCG 966
 Qy 660 TGGGATCTCTTGTGTGTGACTGTTCTCTTTTATGATGCTTGTCTGCAATTTGGC 719
 Db 987 CGGGGGTCCGACATCTCGGCTGTGTAACCGCTGTGCTGCTGCTCCCTCGAATTTG 1046
 Qy 720 CTATAGAGGGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 779
 Db 1047 GGAAGAGGGTGGGCTGTGTGTCTTTCAGCTTCAACATCTG-CGGGATTCAGACGTC 1105
 Qy 780 TTCTGTGTAATGACCTTGTGTAATTTATGATGCGAGC-ACNANTGGGAATGACTG 837
 Db 1106 TTCTGCTGAACACCTTCTGCTGCGAGCTGATGTGCGGCGCACCGCAATGACTG 1165
 Qy 838 NT 839
 Db 1166 TT 1167

RESULT 7
 BH687867/c 823 bp DNA linear GSS 19-FEB-2002
 LOCUS BOHSQ94TR BO 2.3 KB Brassica oleracea genomic clone BOHSQ94,
 DEFINITION genomic survey sequence.
 ACCSSION BH687867
 VERSION BH687867.1 GI:18758304
 KEYWORDS
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 823)
 Town,C.D., Van Aken,S., Utecherback,T., Koo,H. and Fraser,C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished
 Other GSSs: BOHSQ94TR
 COMMENT Contact: Chris Town

TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.

FEATURES
 source location/Qualifiers

1. 823
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="TO100DH3"
 /db_xref="taxon:3712"
 /clone="BOHSQ94"
 /clone_1lb="BO 2.3 KB"
 /note="Vector: pHO5; Site 1: BstXI; 2-3 kb sheared
 genomic DNA inserted into pHO5 using BstXI linkers"
 BASE COUNT 182 a 197 c 283 g 161 t

Query Match 31.9%; Score 281; DB 28; Length 823;
 Best Local Similarity 63.6%; Pred. No. 3.8e-57;
 Matches 439; Conservative 0; Mismatches 250; Indels 1; Gaps 1;
 Qy 1 CGCGCTCCCTCTCTCTCCGCTTCTTCACCTCCACCGCTTTCGACACACCGCTCT 60

Db 705 CCCCTTGAGCACCCCTCTGACAGGCTTCTTCAACCCGCTACACATCGAGATACGAATCT 646
 Qy 61 CGCGCGCTCTCTCGACTACCGGAGCTCTTCGAGCCTTCGCGGCTCAACTCTTCA 120
 Db 645 CCGAGTCTCCGCGACTACCGCGGATGAGCCAGAGATTCGCAAGCTTGGCTCTTC 586
 Qy 121 ACCGAGGCGCACAGAACCTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
 Db 585 AATCGAAGGAGACAAACATCTTACACGCTATCTTCAATGCGCATTTGCGCGGCG 526
 Qy 181 CTGTCTGCGGCGCT 240
 Db 525 TCTCTACGCTGTTTGTGGCGTGCACATCTCTCTCTCTCTCTCTCTCTCTCTCT 466
 Qy 241 TAGGCTTCTCTGATTCAGAGGCGGTGATAGGCGCACATCTCTCTCTCTCTCT 300
 Db 465 TCGGACTCTCTGATTCAGAGGCGGTGATAGGCGCACATCTCTCTCTCTCTCT 406
 Qy 301 TGTCTACGCGCGCTCAACCGCGCAATTCAGATCTCTCTCTCTCTCTCTCTCT 360
 Db 405 TGTGCAACAAGAGATTAACAGATGCGGAGCTCTCTCTCTCTCTCTCTCTCT 346
 Qy 361 TCAAGATCGGCTGTGGAAGTGAACCAACGCGCACCAATTCATGATGCAACAGCT 420
 Db 345 TCTGATCGGCTGTGGAAGTGAACCAACGCGCACCAATTCATGATGCAACAGCT 286
 Qy 421 ACTATGACCTGATCTGAGAGCATATGCGCTCTCTCTCTCTCTCTCTCTCTCT 480
 Db 285 AATGACATCCGATCTGAGAGCATATGCGCTCTCTCTCTCTCTCTCTCTCTCT 226
 Qy 481 CCATTAACCTCTCATTTCTATGAGAGATGAGTTCATTCATTCATTCATTCATTC 540
 Db 225 CGATGACGTACAGCTTCTACATGAGAGTTCATTCATTCATTCATTCATTCATTC 166
 Qy 541 TGTCTACAGCACTTACTTTTACCCGGTAATGTGTGTGCGAGGCTCACTGTATC 600
 Db 165 TTAGCTACAGCACTTACTTTTACCCGGTAATGTGTGTGCGAGGCTCACTGTATTC 106
 Qy 601 TGCAGCAATTCCTGCTATGTTTTCGAGGAAAGTGCAGGATAGAG-CTTGAACATA 659
 Db 105 TGCAGAGCTTCTCTGCTGTCTCTCCGAGCGAGATGAGATCGCGTCTCAACTTC 46
 Qy 660 TGGGATCTCTTGTGTGTGACTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 689
 Db 45 CGGGATCTTGTGTGTGACTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 16

RESULT 8
 BM143768 588 bp mRNA linear EST 29-NOV-2001
 LOCUS saj48e09.y1 Gm-cl072 Glycine max cDNA clone SOYBEAN CLONE ID:
 DEFINITION Gm-cl072-2921 5' similar to FR:082348 082348 PUTATIVE CYTOCHROME
 B5.; mRNA sequence.
 ACCSSION BM143768
 VERSION BM143768.1 GI:17453835
 KEYWORDS
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 588)
 Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
 A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
 Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schuck
 R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
 R., Waterston,R. and Wilson,R.
 Public Soybean EST Project
 Unpublished
 COMMENT Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130
 South Memorial Parkway Huntville, AL 35801 For further information
 call: (800)-533-4363 or contact: cdu@resgen.com web site:
 www.resgen.com
 Seq primer: -40RP from Gibco
 High quality sequence stop: 426.
 Location/Qualifiers

FEATURES

source

1. 588
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="SOYBEAN CLONE ID: Gm-c1071-2921"
 /tissue_type="seedlings induced for symptoms of SDS
 (Sudden Death Syndrome) disease"
 /dev_stage="2-3 weeks old"
 /lab_host="DH10B"
 /clone_lib="Gm-c1071"
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
 XhoI; The cDNA library was constructed from mRNA isolated
 from 2-3 week old seedlings that were induced for symptoms
 of SDS (Sudden Death Syndrome) disease by the
 translocation of culture filtrate of Fusarium solani f.
 sp. glycines (Plant Cell Report 18:375-380). Cultivar PI
 567374 is partially resistant to the disease SDS. Plant
 tissue (expanded leaves, folded leaves, and new shoots)
 were collected at 1, 6, 24, and 48 hrs. after inoculation
 and their mRNA pooled equally for cDNA construction. The
 library was prepared using the Stratagene pBluescript II
 SK(+) library construction kit. Complementary DNA was
 synthesized from mRNA using a primer consisting of a
 poly(dT) sequence with an XhoI restriction site. EcoRI
 adapters were ligated to the blunt-ended cDNA fragments
 followed by XhoI digestion. The cDNA insert is protected
 from XhoI digestion via methylation during first strand
 synthesis. The cDNA fragments were directionally cloned
 into the EcoRI-XhoI restriction site of the pBluescript
 vector. The ligated cDNA fragments were transformed into
 E. coli Electromax DH10B host cells. Plants were inoculated
 by Shuxian Li (Glen Hartman lab, University of Illinois).
 Library was constructed by Steve Clough (Illa Vodkin lab,
 University of Illinois)."

BASE COUNT 124 a 120 c 138 g 205 t 1 others
 ORIGIN

Query Match 31.4%; Score 276.4; DB 12; Length 588;
 Best Local Similarity 67.5%; Pred. No. 4.3e-56;
 Matches 396; Conservative 0; Mismatches 190; Indels 1; Gaps 1;

169 TTTTCTCTCTCTGCTGGCGCTCTTCCGACGACCTTCGTCGACGCTTT 228
 Db 2 TGTTCCTCAATTTGTTTATGATGTCATAGGCTGCTAGTGTGTGGCTCACTTGGTG 61
 229 CCGCTCATGTATGAGCTTCTCTGATTCAGAGCGGCTGATGAGCCAGCTCCGCGC 288
 Db 62 CTGCGCTTTTGTGGGCTTCTTGTGATGCAAGCACTTACGTTGGGTCATCTGGGC 121
 289 ATTACACGTGATGCTCAGCCGCGCTCAACGGCGCATTCGATTCTCTCGGCAACA 348
 Db 122 ACTATAGGTTATGTCTAGCCCTGCTACCAAAATTTGGCAAAATCTTTTGGCAATT 181
 349 TTCTCGCGGAATCAGATCGGCTGGTGAAGTGAACCAAGCCCAACCATTCGAT 408
 Db 182 GCATGATCGGATTAATCATTCATGATGAGAGTCACTCAAAATGCTCACACATCTCAT 241
 409 GCAACAGCCTCGACTATGACCTGATCTGCAGACATGCGGATCTTTGACGTTGCTCG 468
 Db 242 GCAATGATCTTGAATGATCTGATCTCAGACATACCTGCTTTGGCGGTGCAAC 301

QY 469 GGTTCCTCAATTCATTAACCTTCATTTNCTATGAGGAGAAATTGAGTTGATTNCATTG 528
 Db 302 GGTTCCTCAATTCATTAACCTTCATTTNCTATGAGGAGAAATTGAGTTGATTNCATT 361
 QY 529 CTATGTTCTTATGCTGCTACACGACTTACTTTTACCCGGTAAATGTTGTCAGAGG 588
 Db 362 CAAGTTTCTATCAGCTACGACACTTACATTTGACGATTTTGTCTTTGCAAGG 421
 QY 589 TCACTTGTATGCTGACAGCAATTTGCTATTTGTTTTCAGAGGAAAGTCAGATAGAG 648
 Db 422 TCAATTTGATCTCCAGACTTTGTTGCTGTTTCTTCTAGAGAAAGTCAGATAGAG 481
 QY 649 -CTTGAACATAATGGGAGATCTTGTGTTTGGACTGTTCCCTTTAGTACGCTGCT 707
 Db 482 CTTTACATTAATGGGAGATCTTGTGTTTGGACTGTTCCCTTTAGTACGCTGCT 541
 QY 708 GCCAATTTGGGCTGATAGGAGATGTTGACCTTGTGCTTGTGCT 754
 Db 542 TACCAATTTGGGAGAGATGATGTTGTTGCTTGTGCTGCACTTTGCT 588

RESULT 9
 CA935212 449 bp mRNA linear EST 30-DEC-2002
 LOCUS 8au50d04.v1 Gm-c1071 Glycine max cDNA clone SOYBEAN CLONE ID:
 DEFINITION Gm-c1071-4376.5, similar to TR:082348 082348 PUTATIVE CYTOCHROME
 B5.; mRNA sequence.
 ACCESSION CA935212 GI:27423692
 VERSION CA935212.1
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max

REFERENCE 1 (bases 1 to 449)
 AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna,
 A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,
 Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,
 R., Ritter,E., Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,
 R., Waterston,R. and Wilson,R.
 TITLE Public Soybean EST Project
 JOURNAL Unpublished
 COMMENT Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130
 South Memorial Parkway Huntville, AL 35801 For further information
 call: (800)-533-4363 or contact: cdu@resgen.com web site:
 www.resgen.com
 Seq primer: -40RP from Gibco.

FEATURES

source

1. 449
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="SOYBEAN CLONE ID: Gm-c1071-4376"
 /tissue_type="immature pods (~2cm long) of greenhouse
 grown plants"
 /lab_host="DH10B"
 /clone_lib="Gm-c1071"
 /note="Vector: pSPORII; Site 1: NotI; Site 2: SalI; The
 cDNA library was constructed from mRNA isolated from
 immature pods (approximately 2cm long) of greenhouse grown
 plants. The library was prepared using the Life
 Technologies superscript cDNA library construction kit."

ORGANISM

Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE
AUTHORS

1 (bases 1 to 503)
Vodkin, L., Shoemaker, R., Keim, P., Retzel, E., Khanna, A., Shealy, R.,
Clough, S., Thibaud-Nissen, F., Corryell, V., Erpelting, J., Rapp, C.,
Shoop, E., Stromvik, M., Schweitzer, P., Gong, G. and Liu, L.
A Functional Genomics Program for Soybean (NSF 9872565) (2002)
Unpublished
Other ESTs: B1788109 corresponding to Gm-cl065-4163 (5')
Contact: Vodkin, L.O., PI, A Functional Genomics Program for
Soybean (NSF 9872565)
Lewin, H. A., Director, Keck Center for Comparative and Functional
Genomics
University of Illinois
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-6147
Fax: (217) 333-4582
Email: l-vodkin@uiuc.edu

TITLE
JOURNAL
COMMENTFEATURES
source

Insert Length: 503 Std Error: 0.00
Plate: GM80016B20 Row: E Column: 01
Seq primer: 5'-TTTTTTTTTTTTTTTTT(A/C/G)-3'
High quality sequence stop: 503.
Location/Qualifiers
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/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="Gm-r1088-5978"
/clone_1ib="Gm-r1088"
/note="The library Gm-r1088 is a sequence-driven, rerecked
set of 9,216 low redundancy clones selected from cDNA
libraries from various tissues and stages of development
of soybean that consists of 2,706 cDNAs from germinating
cotyledons (source library Gm-cl027); 1,355 cDNAs from
immature seed coats (libraries Gm-cl019 and Gm-cl023); 917
cDNAs from tissue culture derived somatic embryos (source
libraries Gm-cl036 and Gm-cl075); 3,275 cDNAs from
germinating seedlings, shoot tips, or leaves exposed to
various stresses (source libraries Gm-cl064, Gm-cl065,
Gm-cl066, and Gm-cl067; and Gm-cl068); and 963 cDNAs from
young leaves exposed to bacterial and fungal pathogens
(source libraries Gm-cl072, Gm-cl073, and Gm-cl074). The
5' ESTs of the source clones from the different libraries
was used to select singletons, or a representative of each
contig, which were rerecked to form library Gm-r1088 and
the cDNA clones of the rerecked Gm-r1088 library were then
sequenced at the 3' end. The unigene selection and 3'
sequencing was funded by NSF Plant Genome project #9872565
(http://soybeanomics.cropsci.uiuc.edu/) as part of
creation of a low redundancy soybean cDNA set. The source
cDNA libraries were constructed by the laboratories of
Lila Vodkin, University of Illinois, Randy Shoemaker, Iowa
State University, and Paul Keim, Northern Arizona
University as part of the Public EST project,
http://129.186.26.94/soybeanest.htm. The contig analysis
to select unique genes was performed by the laboratory of
Ernest Retzel, Center for Computational Genomics and
Bioinformatics, University of Minnesota.
http://web.ahc.umn.edu/biodata/misoy/. Rerecking and 3'
sequencing were conducted by services of the University of
Illinois Keck Center for Comparative and Functional
Genomics http://www.biotech.uiuc.edu/keck.htm. Note: The
corresponding 5' EST from each clone in the Gm-r1088
library is listed in the 'OTHER EST' field. The detailed
information on the source library for each clone can also
be obtained by referring to the Genome Systems clone ID of
the original cDNA library that is also listed under 'OTHER
EST'."

BASE COUNT
ORIGIN

115 a 110 c 107 g 168 t 3 others

Query Match 29.2%; Score 256.8; DB 13; Length 503;
Best Local Similarity 72.0%; Pred. No. 2,2e-51;
Matches 352; Conservative 0; Mismatches 135; Indels 2; Gaps 2;

QY	306	AGCGCGCGCCCTCAACCGCCCAATTCAGATTCTCTCCGCAACATTCGCGGAATCAAGC	365
DB	10	AGCGCGCGCCCTCAACCAATTCGCAATTCCTTTGGCAATTCATGATCGGGATTAAGC	69
QY	366	ATCGGCTGTGGAAGGAGAACCAACCAACCGCCACCAATTCATGATGCAACGCTCGACTAT	425
DB	70	ATTGCAATGAGGAGAGGAGCTCAATGCTCAACATCTCATGCAATATGCTTGACTAT	129
QY	426	GACCCGTATCTGAGACAGACATGCGGCTTTGAGTTGCGGCGGCTTCAATTCATA	485
DB	130	GATCTGATCTCAGACATACCTGCTTGGCGTTCACACAGGTTCTTCAATTCATC	189
QY	486	ACCTCTCATTCATGAGGAGAAATTGATTCATTCATTCATTCATTCATTCATTC	545
DB	190	AAATCTGTTTCTATGAGAAAGAAATTTGTTGATTCATTCATTCATTCATTCATTC	249
QY	546	TACACGACCTTATCTTTTACCCGTAATGTGTGTTGCCAGGCTCACTGTATCTGACG	605
DB	250	TACACGACCTTATCTTTTACCCGTAATGTGTGTTGCCAGGCTCACTGTATCTGACG	309
QY	606	ACATCTGCTATGTTGTTTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	664
DB	310	ACTTGTCTGTTGTTGTTTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	369
QY	665	ATCTCTGTTTGTGAGACTTGTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	724
DB	370	ATCTCTGTTTGTGAGACTTGTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	429
QY	725	AGGGGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	784
DB	430	AGGGGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	488
QY	785	GTTGAATCA	793
DB	489	TTTGAATCA	497

RESULT 12
BG647198 783 bp mRNA linear EST 24-APR-2001
DEFINITION
EST508817 HOGA Medicago truncatula cDNA clone PHOGA-15P24 5' end,
mRNA sequence.

ACCESSION
BG647198 GI:13782310
VERSION
BG647198.1 GI:13782310
KEYWORDS
EST.
SOURCE
Medicago truncatula (barrel medic)
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosoids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.

1 (bases 1 to 783)
Hahn, M.G., Ojane-Reuhs, T., Samac, D., Town, C.D., Van Aken, S.,
Uteback, T., Cho, J. and Fraser, C.M.
ESTs from roots of Medicago truncatula treated with
oligoalacuronicides of DP 6-20
Unpublished
Contact: Michael G. Hahn
Complex Carbohydrate Research Center
University of Georgia
220 Riverbend Road, Athens, GA 30602-4712, USA
Tel: 706-542-4457
Fax: 706-542-4412
Email: hahn@ccrc.uga.edu
G3908046 TIGR sequence name: MTMBV967K More information is
available at: www.medicago.org
Seq primer: Skmod (CTA GAA CTA gtc gat CC).
Location/Qualifiers

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

```

source
1. .783
/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="A17"
/db_xref="taxon:3880"
/clone="pHOGA-15P24"
/tissue_type="3 day old seedling roots"
/dev_stage="24 hours after treatment in the dark at 26 C
with 0.5 mg/ml oligogalacturonide (DP 6-20) in the
presence of 100 ug/ml Gentamicin"
/lab_host="X10LR"
/clone_lib="HOGA"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in SOLR cells."

BASE COUNT      173 a      142 c      169 g      299 t
ORIGIN
Query Match      29.0%; Score 254.8; DB 10; Length 783;
Best Local Similarity 65.2%; Pred. No. 7.8e-51;
Matches 441; Conservative 0; Mismatches 226; Indels 9; Gaps 5;

207 AGCACTTGTGACGCGCTTCCCGCATGATGAGCTTCTCTCGGATTCAAGCGGC 266
|||
21 AGGTTGGGCTATTAAGTTCTGATGTTGTTGGTTGCTATGAGATCAAGAACT 80
|||
267 TGGATAGGCGACACTCCGCGCATTAACAGTATGCTCAGCCGCGCTCAACCGGCA 326
|||
81 TATATTGCTATGATTTCTGCTATGAGATTATGCGATGGAATTATTAACAATTA 140
|||
327 ATTCAATTTCTCCGGAACATTTCTCCGGAATGAGATCGGCTGGTGAAGTGAC 386
|||
141 GCACAAATTTCTTGTGGTAATGATGATGATGATGATGATGATGATGATGATG 200
|||
387 CACAAGGCCACACATGATGATGATGATGATGATGATGATGATGATGATGATG 446
|||
201 CATTAAGCTCATATGATGCTTCAATGATGATGATGATGATGATGATGATGATG 260
|||
447 CCGGCTTTGCACTTTCGCGCGCTTCTCAATTCATTAATCTCTCAATTCATTA 506
|||
261 CCGTTCGCTCTGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 320
|||
507 AAGTNGAGTTGATTCATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 566
|||
321 CAGTTAAAGTTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 380
|||
567 CCGGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 626
|||
381 CCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 440
|||
627 ---AGGNGAAGAGTGCAGATAGAGCTT-GAACATAATGGGATTCCTGTTGGACT 682
|||
441 CCATCAAGAAATGCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 500
|||
683 TGGTCTCTCTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 742
|||
501 TGGTCTCTCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
|||
743 GCTAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 802
|||
561 GCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 619
|||
803 AAATTTATATGNGGGG--ACNANTGGAGTGACTGGTANATGACAGAG--GGGTC 858
|||
620 AAGCGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 679
|||
859 ATTGATATCTCTTGT 874
|||
680 ATTGATATCACTTGT 695
|||

```

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RESULT 13
BG882077
LOCUS
DEFINITION
  BG882077 494 bp mRNA linear EST 29-NOV-2001
  sae95g06.y1 Gm-cl065 Glycine max cDNA clone GENOME SYSTEMS CLONE
  ID: Gm-cl065-3779 5' similar to TR:082348 082348 PUTATIVE
  CYTOCHROME B5. ; mRNA sequence.
ACCESSION
  BG882077
VERSION
  BG882077.1 GI:114259169
KEYWORDS
  SOURCE
  ORGANISM
    Glycine max (soybean)
    Glycine max
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
    ; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
    Glycine.
  1 (bases 1 to 494)
REFERENCE
  Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
  ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
  Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
  ,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schuck
  ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
  ,R., Waterston,R. and Wilson,R.
  Public Soybean EST Project
  Unpublished
  Contact: Shoemaker R/Public Soybean EST Project
  Public Soybean EST Project
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@waterston.wustl.edu
  This clone is available through: Resgen, Invitrogen Corp. 2130
  South Memorial Parkway Huntville, AL 35891 For further information
  call: (800)-533-4363 or contact via email: ccu@resgen.com
  Insert Length: 1782 Std Error: 0.00
  High quality sequence stop: 415.
  Location/Qualifiers
    1..494
      /organism="Glycine max"
      /mol_type="mRNA"
      /db_xref="taxon:3847"
      /clone="GENOME SYSTEMS CLONE ID: Gm-cl065-3779"
      /tissue_type="germinating shoots"
      /clone_lib="DH10B"
      /lab_host="DH10B"
      /notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
      XhoI; The cDNA library was constructed from mRNA isolated
      germinating shoots of the cultivar Williams. The seeds
      were allowed to germinate for 24 hours prior to being
      cold stressed for 2 days at 4C. Complementary DNA was
      synthesized from mRNA using a primer consisting of a
      poly(dT) sequence with a XhoI restriction site. EcoRI
      adapters were ligated to the blunt-ended cDNA fragments
      followed by XhoI digestion. The cDNA fragments were
      directionally cloned into the EcoRI-XhoI restriction site
      of the pBluescript vector. The ligated cDNA fragments were
      transformed into DH10B host cells (GibcoBRL). This library
      was constructed in the laboratory of Dr. Randy
      Shoemaker."

BASE COUNT      113 a      106 c      105 g      170 t
ORIGIN
Query Match      28.9%; Score 254.2; DB 12; Length 494;
Best Local Similarity 70.6%; Pred. No. 9.2e-51;
Matches 345; Conservative 0; Mismatches 143; Indels 1; Gaps 1;

306 AGCCGCGCTCAACCGCGCATTCGATTCCTCCGGAACATTCCTCCGGAATCAGC 365
|||
3 AGCCCTGGCTACCAAAATGGCAAAATCTTGTGGCAATTCGATGATGAGGATGAGC 62
|||
366 ATGGGCTGGTGAAGTGAACCAACAGCCCAACCATTCGATGCAACAGCTCGACTAT 425
|||

```

Db 63 ATTGCATGGTGAAGGAGTCACTCAGATGCTCACCATCTCATGCAATAGTCTTGACTAT 122
 Qy 426 GACCCGATCTGAGACATGCGGCTTTGGAGTTTGGCGGGTTCTTCAATTCATA 485
 Db 123 GATTCGATCTCAGACATACCTGCTTGGCCGTGACACAGGTTCTTCAATTCATC 182
 Qy 486 ACCTTCATTCATGAGGAGAAATTGATTTGATTCATTCATTCATTCATTCATTC 545
 Db 183 AATCTGTTTCTATGAAAGAAATGCTGTTGATTCATTCATTCATTCATTCATTC 242
 Qy 546 TACACAGACTTACATTTTACCCGTAATGCTGTCAGAGGTCATTCATTCATTCAG 605
 Db 243 TACACAGACTTACATTCATTCACAGTTTGTGCTTGGCAAGGTCATTCATTCATTCAG 302
 Qy 606 ACAATCTGCTATGTTTTCGAGAGNAAAAGTCAGAGATGAG-CTTGAACATATAGGG 664
 Db 303 ACTTGTGCTGCTGTTCTCAGAGAAAGTCCAGATAGACCTTTAACAATATAGGG 362
 Qy 665 ATCTGTTGTTTGAAGTGTCTCTTCTTGTAGTGTGCTGCTGCTGCTGCTGCTGCTG 724
 Db 363 ATCTGTTGTTTGGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 422
 Qy 725 AAGGAGATGTTGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 784
 Db 423 AAGGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 482
 Qy 785 GTTGATCA 793
 Db 483 TTGAAACA 491

RESULT 14
 CB829088 585 bp mRNA linear EST 16-MAY-2003
 LOCUS LjNEST93h9r Lotus japonicus module library 5 and 7 week-old Lotus
 DEFINITION japonicus cDNA 5', mRNA sequence.
 ACCESSION CB829088
 VERSION CB829088.1 GI:29969635
 KEYWORDS EST.
 SOURCE Lotus japonicus
 ORGANISM Lotus japonicus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotceae; Lotus.
 1 (bases 1 to 585)
 Colbatch,G., Freund,S., Trevaekis,B and Urdvardi,M.
 Lotus japonicus root module ESTs: tools for functional genomics
 Unpublished
 Contact: Urdvardi MK
 Molecular Plant Nutrition
 Max Planck Institute of Molecular Plant Physiology
 Am Muehlenberg 1, 14476 Golm, Germany
 Fax: 49 331 567 8250
 Email: urdvardi@pimp-golm.mpg.de
 Seq primer: T7
 High quality sequence stop: 585.
 Location/Qualifiers
 1..585
 /organism="Lotus japonicus"
 /mol_type="mRNA"
 /catalytic="Gifu (B-129)"
 /db_xref="taxon:34305"
 /dev_stage="5 and 7 week-old plants"
 /clone_lib="Lotus japonicus module library 5 and 7
 week-old"
 /note="Organ: Nodule; Vector: pSPORT1; Site: 1; SalI;
 Site: 2; NotI; The library was prepared using mRNA
 extracted from nodules of 5 and 7 week-old Lotus plants.
 Nodules were induced by, and contained Mesorhizobium
 strain R7A."

BASE COUNT
 ORIGIN

122 a 124 c 141 g 198 t

Query Match 28.6%; Score 251.8; DB 14; Length 585;
 Best Local Similarity 64.3%; Pred. No. 3,7e-50;
 Matches 373; Conservative 0; Mismatches 207; Indels 0; Gaps 0;

Qy 75 GACTACCGCAAGCTTCTCCGACCTCCGCGCTCAACCTTTCAACCGCAAGGCCAC 134
 Db 5 GATTACAGGAACCTGTGACGAGTTTGCAAAATTGGGGCTTTTGAAGAAAGAGCAT 64
 Qy 135 ACAACCTGCATCT 194
 Db 65 GTACCTTATACACCTCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 124
 Qy 195 CTTCTTCGACAGCACTTGTGACAGGCTTTCGCGTCAATGATAGCTTCTCTCTCT 254
 Db 125 CTCAGATGCAAGAGCTGTGGCTATTTGGCTCTGCATGTTCTGGGTTTCTTTGG 184
 Qy 255 ATTCAAGCGGCTGTATAGGCCACGACTCCGCGCTTCAACGATGCTCAGCCGCGC 314
 Db 185 ATGACAGACACTTATGTGGTCTATGTTCTGCTACTATGAGGTTATGTCAGTCCGG 244
 Qy 315 CTCACCGCGCAATTCATGCTCTCCGCAATTTCCGCGCAATTCGCGGAATCAGCT 374
 Db 245 TACAAACAATTAGCCCAAGTTTGTGTGGAATTGTATGACTGGGATAGCAATTCG 304
 Qy 375 TGGAGTGGAAACCAACGCGCCACCAATGTCATGCAACAGCTGACTATGACCTGAT 434
 Db 305 TGGAAATGAGACTCACAAATGCTCATCATCTGCTTAAAGTCTTGAATATATCTGAT 364
 Qy 435 CTGACAGCATGCGCGCTCTTTCGATTCGTCGCGTTCTTCAATTCATTAACCTTCAT 494
 Db 365 CTGACAGCATATCCGTTTGTGCTGATCTTCTGTTCTTCAATTCATTAACCTTCAT 424
 Qy 495 TNCATGAGGAGAAATTGAGTTGATTCATTCATTCATTCATTCATTCATTCATTCAT 554
 Db 425 TTCTATGGAGGAGAGCTCAAGTTGATCTTGTCAAGGTTCTGATCAGTTACAGCAG 484
 Qy 555 TTTACTTTTACCCGCTATGCTGTCGAGGCTCACTGATCTGATCTGATCTGATCTG 614
 Db 485 TGGACATTTTACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 544
 Qy 615 CTATGTTTTCGAGGAGAAAGTGCAGATAGAGCTTGA 654
 Db 545 CTCTGTTTTCAGGCGCTTAAAGTCCAGATAGAGCTTTAA 584

RESULT 15
 BF003445 673 bp mRNA linear EST 06-OCT-2000
 LOCUS EST431943 KVI Medicago truncatula cDNA clone pKVI-5L4, mRNA
 DEFINITION
 ACCESSION BF003445
 VERSION BF003445
 KEYWORDS EST.
 SOURCE Medicago truncatula (barrel medic)
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 1 (bases 1 to 673)

REFERENCE 1 Vandenoesch,K., Endre,G., Hur,J., Moore,J., Beremand,P., Ellis,L.,
 Town,C.D., Bowman,C.L., Craeven,M.B., Hansen,T.S., Holt,I.E. and
 Frazer,C.M.
 ESTs from roots of Medicago truncatula 24 hours after inoculation
 with Sinorhizobium meliloti
 Unpublished
 Contact: Vandenoesch K
 Department of Plant Biology
 University of Minnesota
 220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
 Tel: 612 624 2755
 Fax: 612 625 1738

TITLE
 JOURNAL
 COMMENT

Query Match	31.2%;	Score 274.2;	DB 4;	Length 1702
Best Local Similarity	59.6%;	Pred. No. 4e-61;		

Matches 484; Conservative 0; Mismatches 326; Indels 2; Gaps 2;

18 CCGGCTTCACACCTCCCAACCGCTTTCGACACACCGCTTCGCGGCTTCCTCCGAC 77
 267 CCGCTCTTACCGGCTACTACTACTCAAGACTTCAGAGATTCGAGATTCGAGAC 326
 78 TACCGGAGCTCTTCCGACCTTCCGCGCTCAACCTTCAACCGGAGGACACACA 137
 327 TACCGGAGCTTTCGAGAGATTCGCGGCTTCGAGAGAGAGGACACAC 366
 138 ACCTCATCTCTCTCTTATTCACCTTTTCTCTCTCTCTCTCTCTCTCTCTCT 197
 387 ATCATGTGACGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 446
 198 TTCTCCGACGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 257
 447 GCGTCCGAGTCCGCTCGAGTTCACATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 506
 258 CAGAGCGCTGATAGGACGACGCTCGGCTTCAACGATGCTCAGCGCGCTC 317
 507 CAGCGCGCTATGTGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 566
 318 AACCGGCAATTCAGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 377
 567 AACGAGATTCAGGAACTCATAGCAGGCAACATCTCTAATCGGAAATCAGCATCG 626
 378 AAGTGAACCAACCGGCAACATTCATGACGACGCTCTGACGCTTGAACCTGATCT 437
 627 AAGTGAACCAACCGGCAACGCTCTGACGACGCTCTGACGACGCTCTGACGCTCT 666
 438 CAGCAGTCCGCT 497
 687 CAGCAGTCCGCT 746
 498 TATGGAGAGATTCGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 557
 747 TATGGAGAGATTCGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 806
 558 ACTTTTACCGGCTTATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 617
 807 ACTTACTACCGGCTTATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 866
 618 TTGTTTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 676
 867 CTCTCACCAGGCGGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 926
 677 TGAAGTGTCT 736
 927 TGAAGTGTCT 986
 737 GAGCTGTCT 796
 987 GTCTCATCAGCTTCT 1045
 797 TGCTGAATTTATTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 828
 1046 CTCGCGGAGACATACGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAG 1077

RESULT 2
 US-08-831-570-1
 ; Sequence 1, Application US/08831570
 ; Patent No. 5959175
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; APPLICANT: Numborg, Andrew N.
 ; APPLICANT: Beremand, Phillip D.
 ; TITLE OF INVENTION: A SUNFLOWER ALBUMIN 5' REGULATORY REGION
 ; TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: USA
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/831,570
 FILING DATE: 09-APR-1997
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Digilio, Frank S.
 REGISTRATION NUMBER: 31,346
 REFERENCE/DOCKET NUMBER: 10545
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 743-4366
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1684 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 43..1387
 US-08-831-570-1

Query Match 27.9%; Score 245.2; DB 2; Length 1684;
 Best Local Similarity 57.7%; Pred. No. 1.1e-53;
 Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

24 TTCTCCACCTCCGACCGCTCTTTCGACGACGCTCTCGGCGGCTCTCCGCTACCGC 83
 265 TTTTTCACGCGGATTAATCTTAAGATTAATCTCTCTCTCTCTCTCTCTCTCTAAGATTATAG 324
 84 AAGCTCTCTCCGACCTCTCCGCTCAACCTTTCACCGGAGGAGGAGGAGGAGGAGGAGG 143
 325 AAGCTGTGTGATTAATCTTAAGATTAATCTCTCTCTCTCTCTCTCTCTCTAAGATTATAG 384
 144 ATCT 203
 385 GCAACTTGTGCTTATAGCAATGCTGTTGCTATGATGATGATGATGATGATGATGATG 444
 204 GAGAGCACTTGTGAGCGGCTTTCGCGCTGATGATGATGATGATGATGATGATGATGATG 263
 445 GAGGAGTGTGATTAATCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAGGCTTCTGAG 504
 264 GCGTGTATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 323
 505 GGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 564
 324 GCAATTCAGATTCCTCTCGGCAACATTCGCGGGAATAGCATCGGCTGTGGAAGTGG 383
 565 TTATGTGATTTTCTCTCAAAATGCTCTTTCAGGATTAAGATTTGTTGGAATGG 624
 384 AACCAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 443
 625 AACCATATGACATACATGCTCTTAATAGCTTGAATATGACCTCTTAATATACAAATAT 664
 444 ATGCGGCTCTTTCGATTCGCGGCTTCTCAATTCATTAACCTCTCATTTCTATGAGG 503
 685 ATACATTCCTTGTGTGCTTCTCAAGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 744
 504 AGGAGTGTGATGATTCATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 563
 745 AAAAGTTGACTTTGACTTTATCATGATTTCTTGTGAATGATTCATGATTCATGATTCATG 804


```

QY 564 TACCCGTAATGTGTGTGCGAGGTCAATTGTATCTGACAGCAATTCGTATTTT 623
DB 805 TACCTATTATGTGTCTGTAGCTCAATGTATGTATCAATCTCATATGTTGTTG 864
QY 624 TCAGAGGAAAGTGCAGATAGACT-TGAACATATGGGGATCCTTGTGTTGGACT 882
DB 865 ACCAAGAAATGTCTATCAAGCTCAGGAATCTTGGGATGCTTAGTGTCTGATTT 924
QY 683 TGGTTCCTTTAGTGTGTGCTGCTCAATTTGGGCTGATAGGGGAAATGTTGACTT 742
DB 925 TGGTACCGGTGCTTGTCTTCTTGTGCTAATTTGGGGTGAAGAAATATGTTGTTAT 984
QY 743 GCTAGCTTTGCTGTTGTGNCNATCCAGACATTCAGTTCTGTGTAATCAGCTTCTGA 802
DB 985 GCAAGTTATCACTGACTG-GAATGCAACAAGTTCACTTCTCTTGAACCACTTCTTTC 1043
QY 803 AAATTTATGNCGGCA--CNANTGGAAATGACTGANT--GANAATCAGACAGGGGTC 858
DB 1044 AAGTGTATATGTTGGAAGGCTTAAGGGAATATGTTGAGAAACAACGATGGGAC 1103
QY 859 ATTGATATCTCTTGNCCT 880
DB 1104 ACTGACATTTCTGTCTCT 1125

```

RESULT 3

```

US-08-831-575-1
; Sequence 1, Application US/08831575
; Patent No. 5977436
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Li, Zhongsen
; TITLE OF INVENTION: AN OLEOSIN 5'REGULATORY REGION FOR THE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,575
; FILING DATE: 09-Apr-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Digilio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1387
; US-08-831-575-1

```

```

Query Match 27.9%; Score 245.2; DB 2; Length 1684;
Best Local Similarity 57.7%; Pred. No. 1,le-53;
Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

```

```

QY 24 TTTCACCTCCACCGTCTTCCGACCAACCGTCTCCGCCCTCTCCGACTACCG 83
DB 265 TTTTTCACCTGGGTATATCTTAAAGTTACTCTGTTCTTGAGGTTTCTAAAGTTATAG 324
QY 84 AAGCTTCTCCGACCTCTCCGCGTCAACCTTTCAACCGGAGGGCACAACCTCC 143
DB 325 AAGCTTGTTGAGTTTCTAAATAGGTTGTATGACAAAAGATCATATATGTTT 384
QY 144 ATCTCTCTCTCCCTTATTTCTACCTTTTCTCTCTCTCTGCTGGGCGCTCTTCTCC 203
DB 385 GCACCTTGTGTTTATAGCAATGCTGTTTGTATAGAGTTATAGGGGTTTGTGTTTGT 444
QY 204 GACAGACCTTGTGAGAGTGTCTTCCGCTGCAATGATAGGCTTCTCTGATTCAGAGC 263
DB 445 GAGGGTGTGTTGATCATTTGTTTCTGGGTTGTATAGGGGTTCTTGTGATTCAGAT 504
QY 264 GCGTGAATAGCCACGACTCCGCGCATTAACAAGTATGCTCAGCGCGCTCAACCGC 323
DB 505 GGTGGAATGACATGATGCTGGGCAATTAATGTAAGTCTGATCAAGGCTTAATAG 564
QY 324 GCAATTCAGATCTCTCCGCAACATTTCCGCGGATGACATGGCTGTGGAAGTGG 383
DB 565 TTTATGGGTATTTTGTGCAAAATGCTTTTCAAGAAATAGTATGTTGGTGGAAATGG 624
QY 384 AACCAACAGCCACACATTCGATGCAACAGCTCGATATGACCTGATCGACGAC 443
DB 625 AACCAATATGACATCAATTCCTGTATATGACCTTGAATATGACCTGATTAACATAT 684
QY 444 ATGCGGCTTTTTCAGATTTGCTGCGGTTCTTCAATTCATTAACCTCTCATTTCTATGG 503
DB 685 ATACATTCCTTGTGTGTCTTCAAGTTTGTGTTGCTACCTCATATTTCTATAG 744
QY 504 AGAAGTTNAGTTGATTCATTCGTATGTTCTGATCTGCTACCGACACTTACTTTT 563
DB 745 AAAAGTTGACTTTGACTTTATCAAGATTTCTTGTATGATTCACATTTGACATTT 804
QY 564 TACCCGTAATGTGTGTCGAGGTCACCTGTATATCGACACAAATTCGATTTGTT 623
DB 805 TACCTATTATGTGTGTGCTAGGCTCAATATATGTAACAATCTCAATATGTTGTTG 864
QY 624 TCAGAGGAAAGTGCAGATAGACT-TGAACATATAGGGGATCCTTGTGTTGACT 682
DB 865 ACCAAGAAATGTGTCTATGAGCTCAGAACTTGGATGCTTATGTTCTGATTT 924
QY 683 TGGTCTCTTTTAACTGCTTCCCAATTTGGGCTGATAGGGGAAATGTTGACTT 742
DB 925 TGGTACCGGTGCTTGTCTTCTTGTGCTTAATTTGGGGTGAAGAAATATGTTGTTAT 984
QY 743 GCTAGCTTTGCTGTTGTGNCNATCCAGACATTCAGTTCTGTGTAATCAGCTTCTGA 802
DB 985 GCAAGTTATCACTGACTG-GAATGCAACAAGTTCACTTCTTGAACCACTTCTTTC 1043
QY 803 AAATTTATGNCGGCA--CNANTGGAAATGACTGANT--GANAATCAGACAGGGGTC 858
DB 1044 AAGTGTATATGTTGGAAGGCTTAAGGGAATATGTTGAGAAACAACGATGGGAC 1103
QY 859 ATTGATATCTCTTGNCCT 880
DB 1104 ACTGACATTTCTGTCTCT 1125

```

RESULT 4

```

US-08-366-779-4
; Sequence 4, Application US/08366779
; Patent No. 5614393
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Reddy, Avutu S.
; APPLICANT: Nucio, Michael
; APPLICANT: Freysinet, Georges L.
; APPLICANT: Nunberg, Andrew N.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A

```

TITLE OF INVENTION: DELTA 6-DESATURASE
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/366,779
 FILING DATE: 30-DEC-1994
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Presser, Leopold
 REGISTRATION NUMBER: 19,827
 REFERENCE/DOCKET NUMBER: 8383ZYXX
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1685 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-366-779-4

Query Match 27.9%; Score 245.2; DB 1; Length 1685;
 Best Local Similarity 57.7%; Pred. No. 1.1e-53;
 Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

24 TTCTCCACCTCCACCGCTTTTCGACACACCGCTCTCCGCGCTCTCCGACTACCGC 83
 Db 266 TTTTTCACCTGGGATTAATTAAGATTACTGTGTTCTGAGGTTTAAAGATTATAG 325
 Qy 84 AAGCTCTTCGCGACTCTCGCGCTCAACCTCTTCAACCGCAAGGCGACACAACTCC 143
 Db 326 AAGCTTGTGTTGATTTTCAAAATGGGTTGTATGACAAAAAGGTCATATATGTTT 385
 Qy 144 ATCTCTCTCCCTTATCTCACCCCTTTTCCTCTCTCTGCTGCGCGCTCTCTCTCC 203
 Db 386 GCACTTTGTCTTATAGCAATGCTGTTGCTATGATGTTTATGCGGTTTGTGTTGT 445
 Qy 204 GACAGCACTTTCGCGACGTCGCTTCGCTGCAATGATAGGCTTCTCTGATTCAGAGC 263
 Db 446 GAGGCTGTTTGGTACATTTGTTTCTGGGTGTTGATGGGCTTTCTTGGATTCAAGT 505
 Qy 264 GGCTGATAGGCGCAGCTCGCGCATTAACAAGTGAATGCTGACCGCGCGCTCAACGC 323
 Db 506 GGTGGATTGACATGATGCTGGGCATTATAGTAGTGTGATTTCAAGGCTTAATAG 565
 Qy 324 GCAATTCAGATTCTCTCGCGCAATTCGCGCGGAATCAGCATCGCTGGTGAAGTGG 383
 Db 566 TTTATGGGTAATTTTGTGCGAAATGTCTTACAGAAATAGATATGTTGGTGAATGG 625
 Qy 384 AACCAACGCGCCACCATTCATGACAGAGCTCGATGATGACCTGATTCGACAGC 443
 Db 626 AACCATATGACATCATTCATTCCTGTAAATAGCCTTGAATTAATGACCTGATTAAT 685
 Qy 444 ATGCGGCTTTGAGTTGTGCGGCTTCTCAATTCATTAACCTCTCAATTGATGG 503
 Db 686 ATACCATTCCTGTTGTGCTTCCAAAGTTTGTGCTACCTCCTCAATTTCTATAG 745
 Qy 504 AGGAAGTTNAGTTGATTCAATGCTATGTTCTTGAATGCTGCTACGACACTTACTTT 563

Db 746 AAAAGTTGACTTTTGACTCTTTATCAAGATTCTTTGATGATATCAACATTGGACATTT 805
 Qy 564 TACCGGTAATGTTGTTGCGAGGTCACCTGATCTGACAGCAATTCGATTTGTTT 623
 Db 806 TACCTATATATGTTGCTGTAAGCTCAATATATATGATCAATCTTCAATATGTTGTTG 865
 Qy 624 TCGAGNGAAAAGTCAGATAGAGCT-TGAACATATAGGGGATCCTTGTGTTTGGACT 682
 Db 866 ACCAAGAAAAGTGTCTATGAGCTCAGAGACTCTTGGATGCTAGGTTCTGATTT 925
 Qy 683 TGGTTCCTCTTTAGTGNCTTGCTTCGCAATTTGGCCCTGATAGGGGATGTTTNGCTT 742
 Db 926 TGGTACCGCTTGTGTTCTTGTGTTGCTTAATTTGGGGTGAAGATTAATGTTTATTT 985
 Qy 743 GCTAGCTTTGCTGTTTGNCAATCCAGACATTCAGTTCTGTTGATATCACTTCTGA 802
 Db 986 GCAAGTTATCAATGACTG-GAATGCAACAAGTTCAATCTTCAACCACTTCTCTTC 1044
 Qy 803 AAATTATATGNCGGCA--CNAMTGGAAATGACTGANT--GAMAAATCAGACAAGGGGTC 858
 Db 1045 AAGTTTATGTTGGAAGGCTTAAGGGAATATGTTTGAAGAAACAACGATGGAG 1104
 Qy 859 ATTGATATCTCTTGACCCCT 880
 Db 1105 ACTTGACATTTCTTGTCTCTCT 1126

RESULT 5
 US-08-789-936-4
 Sequence 4, Application US/08789936
 Patent No. 5789220
 GENERAL INFORMATION:
 APPLICANT: Thomas, Terry L.
 APPLICANT: Nuccio, Avutu S.
 APPLICANT: Freysinet, Georges L.
 APPLICANT: Nuberg, Andrew N.
 TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 TITLE OF INVENTION: DELTA 6-DESATURASE
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/789,936
 FILING DATE: 28-JAN-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/366,779
 FILING DATE: 30-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Presser, Leopold
 REGISTRATION NUMBER: 19,827
 REFERENCE/DOCKET NUMBER: 8383ZYXX
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1685 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-789-936-4

Query Match 27.9%; Score 245.2; DB 1; Length 1685;
Best Local Similarity 57.7%; Pred. No. 1.1e-53;
Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

24 TTCTCCACCTCCACCGCTCTTCCGACCAACACCGCTCCGCGCTCTCCGACTACCGC 83
266 TTTTTCACCTGGGATTAATCTTAAGATTAATCTCTGAGTTTCTTAAGTTATAG 325
84 AACCTCTCTCCGACCTCTCCGCTCAACCTCTTCAACCGCAAGGCCACACACCTCC 143
326 AAGCTTGTTGATGATTTCTTAATAAGGTTGTATAGCAAAAAGATGATATATAGTT 385
144 ATCCCTCTCTCTTATCTACACCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 203
386 GCAACTTGTGCTTATAGCAATGCTGTTGCTATAGATGTTATGAGGTTTGTGTTGT 445
204 GACAGCACTTGTGACGCTTCTCCGCTGATGATAGGCTTCTCTGATTCAGAG 263
446 GAGGCTTTTGTATCAATTTGTTTCTGAGTGTGTTGAGGCTTCTTGGATTCAGAT 505
264 GGGTGTATAGGCGACACTCCGCGCATTAACAGTATGCTCAAGCCGCTCAACCCG 323
506 GGTGATGATGACATGATGCTGGCATTAATGATGATGATGATGATGATGATGATG 565
324 GCAATTCAGATTTCTCTCCGCAATCTCTGCGGATCAAGCATCGGCTGTGGAAGTG 383
566 TTATGCGTATTTTCTCTGCAATTTCTTTCAGGATTAAGTATGTTGTGGAATG 625
384 AACCAAGCGCCACCAATGATGATGATGATGATGATGATGATGATGATGATGATG 443
626 AACCAATATGACATCAATGCTGCTTAATGATGATGATGATGATGATGATGATGAT 685
444 ATGCGGCTCTTTCAGATTTCTGCGGCTTCTTCAATTCATCACTCTGATTTCTGAG 503
686 ATACATTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 745
504 AGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 563
746 AAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 805
564 TACCGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 623
806 TACCTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 865
624 TCGAGGCAAAAGTGCAGATAGAGCT-TGAACATATGAGGATCCTTGTGTTTGGACT 682
866 ACCAAGAAATGTGCTATGAGCTCAAGACTCTTGGAGTCTGATGTTCTGATTT 925
683 TGGTCTCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 742
926 TGGTATCCCTGCTTGTCTTCTTGTGCTTAATGAGGATGAAGATTAATGTTTAT 985
743 GCTAGCTTGTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 802
986 GCAAGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1044
803 AAATTTATATGAGGCA--CNANTGGGAATGACTGANT--GANANTTCAGACAAGGGT 858
1045 AAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1104
859 ATGATATCTCTTGTGATGCT 880
1105 ACTTGACATTTCTGCTCTCT 1126

RESULT 6
US-08-934-254-4
Sequence 4, Application US/08934254
Patent No. 6355861
GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934.254
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXWV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1685 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-934-254-4

Query Match 27.9%; Score 245.2; DB 4; Length 1685;
Best Local Similarity 57.7%; Pred. No. 1.1e-53;
Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

24 TTCTCCACCTCCACCGCTCTTCCGACCAACACCGCTCCGCGCTCTCCGACTACCGC 83
266 TTTTTCACCTGGGATTAATCTTAAGATTAATCTCTGAGTTTCTTAAGTTATAG 325
84 AACCTCTCTCCGACCTCTCCGCTCAACCTCTTCAACCGCAAGGCCACACACCTCC 143
326 AAGCTTGTTGATGATTTCTTAATAAGGTTGTATGACAAAAGATGATATATAGTT 385
144 ATCCCTCTCTCTTATCTACACCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 203
386 GCAACTTGTGCTTATAGCAATGCTGTTGCTATAGATGTTATAGGCTTGTGTTGT 445
204 GACAGCACTTGTGACGCTTCTCCGCTGATGATAGGCTTCTCTGATTCAGAG 263
446 GAGGCTTTTGTATCAATTTGTTTCTGAGTGTGTTGAGGCTTCTTGGATTCAGAT 505
264 GGGTGTATAGGCGACACTCCGCGCATTAACAGTATGCTCAAGCCGCTCAACCCG 323
506 GGTGATGATGACATGATGCTGGCATTAATGATGATGATGATGATGATGATGATG 565
324 GCAATTCAGATTTCTCTCCGCAATCTCTGCGGATCAAGCATGCGCTGTGGAAGTG 383
566 TTATGCGTATTTTCTCTGCAATTTCTTTCAGGATTAAGTATGTTGTGGAATG 625
384 AACCAAGCGCCACCAATGATGATGATGATGATGATGATGATGATGATGATGATG 443
626 AACCAATATGACATCAATGCTGCTTAATGATGATGATGATGATGATGATGATGAT 685
444 ATGCGGCTCTTTCAGATTTCTGCGGCTTCTTCAATTCATCACTCTGATTTCTGAG 503
686 ATACATTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 745

QY	AGGAAGTNGAGTTGATTNCAATCTNAGTCTTGATCTGGTACAGACATTACTTTT	563
Db	AAAGGTGACTTTTGACTCTTTATCAAGATTCTTTGAAGTTATCAACATTGGACATTT	805
QY	TACCGGTAATGTGTGTGCCAGGGTCAACTGTATCTGCAGACAATTCGTATGTGTT	623
Db	TACCTATTATGTGTGTCTAGAGCTCAATATGATATCAATCTCTCATATATGTGTTG	865
QY	TCGAGAGNAAAAGTGCAGATAGACT-TGAACATTAATGGGGATCTCTGTGTTTGA	682
Db	ACCAAGAAATGTGTCTTATCGAAGCTCAGGAACCTTGGAGTGGCTGTGTGTCGATT	925
QY	TGGTTCCCTCTTTTAGTGNCTGCCCAATTTGGGCGCTGAATAGGGNATGTTNGCCT	742
Db	TGGTACCCTGTGCTTTGTTTCTTTGTTCCTAATTTGGGGTGAAGAATTAATGTTTAA	985
QY	GCTAGCTTGTGCTTTGTGNCNATCCAGACACTTCAGTTCTGGTGAATCACTTGCTGA	802
Db	GCAAGTTTATCAGTACTG-GAATGCACAAAGTTCAAGTTCTCTGAAACACTTCTCTTC	104
QY	AAATTATATGNCGGGCA--CNANTGGGAATGACTGAGT--GANAATGACAAAGGGTTC	858
Db	AAGTGTATTATGTGGAAAGCCTAAGGGAAATTAATGTTTGAGAAACAACGATGGGAC	1104
QY	ATTGGATATCTCTGTGNCCTT	880
Db	ACTTGACATTTCTGTCTCTCTT	1126

RESULT 7
 US-08-232-463-14
 Sequence 14, Application US/08232463
 Patent No. 5670367
 GENERAL INFORMATION:
 APPLICANT: DORNER, F.
 APPLICANT: SCHEIFLINGER, F.
 APPLICANT: FALKNER, F. G.
 TITLE OF INVENTION: RECOMBINANT FOAMPOX VIRUS
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 1800 Diagonal Road, Suite 500
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22313-0299
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.255
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,463
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/935,313
 FILING DATE:
 APPLICATION NUMBER: EP 91 114 300.6
 FILING DATE: 26-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 30472/114 IMMU
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)816-9300
 TELEFAX: (703)683-4109
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7218 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

;
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PTZgpt-Fls
US-08-232-463-14

Query Match 9.6%; Score 84.8; DB 1; length 7218;
Best Local Similarity 2.2%; Pred. No. 2,8e-12;
Matches 8; Conservative 246; Mismatches 118; Indels 0; Gaps 0.

[illegible]

```

RESULT 8
US-09-249-585A-4
Sequence 4, Application US/09249585A
Patent No. 6417002
GENERAL INFORMATION:
APPLICANT: Horlick, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/0D905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 1926
TYPE: DNA
ORGANISM: Epstein Barr Virus
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(1926)
OTHER INFORMATION: template strand of EBNA-1 DNA
US-09-249-585A-4

```

[illegible]


```

1 ADDRESS: Woodcock, Washburn, Kutz, Mackiewicz & No. 582133918
2 STREET: One Liberty Place, 46th floor
3 CITY: Philadelphia
4 STATE: PA
5 COUNTRY: USA
6 ZIP: 19103
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: Wordperfect 5.1
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/08/458,568A
14 FILING DATE: 02-JUNE-1995
15 CLASSIFICATION: 435
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: US 08/065,146
18 FILING DATE: 05-MAY-1993
19 CLASSIFICATION: 435
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Leary Ph.D., Kathryn R.
22 REGISTRATION NUMBER: 36,317
23 REFERENCE/DOCKET NUMBER: DPCI-0029
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (215) 568-3100
26 TELEFAX: (215) 568-3439
27 INFORMATION FOR SEQ ID NO: 11:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 12001 base pairs
30 TYPE: nucleic acid
31 STRANDEDNESS: double
32 TOPOLOGY: linear
33 MOLECULE TYPE: DNA (genomic)
34 HYPOTHEICAL: NO
35 ANTI-SENSE: NO
36 ORIGINAL SOURCE:
37 ORGANISM: Herpes simplex virus
38 STRAIN: Herpes Simplex Virus Type 1
39 US-08-458-568A-11

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Query Match Similarity      6.2%; Score 54.4; DB 1; Length 12001;
Best Local Similarity      52.2%; Pred. No. 0.00021;
Matches 121; Conservative   0; Mismatches 111; Indels    0; Gaps    0

QY      1 CCGCCTCCCTCTCTCTCTCTCCGCGCTTCTGCACCTGCCAGCGTTCTTCGACCAACAACGGTCT 60
DB      1247 CCCCCTCTCTCCCCCGCGCTCTCCCCCGGTCTCTCCCCCGGTCTCTCCCCCGGTCTCTCC 1306

QY      61 CCGCGCGCTCTCTCGACTAACCGAAAGCTTTCTTCGACGCTCTCGCGGTCAACGTTCA 120
DB      1307 CCGGCTCTCTCCCCCGGCTCTCTCCCCCGGTCTCTCCCCCGGTCTCTCCCCCGGTCTCTCC 1366

QY      121 ACCGAAGGGGCAACAACAACGTCAATCTCTCTCTCTCTCTCTTAATTCTAACCCTTTTCTCTCT 180
DB      1367 CCGGCTCTCTCCCCCGGCTCTCTCCCCCGGTCTCTCCCCCGGTCTCTCCCCCGGTCTCTCC 1428

QY      181 CTGTCTGGGGGCTCTCTTCTTCCGACAGACTTTCGTGACAGTGCTTTCGCC 232
DB      1427 CCGGCTCTCTCCCCCGGCTCTCTCCCCCGGTCTCTCCCCCGGCTCTCCCCCGGTCTCTCC 1478

US-08-814-655-1
Result 13
US-08-814-655-1
Sequence 1, Application US/08834655
Patent No. 5968809
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

```

NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-08-834-655-1

Query Match 6.0%; Score 53; DB 2; Length 1617;
Best Local Similarity 51.0%; Pred. No. 0.00023;
Matches 125; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
QY 210 ACTTTCGTGACAGTCTTCCGCTGATGATAGCTTCTCTGATTCAGACCGGCTGG 269
DB 518 ACCCTCGCCACAGTGCTCTGCGCTGGCTTTGGGCTGCTTTGCGACAGTGGCGATGG 577
QY 270 ATAGCCACAGCTCCGGCCATTACAGTGATGCTCAGCGCGGCTCAACCGCGCAATT 329
DB 578 TTGGCTCAGACTTTTTCATCACCAGTCTTCCAGACCGTTTTCGGGCTATCTTTTC 637
QY 330 CAGATTCTCTCCGGCAACATTTCTCGCCGGAATCAGATCGGCTGTGAAGTGAACAC 389
DB 638 GCGGCTCTTGGGAGGTGTCTGCCAGGGCTTCTGCTCGTGTGGAAGGACAAAGCAC 697
QY 390 AACGCCACACATTTGATGACGACAGCTTGAATGATCCCTGATCTGACGACATGCCG 449
DB 698 AACACTCACCAGCGCCGCCCAACGTCACAGCGGAGATCCGACATTCACACCCACCT 757
QY 450 GTCTT 454
DB 758 CTGTT 762

RESULT 14
US-08-834-033A-1
Sequence 1, Application US/08834033A
Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300.USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-834-033A-1

Query Match 6.0%; Score 53; DB 3; Length 1617;
Best Local Similarity 51.0%; Pred. No. 0.00023;
Matches 125; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
QY 210 ACTTTCGTGACAGTCTTCCGCTGATGATAGGCTTCTCTGATTCAGACCGGCTGG 269
DB 518 ACCCTCGCCACAGTGCTCTGCGCTGGCTTTGGGCTGCTTTGCGACAGTGGCGATGG 577
QY 270 ATAGCCACAGCTCCGGCCATTACAGTGATGCTCAGCGCGGCTCAACCGCGCAATT 329
DB 578 TTGGCTCAGACTTTTTCATCACCAGTCTTCCAGACCGTTTTCGGGCTATCTTTTC 637
QY 330 CAGATTCTCTCCGGCAACATTTCTCGCCGGAATCAGATCGGCTGTGAAGTGAACAC 389
DB 638 GCGGCTCTTGGGAGGTGTCTGCCAGGGCTTCTGCTCGTGTGGAAGGACAAAGCAC 697
QY 390 AACGCCACACATTTGATGACGACAGCTTGAATGATCCCTGATCTGACGACATGCCG 449
DB 698 AACACTCACCAGCGCCGCCCAACGTCACAGCGGAGATCCGACATTCACACCCACCT 757
QY 450 GTCTT 454
DB 758 CTGTT 762

RESULT 15
US-09-363-574-1
Sequence 1, Application US/09363574
Patent No. 6136574
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING

CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-09-363-574-1

Query Match 6.0%; Score 53; DB 3; Length 1617;
Best Local Similarity 51.0%; Pred. No. 0.00023;

Matches 125; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY	210	ACTTTGTCGACGCTCTTCCGCTGCAATTAAGGCTTTCTCTGATTCAGACGCGCTGG	269
DB	518	ACCTTGCCCAACGCTCTGCGCTTTGGCTTGTCTGCGCAGCAGTCGGATGG	577
QY	270	ATAGGCGACGACTCCGGCCATTCAACGATGCTCAGCCGCGCCCAACCGGCAATT	329
DB	578	TTGGCTCAGCACTTTTTCATCAACAGTCTTCCAGGACCGTTTCTGGGGTGAATCTTTTC	637
QY	330	CAGATTCTCCGCGCAACATTTCTGCCGGAATCAGCATCGCTGTGGAAGTGAACAC	389
DB	638	GGCGCTTCTTGGAGAGTGTCTGCCAGGCTTCTGCTCGTGTGGAAGACAGCAC	697
QY	390	AAGCCCACTGACATTTGATGACCAAGCTTGACTATGACCTGATCTGCACACATGCCG	449
DB	698	AACACTCACCACCGCCGCCCAAGTTCACGCGAGGATCCGACATTTGACACCCCTT	757
QY	450	GTCTT 454	
DB	758	CTGTT 762	

Search completed: January 1, 2004, 00:05:26
Job time : 45.6671 secs

LENGTH: 1702 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 48..1406
 NAME/KEY: CDS
 LOCATION: 48..1406
 SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 us-10-029-756-26

Query Match 31.2%; Score 274.2; DB 14; Length 1702;
 Best Local Similarity 59.6%; Pred. No. 3.2e-74;
 Matches 484; Conservative 0; Mismatches 326; Indels 2; Gaps 2;

18 CCCGCTTCTCCACCTCCACCGCTTTCGACACACCGCTCCGCGCTCTCCGAC 77
 267 CCGCTCTTCCACCGGCTACTACTACTCAAGACTTGAAGTGTGAGATCTTCAAGAC 326
 78 TACCGAAGCTTCTTCCGACTCTCCGCGCTCAACCTTTCAACGCGAAGGCGCACACA 137
 327 TACCGAAGCTTCTTGAACGAGATGTGCGGCTCCGGGATCTTCAAGAAAGGCGCACAC 386
 138 ACCTCATCTCTCTCCCTTATCTACCCCTTTTCTCTCTCTCTCTCTCTCTCTCTCT 197
 387 ATATGTGACGTTCTGCGCGCTTGCCTATATGCGGCAATCGTACGCGCTCTG 446
 198 TTCTCCGACAGCACTTTCGTCAGAGTCTTCCGCTGATGATGAGGCTTCTCTGATT 257
 447 GCGTCGAGTCCGTCGGAAGTTCATCTCTGCGGCGCACTGCTGGCTTGTGTGATC 506
 258 CAGAGCGGCTGATGAGCCACGACTCCGCGCATTAACGTAATGCTCAGCGCGCTC 317
 507 CAGCGCGGCTATGTGGCCATGACTCCGCGCATTAACGTAATGCTCAGCGCGCTC 566
 318 AACCGCGCATTTGATGATCTCTCCGCAATCTCGCGGAATTCAGATCGGCTGTG 377
 567 AACGAAATCCGCACTCATAGAGGACATCTTAACCGGAATTCAGATCGGCTGTG 626
 378 AAGTGAAACCAACGCGCCACCATTTGATGATGATGATGATGATGATGATGATGATG 437
 627 AAGTGAAACCAACGCGCCACCATTTGATGATGATGATGATGATGATGATGATGATG 686
 438 CAGCAATGCGGCTTGTGAGTTGCTGCGGCTTCTCAATTCATTAACCTCTCATTTNC 497
 687 CAGCAATGCGGCTTGTGAGTTGCTGCGGCTTCTCAATTCATTAACCTCTCATTTNC 746
 498 TATGGAGAGAGTTNAGTTGATTCATGCTATGCTATGCTATGCTATGCTATGCTATG 557
 747 TATGGAGAGAGTTNAGTTGATTCATGCTATGCTATGCTATGCTATGCTATGCTATG 806
 558 ACTTTTAAACCGGTAATGTTGTTGACAGGATCAACTTATGATGATGATGATGATGATG 617
 807 ACTTACTACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 866
 618 TTGTTTTCAGAGGAAAGTGCAGATGAGCT-TGAACATTAATGGGATCTTGTGTTT 676
 867 CTCTCTCAACGAGGCGAGCTCCCTGACCGGCTCTAACTTAATGAGGATTCGGGTTTC 926
 677 TGAATTTGTTCTCTTTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 736
 927 TGAATTTGTTCTCTTTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 986
 737 GAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 796
 987 GTCTCTATCAAGCTTTGCT-GGTACGCGGATGATGATGATGATGATGATGATGATGAT 1045
 797 TGTGAAATTTATATGTCGAGGACAAATGAG 828
 1046 CTCGCGGAGACATAGTGTGGCCCCCAAGG 1077

RESULT 2
 us-10-029-756-4
 ; Sequence 4, Application US/10029756
 ; Publication No. US20020108147A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; DELTA 6-DESATURASE
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/029, 756
 ; FILING DATE: 21-Dec-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/934,254
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1685 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 us-10-029-756-4

Query Match 27.9%; Score 245.2; DB 14; Length 1685;
 Best Local Similarity 57.7%; Pred. No. 3.2e-65;
 Matches 497; Conservative 0; Mismatches 359; Indels 6; Gaps 4;

24 TTCTCCACCTCCACCGCTTTCGACCAACCGCTCCGCGCTCTCCGACTACCGC 83
 266 TTTTACAGGGATATATCTAAAGATTAATCTGTTCTGAGGTTTCTAAAGATTATAGG 325
 84 AAGCTTCTCCGACTCTCCGCGCTCAACCTTTCAACCGCAAGGCGCAACAACTCC 143
 326 AAGCTTGTGTGAGTTTCTAAATGGGTTGTATGACAAAAAAGGTATATATGTTT 385
 144 ATCTCTCTCCCTTATTTCAACCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 203
 386 GCACTTGTGCTTTATAGCAATGCTGTTTGTCTATAGTGTATATAGGGTTTGTGTTGT 445
 204 GACAGCACTTTCGTCAGCTGCTTCCGCTGATGATGATGATGATGATGATGATGATGATG 263
 446 GAGGAGTTTGTGTAATTTGTTTCTGGGTTGTATGAGGTTTCTTTGATTCAGAGT 505
 264 GCGTGATGAGCGCAACATTCGCGCATTAACATGATGATGATGATGATGATGATGATGATG 323
 506 GGTGTGATGAGCATATGCTGGGCAATTAATGATGATGATGATGATGATGATGATGATGATG 565
 324 GCAATTCAGATTCTCTCCGCAACATTTCCGCGGAATGAGCATCGGCTGTGGAAGTGG 383

Db 566 TTATATGATATTTCTGCAAAATGTCCTTTGAGAAATGATGTTGGTGAATG 625
 Qy 384 AACCAAGCCGACCAATGTCATGCAACAGCTGACATGACCTGATCGACAC 443
 Db 626 AACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 685
 Qy 444 ATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 503
 Db 686 ATACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 745
 Qy 504 AGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 563
 Db 746 AAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 805
 Qy 564 TACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 623
 Db 806 TACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 865
 Qy 624 TCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 682
 Db 866 ACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 925
 Qy 683 TGGTCTCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 742
 Db 926 TGGTACCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 985
 Qy 743 GCTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 802
 Db 986 GCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1044
 Qy 803 AAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 858
 Db 1045 AAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1104
 Qy 859 ATGGATATCTCTTGTGACCT 880
 Db 1105 ACTTGACATTTCTTGTCTCT 1126
 RESULT 3
 US-09-938-842A-558
 ; Sequence 558, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Krepes, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 558
 ; LENGTH: 1350
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-558

Query Match 27.7%; Score 244.2; DB 10; Length 1350;
 Best Local Similarity 57.2%; Pred. No. 5,9e-65;
 Matches 469; Conservative 0; Mismatches 349; Indels 2; Gaps 2;

1 CCGGCTCCCTCTCTCCGCGCTTCCACCTCCACCGCTTTTCCGACCAACCGCT 60

Db 203 CCGCTTGGACCATCTCGACCATCTCTTCCACCGGTTACCAATCAAGATTTCCAGTCT 262
 Qy 61 CCGGCGCTCTCTCGACCATCTCGACCATCTCTTCCGACCTCTCGGCTCAACCTCTCA 120
 Db 263 CCGAGCTCTACCGGATTAACCTCTGATGCTGCGGAGTTTGTAACCTGCTCTTGG 322
 Qy 121 ACCGAGGCGGACCAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
 Db 323 AAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 382
 Qy 181 CTGTCTGCGGCT 240
 Db 383 TTCTCTACCGGATTTTGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 442
 Qy 241 TGGGCTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
 Db 443 TGGGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 502
 Qy 301 TGGTACCGGCGGCTCTCAACCGGATTTCAAGATTTCTCTCTCTCTCTCTCT 360
 Db 503 TGTGCAACAAATCTTATACAAATTCGCTCTCTCTCTCTCTCTCTCTCTCTCT 562
 Qy 361 TCGACATGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 Db 563 TGTCAATGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 622
 Qy 421 ACTATGACCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
 Db 623 ATTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 682
 Qy 481 CCATTAACCTCTCTATTTATGATGATGATGATGATGATGATGATGATGATGAT 540
 Db 683 CATTAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 742
 Qy 541 TGTGATACCAAGATTTTATGATGATGATGATGATGATGATGATGATGATGATG 600
 Db 743 TCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 802
 Qy 601 TCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 659
 Db 803 TTCAAGCTTTCT 862
 Qy 660 TGGGATCT 719
 Db 863 CCGGATCT 922
 Qy 720 CTGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 779
 Db 923 CTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 981
 Qy 780 TTCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 819
 Db 982 TTCAAGCTTTATCAATTTGCTGATGATGATGATGATGATGATGATGATGATG 1021

RESULT 4
 US-09-878-574-9255
 ; Sequence 9255, Application US/09878574
 ; Patent No. US20020110548A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Byrum, Joseph R.
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Thompson, Michael D.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(15401)B
 ; CURRENT APPLICATION NUMBER: US/09/878,574
 ; PRIOR FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: 09/333,535
 ; PRIOR FILING DATE: 1999-06-14
 ; NUMBER OF SEQ ID NOS: 15775
 ; SEQ ID NO 9255
 ; LENGTH: 263

TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701102270H1
US-09-878-574-9255

Query Match 15.0%; Score 132.4; DB 10; Length 263;
Best Local Similarity 72.0%; Pred. No. 1.3e-30;
Matches 183; Conservative 0; Mismatches 70; Indels 1; Gaps 1;

QY 315 CTGACCGCGCAATTGATTTCTCCGGCAACATTCGCCCGAATCAGCATCGCTGG 374
DB 11 CTGACCGCGCTCAGCAAAATCTTTGGCAATTGCAATGAGTGGGATTAACATGATG 70
QY 375 TGGAGTGGAGCAACGACCCCAACATGATGCAAGCCTCGACTATGACCCGAT 434
DB 71 TGGAGTGGAGCTACATGCTCAGCAACATCTCAATGATGCTTGAATGATCTGAT 130
QY 435 CTGACGACATGCGCGCTTTGGAGTTTCTGCGCGGTTTCAATTCATACCTCTCAT 494
DB 131 -TGCAGCAATACCTGCTTTGCGGTGTGACACAGGTTCTCAATTCATCAATCTGT 189
QY 495 TNCATGGAGGAAGTTTGAATTCATTCATGCTAATGTTCTTGAATCTGTAACGAC 554
DB 190 TTCTATGGAAGGAATTTGTTGATTCATTAAGGTTTCAAGCTACAGCTACGAC 249
QY 555 TTTACTTTTACCC 568
DB 250 TTCACTTCTACCC 263

RESULT 5

US-10-369-493-27824
Sequence 27824, Application US/10369493
Publication No. US2003023675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianning
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 27824
LENGTH: 1098
TYPE: DNA
ORGANISM: Neurospora crassa
US-10-369-493-27824

Query Match 12.7%; Score 111.6; DB 12; Length 1098;
Best Local Similarity 53.2%; Pred. No. 8.2e-24;
Matches 231; Conservative 0; Mismatches 203; Indels 0; Gaps 0;

QY 167 CCTTTTCTCTCTCTGTCGCGCGCTCTTCTTCGACAGACATTTCTGACGTCCT 226
DB 96 CCGCTATACCTCTCTCTGCGGGGTCTTCTGTTCTTAATAATGGGGTTGTAGCTTC 155
QY 227 TTCGCTGATTTATAGGCTTTCTTGGATTCAGAGGGGTGATAGGCGACAGATTCGG 286
DB 156 TAGTGGTCTGCTCGGCTTTTGGACACAGCTAGTTCATGCGCATACGCGCG 215
QY 287 CCAATCAAGTATGTCGACCGCGCTCAACCGCGCAATCAATCTCTCCGCAA 346
DB 216 ACATAGGGCATACGACCATTTTCAATGCTATGCTATGCGCATATCTTCCGA 275
QY 347 CATCTCGCGGATGAGCATCGCTGTGGAGTGGAAACACACGCGCCACCATTTGC 406
DB 276 CTTCATCGGAGTCTAGTCTAGTGTGGAGGCGGAACACACAGTTTACCATATCAT 335

QY 407 ATGCAAGCCTGACTATGACCTGATGAGACATGCGGCTCTTGGACATTCGTC 466
DB 336 CACCAACAGCCTCGACAGATTCGACATGAAACCTCCCTTTTGCCATTTCCCA 335
QY 467 GCGGTTCTTCAATTCATTAACCTGCTATTCATGAGAGGAAGTTAGTTGATTCAT 526
DB 396 TGCTTTCTTCAATTAATCTGGGTGTCATATGACCGGTGATGAGTACGACATCTT 455
QY 527 TGTGATTTGATTTGCTGCTACGACATTTACTTTTACCCGTAATGTGTGCGAG 586
DB 456 TGCCAAATTTCTGCTCTCCCTCCGACGATTAACCTTATCATCATGATGATGTCGCC 515
QY 587 GGTCACTGTATC 600
DB 516 CCGTAACCTCTAC 529

RESULT 6

US-09-770-444-39
Sequence 39, Application US/09770444
Patent No. US2002023280A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Joern
APPLICANT: An, Yong-Olang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Matthew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Woessner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Krieger, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2027 (PARA-016PRV)
CURRENT APPLICATION NUMBER: US/09/770,444
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 39
LENGTH: 476
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(476)
OTHER INFORMATION: n = A,T,C or G
US-09-770-444-39

Query Match 12.6%; Score 111.2; DB 9; Length 476;
Best Local Similarity 54.4%; Pred. No. 6.9e-24;
Matches 221; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

QY 1 CCGCTCTCTCTCTCTCCCGCTTCTCCACCTCCACCGTCTTTCCGACCAACCGCT 60
DB 70 CCGCTTGGACATCTCTGACATCTCTTACCGGGTTACACATCAAGATTTTCAAGTCT 129
QY 61 CCGCGCTCTCTCCGATACCGCAAGCTTTCTCGACCTCTCCGCTCAACCTTTCA 120
DB 130 CCGAAGTCTACGCGATTAACCGTGTAGCTGCGAGTTGTGTAATCTCGGCTCTCG 189

QY 121 ACCGAGAGGCGCACACACCTCCATCTCTCCCTTATTCACCTTTTCTCTCT 180
 DB 190 AAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 249
 QY 181 CTGTCTGCGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
 DB 250 TTCTCTACGAGT 309
 QY 241 TGGGCTTTCTGAGATTCAGAGGCGGTGATGAGGAGGAGGAGGAGGAGGAGG 300
 DB 310 TCGGTTCTCTGAGATTCAGAGGCGGTGATGAGGAGGAGGAGGAGGAGGAGG 369
 QY 301 TCGTCAAGCGCGCGCTCAACCGCGCAATTCAGATTCCTCCGCAATTCCTCGCGGAA 360
 DB 370 TGTGCAAGCAATTCATTAACAGATTCGCTCAGCTTCTCTCTCTCTCTCTCTCT 429
 QY 361 TCAGCATCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 406
 DB 430 TCTCATCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 475

RESULT 7

US-09-923-876-5116
 ; Sequence 5116, Application US/09923876
 ; Patent No. US20020013958A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Laligudi, Raghunath V.
 ; APPLICANT: Kamigaki, Laura Y. (Ito)
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
 ; FILE REFERENCE: PL-0012-1 CON
 ; CURRENT APPLICATION NUMBER: US/09/923,876
 ; PRIOR FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: 09/298,329
 ; PRIOR FILING DATE: 1999-04-21
 ; PRIOR APPLICATION NUMBER: 60/085,331
 ; PRIOR FILING DATE: 1998-05-05
 ; NUMBER OF SEQ ID NOS: 6332
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 5116
 ; LENGTH: 265
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. US20020013958A1 700456385H1
 ; US-09-923-876-5116

Query Match 10.6%; Score 93; DB 9; Length 265;
 Best Local Similarity 60.7%; Pred. No. 2.3e-18;

Matches 147; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 402 ATTGATGCAAGAGCTGCACTATGACCTGATCTGAGACATGCGGCTTTGAGTT 461
 DB 1 ATCGGCTGCAAGAGCTGAGCATGACCGGACCTCGACAGATGCGCTCTTCGTTGTC 60
 QY 462 TCGTGGCGGCTTCTCAATTCATACCTCTCATTCATGAGGAGAGTTGAGTTGAT 521
 DB 61 TCCCCCAACCTGTTCGCAACATATGCTCTTCTTACAGAGGAGCCCTGGGCTTCGAC 120
 QY 522 TNCATTTGCTGATGTTCTGATCTGCTACGACATTTACTTTTACCGGGTAATGTGTT 581
 DB 121 GCGGCTCGAATTTCTCTATCACTACGACGAGCTGAGCTTCTTACCGGGTAATGTGATC 180
 QY 582 GCCAGGTCACCTTGTATCTGACAGCAATTCGCTATGTTGTTGAGGAGAAAGTGAC 641
 DB 181 GCCAGATTAATCTTGTGGGAGAGTGGGCTGTCTTGTCTCTGACGAGAGAGGGTGGC 240
 QY 642 GA 643
 DB 241 CA 242

RESULT 8

US-09-923-876-5116
 ; Sequence 5116, Application US/09923876
 ; Publication No. US20030237110A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Laligudi, Raghunath V.
 ; APPLICANT: Kamigaki, Laura Y. (Ito)
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
 ; FILE REFERENCE: PL-0012-1 CON
 ; CURRENT APPLICATION NUMBER: US/09/923,876
 ; PRIOR FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: 09/298,329
 ; PRIOR FILING DATE: 1999-04-21
 ; PRIOR APPLICATION NUMBER: 60/085,331
 ; PRIOR FILING DATE: 1998-05-05
 ; NUMBER OF SEQ ID NOS: 6332
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 5116
 ; LENGTH: 265
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. US20030237110A9 700456385H1
 ; US-09-923-876-5116

Query Match 10.6%; Score 93; DB 12; Length 265;
 Best Local Similarity 60.7%; Pred. No. 2.3e-18;

Matches 147; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 402 ATTGATGCAAGAGCTGCACTATGACCTGATCTGAGACATGCGGCTTTGAGTT 461

DB 1 ATCGGCTGCAAGAGCTGAGCATGACCGGACCTCGACAGATGCGCTCTTCGTTGTC 60

QY 462 TCGTGGCGGCTTCTCAATTCATACCTCTCATTCATGAGGAGAGTTGAGTTGAT 521

DB 61 TCCCCCAACCTGTTCGCAACATATGCTCTTCTTACAGAGGAGCCCTGGGCTTCGAC 120

QY 522 TNCATTTGCTGATGTTCTGATCTGCTACGACATTTACTTTTACCGGGTAATGTGTT 581

DB 121 GCGGCTCGAATTTCTCTATCACTACGACGAGCTGAGCTTCTTACCGGGTAATGTGATC 180

QY 582 GCCAGGTCACCTTGTATCTGAGCAATTCGCTATGTTTTCAGAGGAGAAAGTGAC 641

DB 181 GCCAGATTAATCTTGTGGGAGAGTGGGCTGTCTTGTCTCTGACGAGAGAGGGTGGC 240

QY 642 GA 643

DB 241 CA 242

RESULT 9

US-10-156-761-2285
 ; Sequence 2285, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; PRIOR FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 2285
 LENGTH: 1095
 TYPE: DNA
 ORGANISM: Streptomyces avermectilis
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1095)
 US-10-156-761-2285

Query Match 8.4%; Score 74.2; DB 15; Length 1095;
 Best Local Similarity 49.9%; Pred. No. 3.4e-12;
 Matches 187; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 59 CTCGCGCGCTCTCCGACTACGCAAGCTCTTCTCCGACTCTCCGCGCTCAACCTCTT 118
 DB 54 CACCGGGCTTGGCGCCACGTTCCGCCGCACTGCTCAAGCGGTAAGCGGAGCCCTTCT 113
 QY 119 CAACCGCAAGGGGCAACCAACCTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 178
 DB 114 CGACCTCGATCCCGCTACTACATAGGCGGCTGGCGCTGACCAACGCGCTGCTGCT 173
 QY 179 CTCTGTCTGGGGGCT 238
 DB 174 CGGGTTCGCGCGCT 233
 QY 239 GATAGGCTTCTCTGATTCAGAGCGGCTGATAGGCGGCAAGCTCCGCGCATTAACAAGT 298
 DB 234 GATGGGCTCTGGCGCGGCTAGTCCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 233
 QY 299 GATGCTCAGCGCGCGCTCAACCGCGCAATTCTCTCTCTCTCTCTCTCTCTCTCTCT 358
 DB 294 GTTCCGAGCAAGAGGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 353
 QY 359 AATCAGATCGGCTGTGGAAGTGAACCAAGCCCAACATTCATGCAACAGCTT 418
 DB 354 GGTGAGCTTGGGTGGGTGATCAACCAACCGGCGACCAAGCCCAACCAAGCTT 413
 QY 419 CGACTATGACCTGA 433
 DB 414 GGACATGACCCGA 428

RESULT 10
 US-10-156-761-1/c
 ; Sequence 1, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; PRIOR FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 1
 ; LENGTH: 9025608
 ; TYPE: DNA
 ; ORGANISM: Streptomyces avermectilis
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (4187715)
 ; OTHER INFORMATION: a, t, c, g, other or unknown
 US-10-156-761-1

Query Match 8.4%; Score 74.2; DB 15; Length 9025608;
 Best Local Similarity 49.9%; Pred. No. 4.8e-10;
 Matches 187; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 59 CTCGCGCGCTCTCCGACTACGCAAGCTCTTCTCCGACTCTCCGCGCTCAACCTCTT 118
 DB 2801106 CACCGGGCTTGGCGCCACGTTCCGCCGCACTGCTCAAGCGGTAAGCGGAGCCCTTCT 2801047
 QY 119 CAACCGCAAGGGGCAACCAACCTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 178
 DB 2801046 CGACCTCGATCCCGCTACTACATAGGCGGCGGCTGAGGCTGGAACCAACGCTGCTGCT 2800987
 QY 179 CTCTGTCTGGGGGCT 238
 DB 2800986 CGGGTTCGCGCGCT 2800927
 QY 239 GATAGGCTTCTCTGATTCAGAGCGGCTGATAGGCGGCAAGCTCCGCGCATTAACAAGT 298
 DB 2800926 GATGGGCTCTGGCGGCTAGTCCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 2800867
 QY 299 GATGCTCAGCGCGCGCTCAACCGCGCAATTCTCTCTCTCTCTCTCTCTCTCTCTCT 358
 DB 2800866 GTTCCGAGCAAGAGGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2800807
 QY 359 AATCAGATCGGCTGTGGAAGTGAACCAACCGCCCAACATTCATGCAACAGCTT 418
 DB 2800806 GGTGAGCTTGGGTGGGTGATCAACCAACCGGCGACCAAGCCCAACCAAGCTT 2800747
 QY 419 CGACTATGACCTGA 433
 DB 2800746 GGACATGACCCGA 2800732

RESULT 11
 US-10-156-761-1580
 ; Sequence 1580, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; PRIOR FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 1580
 ; LENGTH: 1059
 ; TYPE: DNA
 ; ORGANISM: Streptomyces avermectilis
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1059)
 US-10-156-761-1580

Query Match 8.2%; Score 72.2; DB 15; Length 1059;
 Best Local Similarity 55.9%; Pred. No. 1.4e-11;
 Matches 137; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 189 GCGCTCTCTCTCCGACGACTTTCGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 248
 DB 184 GCGCTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 243
 QY 249 CTCTGATTCAGAGCGGCTGATAGGCGGCAAGCTCCGCGCATTAACAAGTATGATCAGC 308

Db	244	CTCTCAGCGGACGCGGTTTCATAGGTACAGAGCGGTCACCTCCAGATACCGGGGAC	303
Qy	309	CGCGCGCTCAACCGGCAATTCAAGTTCTCTCGGCAACATTCTGCGGAAATCAGATC	368
Db	304	AGTTCGGTCAGCCGCTCATCGGACTGATTCACGCGCAACTTCTCTCGGATGAGTTAT	363
Qy	369	GGGTGGTGAAGTGGAAACCAACGCGCCACCAATTGCATGCACAGGCTTGATATGAC	428
Db	364	GCGTGGTGGAAACGACAAAGACAAACGGTCCACGCGCAACCCCAACCATGACAAAGAC	423
Qy	429	CTTGA	433
Db	424	CCCGA	428

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RESULT 12
US-10-184-644-332/c
/ Sequence 332, Application US/10184644
/ Publication No. US20030044930A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3430R1C27
/ CURRENT APPLICATION NUMBER: US/10/184,644
/ CURRENT FILING DATE: 2002-06-28
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 332
/ LENGTH: 520
/ TYPE: PRT
/ ORGANISM: Homo Sapien
/ US-10-184-644-332

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Query Match	7.7%	Score 67.6;	DB 15;	Length 520;
Best Local Similarity	25.9%	Pred. No. 2.6e-10;		
Matches	82;	Conservative	61;	Mismatches 174;
			Indels	0;
			Gaps	0

Oy		CGGCTCCATCCTCTCTCCGGCTTTGCACCTTCCAGCAAGCTTC	61
Db		406 GSSCMBC.HCM.CT.C.TCM.CT.C.SC..CMBC.T.C.BCS.CMYC..C.CAHCMSM.	3478
Oy		62 CGCGGCTCTCTCGGAATAACGAAAGCTTTCTTCGAGACTTTCCGGGTAACAATTTCAA	1219
Db		346 GATC.SC.SC..CTYC.SCTSC..CMTC.DCBYTC..C.BC..C..C.HMTS..CT.C..	287
Oy		122 CGGCAAGGGCACAAACCTCATCTCTCTCCCTTAATGTACACCCTTTTGCTCTC	181
Db		286 C.YC.HCMS.TC..CKBTHCKKTHCMSC..C.HCM.SMAA.CM.C..CHCMSM.	227
Oy		182 TGTCGCGGCTCTCTCTTCGGAAGCACTTTGTGACAGTCTTTCCGCTGCAATGAT	241
Db		226 C..C.ACATC.MC.TC..C..CT.CMBC..C..CS.CATHCYKCTMCTM.T..C..C.T	167
Oy		242 AGGCTTTCTTGATTCAGAAGGGCGGTGATAGCACAAGCTCCGGGCAATTACAAGTAT	301
Db		166 C.KCKTCMDC..C.TC..CM.Y.KC.N.A.NHBY..D.DSBYBA..T..B..YSTC.T	107
Oy		302 GCTCAGCGCGGCTCTCA	318
Db		106 .D.C.DYS...S.S.SH	90

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RESULT 13
US-10-184-634-332/C
, Sequence 332, Application US/10184634
, Publication No. US2003006864A1
, GENERAL INFORMATION:
, APPLICANT: Baker, Kevin P.
, APPLICANT: Chen, Jian
, APPLICANT: Desnoyers, Luc
, APPLICANT: Goddard, Audrey
, APPLICANT: Godowski, Paul J.
, APPLICANT: Gurney, Austin L.
, APPLICANT: Pan, James
, APPLICANT: Smith, Victoria
, APPLICANT: Watanabe, Colin K.
, APPLICANT: Wood, William I.
, APPLICANT: Zhang, Zemin
, TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
, TITLE OF INVENTION: ACIDS ENCODING THE SAME
, FILE REFERENCE: P3430R1C217
, CURRENT APPLICATION NUMBER: US/10/184,634
, CURRENT FILING DATE: 2002-06-28
, Prior Application removed - See File Wrapper or Palm
, NUMBER OF SEQ ID NOS: 612
, SEQ ID NO 332
, LENGTH: 520
, TYPE: PRT
, ORGANISM: Homo Sapien
US-10-184-634-332

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Query Match	7.7%	Score 67.6;	DB 15;	Length 520;
Best Local Similarity	25.9%	Pred. No. 2.6e-10;		
Matches	82;	Conservative	61;	Mismatches 174;
			Indels	0;
			Gaps	0;

Qy	CGGCTCCATCCTTCCTCCGGACCTTTCAGCTCCACGCATTTTCGGACACAGCTTC	61
Db	CSSCMBC.HCM.CT.C.TCM.CT.C.SC..CMBCI.C.BCS.CMYC..C.CANOMGM.	347
Qy	CGCGGCTCTCTCCGACTACCGAAGCTTTCTTCGAGCTCTCCGGGCTCAACTCTTCAA	122
Db	346 GATC.SC.SC..CTYC.SETSC..CMTC.DBTIC.C.BC..C.C.HOMTC.CT.C..	287
Qy	CCGAGAAGGACACACAACCTCCATCCTCTCTCCCTTAATTCTCACCTTTTTCCTCTTC	181
Db	286 C.YC.HOMSC.TC..CKBCTHOMKCYHOMSC..C.HCM.CMAA.CM.C..CCHMSGM.	227
Qy	TGTCTGGGGCGTCTCTTCTCCGAAGAAGCATTTGTGTGACCTGCTTTCGGCTGATTGAT	247
Db	226 C..C.ACATC.MC.TC..C..CT..CMBC..C..CS.CATGCHKTCMTCM.T..C..C.T	167
Qy	AGGCTTTCTTGATTCAGAGCGGCTGTGATGAGCCACAGCTCCGGCAGATTACAGATGAT	301
Db	166 C.KKCTCMDC..C.TC..CM.Y.KC.N.A.NHBV...D.DSBYBWA..T..B..YSTC.T	107
Qy	GCTCAAGCCGCCGCTTCA	318
Db	106 .D.C.DTS...S.S.SH 90	

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RESULT 14
US-10-101-487-74/c
; Sequence 74, Application US/10101487
; Publication No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: MAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; TITLE OF INVENTION: THERMOF
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487

```

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: CURRENT FILING DATE: 2002-03-20
: PRIOR APPLICATION NUMBER: 60/277,705
: PRIOR FILING DATE: 2001-03-21
: NUMBER OF SEQ ID NOS: 116
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 74
: LENGTH: 720
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: OTHER INFORMATION: oligonucleotide
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (2)..(718)
: US-10-101-487-74

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Query Match	7.5%	Score 65.6	DB 14	Length 720
Best Local Similarity	48.6%	Pred. No. 1.3e-09		
Matches 179; Conservative	0	Mismatches 189	Indels 0	Gaps 0

QY	5	CTCCCTCCCTCCCGCCGCTTCCACGCTCCACGCGTCTTCCGACCAACACGCTCCCG	64
Db	719	CTTCTCTTCT	660
QY	65	CGCCTCTCCGAGTACCGGACGCTTTCGGAAGCTCTCCGGGCTCAACCTCTTCAACG	124
Db	659	CCTCTTCTCCGCTTCT	600
QY	125	CAAGGGCCACACACTGCATCT	184
Db	599	CTTCT	540
QY	185	CTGGCGGCGGCTCTCTCTCGACAGCACTTCGACGAGCTTTCGGCGCATGTAGAG	244
Db	539	CCT	480
QY	245	CTTCTCTGATTCAGAGCGCGGTAGAGCAAGCACTCCGGGCATTAAACGTGATGCT	304
Db	479	CTTCTCTTCT	420
QY	305	CAGCCGCGGCTCAACCGGCAATTGATTTCTCTCGGGAACATTTGCGCGGAATCAG	364
Db	419	CCT	360
QY	365	CATGGGCT	372
Db	359	CTTCTCTCT	352

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RESULT 15
US-10-101-487-76
: Sequence 76, Application US/10101487
: Publication No. US20020169125A1
GENERAL INFORMATION:
: APPLICANT: LEUNG, DAVID W.
: APPLICANT: BERGMAN, PHILIP A.
: APPLICANT: LOFOUJIST, ALAN
: APPLICANT: PIETZ, GREGORY E.
: APPLICANT: TOMPKINS, CHRISTOPHER K.
: APPLICANT: MAGGONER JR., DAVID W.
: TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
: TITLE OF INVENTION: THERCOSF
: FILE REFERENCE: 077319/0329
: CURRENT APPLICATION NUMBER: US/10/101,487
: CURRENT FILING DATE: 2002-03-20
: PRIOR APPLICATION NUMBER: 60/277,705
: PRIOR FILING DATE: 2001-03-21
: NUMBER OF SEQ ID NOS: 116
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 76
: LENGTH: 720
: TYPE: DNA

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; ORGANISM: Artificial Sequence
;
; FEATURES:
;
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;
; OTHER INFORMATION: oligonucleotide
US-10-101-487-76

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Query Match	7.5%	Score 65.6	DB 14	Length 720
Best Local Similarity	48.6%	Pred. No. 1	3e-09	
Matches 179, Conservative	0	Mismatches 189	Indels 0	Gaps 0

Oy	5	CTCCGCTCTCTCCCGCCTTCTGACACTCCACCGTCTTTCGACACACACCGTCTCCGC	64
Db	6	CTTCCCT	65
Oy	65	CGCCTCTCTCCGACTACCGGAGCTTCTCTCGACCTCTCGCGGCTCAACCTCTTCAACG	124
Db	66	CGCTTCT	125
Oy	125	CAAGGGGCACACACTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	184
Db	126	CTTCT	185
Oy	185	CTGCGGCGTCT	244
Db	186	CGCTTCT	245
Oy	245	CTTCTCTCTGATTTCAAGAGCGAGTGATAGGCCACGACTCTCGGCAATTACAACGTGATCT	304
Db	246	CTTCT	305
Oy	305	CAAGCGCGGCTCTCAACCGGCAATTCAATTTCTCTCGGGCAAACTTCTCGCGGAATCAG	364
Db	306	CGCTTCT	365
Oy	365	CATCGGCT	372
Db	366	CTTCTCTCT	373

Search completed: January 1, 2004, 05:19:32
Job time : 238.488 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 23.293 Seconds
(without alignments)
1724.030 Million cell updates/sec

Title: US-09-857-524B-6

Perfect score: 1318
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Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	899.5	68.2	450	21	AAV71554 Soybean sphingolip
3	789.5	59.9	449	21	AAAG29290 Arabidopsis thalia
4	780.5	59.2	449	21	AAAG07392 Arabidopsis thalia
5	780.5	59.2	449	21	AAV51333 B. napus sldi prot
6	780.5	59.2	517	21	AAAG07391 Arabidopsis thalia
7	778.5	59.1	449	21	AAAG53861 Arabidopsis thalia
8	778.5	59.1	449	21	AAV51334 A. thaliana sldi p
9	753.5	57.2	452	23	AAU79851 Evening primrose d

10	753.5	57.2	452	24	ABG73416 Evening primrose d
11	747.5	56.7	458	21	AAV51348 Sphingolipid desat
12	741	56.2	353	21	AAAG07393 Arabidopsis thalia
13	739	56.1	353	21	AAAG53862 Arabidopsis thalia
14	730.5	55.4	448	17	AAAG98455 Borage delta-6-des
15	730.5	55.4	448	19	AAAG67471 Borage delta-6-des
16	730.5	55.4	448	23	AAAG98430 Borage delta-6-des
17	730.5	55.4	448	23	AAU79830 Borage officialis
18	730.5	55.4	448	24	ABG73095 Borage delta-6-des
19	725.5	55.0	448	21	AAV51349 Sunflower HADS pr
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21	719	54.6	450	24	ABG73418 Evening primrose d
22	716.5	54.4	448	24	ABG73417 Borage delta-6-des
23	706.5	53.6	326	21	AAAG29291 Arabidopsis thalia
24	696.5	52.8	326	21	AAAG53863 Arabidopsis thalia
25	689.5	52.3	469	21	AAV71555 wheat sphingolipid
26	688.5	52.2	462	21	AAV71552 Desaturase enzyme
27	682.5	51.8	252	19	AAW84141 Corn sphingolipid
28	632	48.0	448	21	AAV71551 Florida bitterbush
29	620.5	47.1	224	21	AAV51350 Protein b51pu with
30	572.5	43.4	284	21	AAV51351 Protein b52pu with
31	515.5	39.1	222	21	AAV51352 Protein delta-6-des
32	348.5	26.4	178	22	AAAB46439 C. purpureus delta
33	291	22.1	104	19	AAW84140 Desaturase enzyme
34	287	21.8	76	21	AAV83238 Sunflower hypothet
35	279	21.2	68	21	AAV83244 Delta 6 desaturase
36	263	20.0	467	24	AAAB99479 Amino acid sequenc
37	258.5	19.6	453	24	AAAB31500 Saponolegna diclin
38	247.5	18.8	457	19	AAW84137 A delta-6 desatura
39	247.5	18.8	457	20	AAW95504 Mortierella alpina
40	247.5	18.8	457	21	AAV92599 M. alpina delta-6
41	247.5	18.8	457	21	AAV56045 Fungal delta6-deasa
42	247.5	18.8	457	22	AAAB31684 Amino acid sequenc
43	247.5	18.8	458	23	AAAG94693 Human delta5-desat
44	247.5	18.8	458	23	AAAG94707 Human delta5-desat
45	247.5	18.8	458	23	ABG96509 M. alpina delta6 d

ALIGNMENTS

RESULT 1	AAV71553	standard; Protein; 253 AA.
ID	AAV71553	
XX	AAV71553	
AC	AAV71553	
XX		
DT	12-OCT-2000	(first entry)
XX		
DE	Soybean sphingolipid desaturase #1.	
XX		
KW	Soybean; sphingolipid desaturase; membrane-bound desaturase;	
XX	transgenic plant; fatty acid.	
OS	Glycine max.	
XX		
PH	Key	Location/Qualifiers
FT	Misc-difference 161	/label= Unknown
FT	Misc-difference 166	/note= "Encoded by TNC"
FT	Misc-difference 170	/label= Unknown
FT	Misc-difference 173	/note= "Encoded by TNC"
FT	Misc-difference 206	/label= Unknown
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FT      /note= "Encoded by TG"
FT      Misc-difference 227..228
FT      /note= "Encoded by TTGATGATGCTGCTGCCAATATGGGCC
FT      TCGATGAGGAGATGTTTNGC"
FT      Misc-difference 252
FT      /label= "Unknown
FT      /note= "Encoded by GNC"
XX      WO200032790-A2.
XX      PD      08-JUN-2000.
XX      PF      02-DEC-1999; 99WO-US28589.
XX      PR      03-DEC-1998; 98US-0110784.
XX      PA      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX      PI      Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;
XX      DR      WPI; 2000-412336/35.
XX      DR      N-PSDB; AAD01351.
XX      PS      Claim 10; Page 45-46; 57pp; English.
XX      CC      The present sequence is a sphingolipid desaturase
XX      CC      derived from a contig of clones sfil.pK0012.c5 and sfil.pK0031.d11
XX      CC      isolated from soybean immature flower cDNA library, sfil.
XX      CC      The present sequence is useful for producing
XX      CC      transgenic plants having altered levels of sphingolipid desaturase which
XX      CC      in turn would alter the fatty acid composition. The enzyme is also useful
XX      CC      for producing polyclonal or monoclonal antibodies. The polynucleotide
XX      CC      is useful as primer or probe for screening cDNA libraries to
XX      CC      isolate desired full-length cDNA clones.
SQ      Sequence 253 AA;
Query Match 99.1%; Score 1306; DB 21; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.7e-137;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 LPAFSTSHRLSDHTVSAASDYSKLFSDLSALNLFNRKHTTSLILSLITLFPPLSVCGV 60
DB      1 LPAFSTSHRLSDHTVSAASDYSKLFSDLSALNLFNRKHTTSLILSLITLFPPLSVCGV 60
QY      61 LFSSTFVHVLSAALIGFLMIOGMIHDSGHYVWLSRRLNRAIOILSGNIIAGISIGW 120
DB      61 LFSSTFVHVLSAALIGFLMIOGMIHDSGHYVWLSRRLNRAIOILSGNIIAGISIGW 120
QY      121 WKNNNAHHIACNSLDYDPLQHPVFAVSSRFNSITSHXGKKEFDXIAKFLICYQH 180
DB      121 WKNNNAHHIACNSLDYDPLQHPVFAVSSRFNSITSHXGKKEFDXIAKFLICYQH 180
QY      181 FTFYPVWCARVNLVYOTILLFSRXKYODRALNIMGILVFWTWFLFLALLFVPIQHIO 240
DB      181 FTFYPVWCARVNLVYOTILLFSRXKYODRALNIMGILVFWTWFLFLALLFVPIQHIO 240
QY      241 FWLNHLAENLYXG 253
DB      241 FWLNHLAENLYXG 253

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RESULT 2

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AAV71554
ID      AAV71554 standard; Protein; 450 AA.
XX      AC      AAV71554;
XX      DT      12-OCT-2000 (first entry)

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XX      DE      Soybean sphingolipid desaturase #2.
XX      KW      Soybean; sphingolipid desaturase; membrane-bound desaturase;
XX      KW      transgenic plant; fatty acid.
XX      OS      Glycine max.
XX      PN      WO200032790-A2.
XX      PD      08-JUN-2000.
XX      PF      02-DEC-1999; 99WO-US28589.
XX      PR      .03-DEC-1998; 98US-0110784.
XX      PA      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX      PI      Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;
XX      DR      WPI; 2000-412336/35.
XX      DR      N-PSDB; AAD01352.
XX      PS      Claim 10; Page 47-48; 57pp; English.
XX      CC      The present sequence is a sphingolipid desaturase
XX      CC      from clone sfil.pK0017.b4.f1e isolated from soybean seedling cDNA
XX      CC      library, sfil. The present sequence is useful for producing
XX      CC      transgenic plants having altered levels of sphingolipid desaturase which
XX      CC      in turn would alter the fatty acid composition. The enzyme is also useful
XX      CC      for producing polyclonal or monoclonal antibodies. The polynucleotide
XX      CC      is useful as primer or probe for screening cDNA libraries to
XX      CC      isolate desired full-length cDNA clones.
SQ      Sequence 450 AA;
Query Match 68.2%; Score 899.5; DB 21; Length 450;
Best Local Similarity 65.3%; Pred. No. 1.6e-91;
Matches 175; Conservative 20; Mismatches 58; Indels 15; Gaps 2;
QY      1 LPAFSTSHRLSDHTVSAASDYSKLFSDLSALNLFNRKHTTSLILSLITLFPPLSVCGV 60
DB      74 LKRFPTGTHSDPKVSEVSKDYRKLSSEFSKGLFDTKGHVISTLAVAVMFLIVYGV 133
QY      61 LFSSTFVHVLSAALIGFLMIOGMIHDSGHYVWLSRRLNRAIOILSGNIIAGISIGW 120
DB      134 LRCTVMAHLGSGMLGLMGSAYVGHDSGHVVTWTTGPNKVAQIISGNCLTGISIAM 193
QY      121 WKNNNAHHIACNSLDYDPLQHPVFAVSSRFNSITSHXGKKEFDXIAKFLICYQH 180
DB      194 WKNTNNAHHIACNSLDHDPDQHPVFAVSSRFNSITSHFYGRKLEFDIAKFLICYQH 253
QY      181 FTFYPVWCARVNLVYOTILLFSRXKYODRALNIMGILVFWTWFLFLALLFVPIQHIO 240
DB      254 FTFYPVWCARVNLVYOTILLFSRXKYODRALNIMGILVFWTWFLFLALLFVPIQHIO 240
QY      227 FLTALLFV-PIQHIOFWLNHLAENLYXG 253
DB      314 FVLASPAVCSIQHIOFCLNHFAANVYVG 341

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RESULT 3

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AAG29290
ID      AAG29290 standard; Protein; 449 AA.
XX      AC      AAG29290;
XX      DT      17-OCT-2000 (first entry)

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DE Arabidopsis thaliana protein fragment SEQ ID NO: 34824.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
XX EPI33405-A2.
PN
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
PF
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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QY 1 LPAFSTSHRLSDHTVASASDYKRLFSALNLFNRKGGHTTSILSLITLTFPLSVCGV 60
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QY 61 LFSDSFFVAVLSAALIGFLMIGSGWIGHSGHYNWMLSRRLRAIOTLSGNIAGISIGW 120
DB 133 LACTSTWALHISAVLLGLMIGSAYVGHSGHYTSTKPCNGLDILLGNCITGISIAM 192
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DB 193 WKMTNHAHHIACNSLDHDPDLOHPIPIFAVSTKFNSTSTFGKRLTFDPLAFLISYOH 252
QY 181 FTFYPMCAVAVNLVLTILLFSSRXKVDRAINIGILVFTWFTFLALL----- 232
DB 253 WFFYPMCAVAVNLVLTILLFSSRXKVDRAINIGILVFTWFTFLAVSFLPMQGRPI 312
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DB 313 FVFSFAVTAIOHVFQCLNHFADVYTG 340
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RESULT 4
AAG07392
ID AAG07392 standard; Protein; 449 AA.
XX
AC AAG07392;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4528.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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 PR 20-AUG-1999; 99US-0149722.

PR 20-AUG-1999; 99US-0149723.
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 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
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 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
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 PR 13-SEP-1999; 99US-0153758.
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 PR 04-OCT-1999; 99US-0157117.
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 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 59.2%; Score 780.5; DB 21; Length 449;
 Best Local Similarity 54.8%; Pred. No. 3, 1e-78;
 Matches 144; Conservative 37; Mismatches 67; Indels 15; Gaps 2;

QY 6 TSHRLSDHTVSAASDDYRKLFSDSLALNPNKRGHTTSLLSLILTLFPLSCGVLFSS 65
 DB 78 TGYHTRDPQVSESVSDYRMALEFRKLGFEKKGVTLYTLAFVAMFLRVLYGVACTS 137
 QY 66 TFVHLSAALIGFLFIOSGIMGHDSGHVVMLSRRLNRAIOLSGNLAGISGMMKMH 125
 DB 138 VFAHQIAALGLGLWIOSAYIGHDSGHVYINSKSNRAQLSGNCLTGISIAAMKMH 197
 QY 126 NAHHTACNSLDYDPLQHPVFAVSRRFENSITSHXGKXEPDIXAFELICYOHTFPY 185
 DB 198 NAHHTACNSLDYDPLQHPVFAVSTKFFSLTSRFDYRKLTFDPVARFLVSYQHTTYP 257

QY 186 VMCVARVNLVLTITLLFSRXKVDRAINMGILVFWTWFLPLALL-----FV---- 234
DB 258 VMCFGINLFIQTLLFSRGVPPDRALNPAIGILVFWTWFLPLVSCLPMPKPERFFVFTG 317
QY 235 ---PIQHIQFWNLHLENLYXG 253
DB 318 FVTALQHIQFTLNHFADVYVG 340

RESULT 5
AA51333
ID AA51333 standard; Protein; 449 AA.
XX
AC AA51333;
XX
DT 27-APR-2000 (first entry)
XX
DE B. napus sld1 protein.
XX
KM Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
KM transgenic plant; crop plant; delta-8-unsaturated long-chain base;
KM tolerance; resistance; soil salinity; ion stress; toxicity; drought;
KM cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
KM pharmaceutical; food; chemical raw material.
XX
OS Brassica napus.
XX
PN DE19628850-A1.
XX
PD 30-DEC-1999.
XX
XX 27-JUN-1998; 98DE-1028850.
PF
XX 27-JUN-1998; 98DE-1028850.
PR
XX (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
PA
PI Heinz E, Zaehring U, Schmidt H, Sperling P;
XX
DR WPI; 2000-127549/12.
DR N-PSDB; AA244832.
XX
PT New sphingolipid desaturase that selectively introduces double bond
into sphingolipide and capnoids -
XX
PS Claim 8; Fig 2; 62pp; German.
XX
CC This invention describes a novel sphingolipid desaturase that selectively
introduces a double bond into the sphingobase of the ceramide residue of
sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
desaturase, or a vector containing the DNA sequence, can be used to
produce transgenic plants, especially crop plants, with an increased or
decreased delta-8-unsaturated long-chain base content or an altered
delta-8-unsaturated long-chain base cis/trans ratio, especially to
compensate for a delta-8-unsaturated long-chain base deficiency, to
exclude production of delta-8-unsaturated bases, to increase tolerance
or resistance to soil salinity, ion stress or toxicity, drought, wet
conditions, cold or frost and/or phytopathogenic microorganisms, or to
alter size growth and flowering time. Cells, transgenic organisms or
plants containing the DNA sequence can be used to produce sphingolipids
and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
can be used in cosmetics, pharmaceuticals and foods and as chemical raw
materials. This sequence represents the Brassica napus sphingolipid
desaturase sld1 protein described in the method of the invention.
XX
SQ Sequence 449 AA;

Query Match 59.2%; Score 780.5; DB 21; Length 449;
Best Local Similarity 54.0%; Pred. No. 3,1e-78;
Matches 141; Conservative 44; Mismatches 61; Indels 15; Gaps 2;

QY 8 HRLSDHTVASASDVKRLFSDSLALNLFNRKHTTSLILSLTLFPLSVCGVLPSDSRF 67

DB 80 YHKDHDVSDVSDRYRLAAEFSSKGLFDKGGVTLVTLTCAVAAALAAVVGVACTSTW 139
QY 68 VHTLSAALIGFLWISGMIQGHDSGHYNNVLSRLNRAIQILSLNIIAGISIGWKKNNHA 127
DB 140 AHLISAVLLGLWIOSAVYGHDSGHYNNVTSRCNKLVOILSGNCTGISIAWKKWTHNA 199
QY 128 HHACNSLDYDDPDLQMPVFAVSSREFNSITSHXGKKEPDXIAXFLICYOHFTFPVW 187
DB 200 HHISCNSLDHPDQHIPTVLAVSNKFEKSMTSRFTGRKLTDPDLARFLISYOHMSFPYPLW 259
QY 188 CVARVNLVLTITLLFSRXKVDRAINMGILVFWTWFLPLLA-----LLFV----- 234
DB 260 CVGRINLFIQTLLFSRRYVPPDRALNPAIGILVFWTWFLPLVSLPNNQERIIFVFLSMA 319
QY 235 ---PIQHIQFWNLHLENLYXG 253
DB 320 VTAIQHVQPCLNHFADVYTG 340

RESULT 6
AAG07391
ID AAG07391 standard; Protein; 517 AA.
XX
AC AAG07391;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4527.
XX
KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
PF
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
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PR 23-APR-1999; 99US-0130510.
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PR 21-MAY-1999; 99US-0135353.

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 PR 06-OCT-1999; 99US-0157865.
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 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
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 PR 21-OCT-1999; 99US-0160770.
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 PR 22-OCT-1999; 99US-0160989.
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 PR 28-OCT-1999; 99US-0161920.

PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 59.2%; Score 780.5; DB 21; Length 517;
Best Local Similarity 54.8%; Pred. No. 3,6e-78;
Matches 144; Conservative 37; Mismatches 67; Indels 15; Gaps 2;

QY 6 TSHRLSDHTVSAASDPYKLFSDLSALNPNRKHGHTTSLTSLTLTLPVSGVLFSDS 65
DB 146 TGHINDFOVSEVSRDPRMAAFKRLGLENKGHVTLTLAVAAFLRVLYGLACTS 205
QY 66 TFWVLSAALIGFLMTIOSGWIIGDSGHYNVMSRLNRAIOILSGNLIAGISIGWKMNH 125
DB 206 VFHNGIAAALLGLMTIQSAVIGHDSGHYVIMNSKYNRFQOLSGNLTGSIAMWKWTH 265
QY 126 NAHHIHCNSLDYDPDIQHMFPVAVSSRFNSITSHXGKKEPDIXALFLICYQHTFYP 195
DB 266 NAHHIHCNSLDYDPDIQHTFVFAVSTFFSLSLTSRFPDRKLTDPVAFVLSYQHFTYYP 325
QY 186 VMCVARVNLVLTOTLLLSFRXKQDRALNTMGILVFWTWFLFLALL-----FV--- 234
DB 326 VMCFGRIINFIOFLLFSKREVPDRALNAGILVFWTWFLVSCLPNMPERFFVFTG 385
QY 235 ----PIQHIQFWMNLHAENLYXG 253
DB 386 FVTVALQHIQFTLNHFADYYVG 408

RESULT 7
AAG53861
ID AAG53861 standard; Protein; 449 AA.
XX AAG53861;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 68613.

KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD -06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
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 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151086.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158332.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159337.
 PR 14-OCT-1999; 99US-0159637.
 PR 18-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.

PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161922.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 59.1%; Score 778.5; DB 21; Length 449;
 Best Local Similarity 54.8%; Pred. No. 5, 1e-78;
 Matches 144; Conservative 37; Mismatches 67; Indels 15; Gaps 2;

QY 6 TSHRLSDHTVSAASDYLKFDLSALNLFNRKGTTSILSLITLFPPLVCGVLFSDS 65
 DB 78 TGYHIDPQVSEVSRYRMAALEFRKLGFEKKGHTLVTLAVFAAMFGLVGLACTS 137
 QY 66 TPVHVLSALLIGFLWQSGMIGHDSCHYVNLRLRAIQILSGNITLAGISGMKWNH 125
 DB 138 VFAHQIAAALGLWIOSAYIGHDSCHYVIMSNKSYRPAQLSGNLTGISIAMMKWT 197
 QY 126 NAHILACSLDYPDLOHMPVFAVSRRFNSITSHYGRKXERFDXAFICQYHFTFP 185
 DB 198 NAHILACSLDYPDLOHMPVFAVSRRFNSITSHYGRKXERFDXAFICQYHFTFP 257
 QY 186 VMCVARVNLQTLITLFFSRXKVDALNIMGLVETWFLFLALL-----FY--- 234
 DB 258 VMCGRINFLQTFLLFSKREVPDALNPAQILVETWFLFLVSCLPMMPEFFVFTS 317
 QY 235 ----PIQHIFWNLHAEVLYXG 253
 DB 318 FTVALQHIQTLNHPADVVYG 340

RESULT 8
 AA51334
 ID AA51334 standard; Protein; 449 AA.
 XX
 AC AA51334;
 XX
 DT 27-APR-2000 (first entry)
 XX
 DE A. thaliana sidi protein.
 XX
 KW Sphingolipid desaturase; sidi; sphingobase; ceramide; capnoid;
 KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
 KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KW pharmaceutical; food; chemical raw material.
 XX
 OS Arabidopsis thaliana.
 XX
 PN DE19628850-AL.
 XX
 PD 30-DEC-1999.
 XX
 PF 27-JUN-1998; 98DE-1028850.
 XX
 PF 27-JUN-1998; 98DE-1028850.
 XX
 PA (GVSE-) GVS GBS ERWERB & VERW LANDWIRTSCHAFTLICH.
 XX
 PI Heinz E, Zaehneringer U, Schmidt H, Sperling P;
 XX WPI, 2000-127549/12.
 DR N-PSDB; AA244833.
 XX
 PT New sphingolipid desaturase that selectively introduces double bond
 into sphingolipide and capnoids -

XX Claim 8; Fig 4; 62pp; German.
 CC This invention describes a novel sphingolipid desaturase that selectively
 CC introduces a double bond into the sphingobase of the ceramide residue of
 CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to
 CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered
 CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
 CC compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 CC materials. This sequence represents the Arabidopsis thaliana sphingolipid
 CC desaturase sld1 protein described in the method of the invention.
 CC
 SQ Sequence 449 AA;
 Query Match 59.1%; Score 778.5; DB 21; Length 449;
 Best Local Similarity 54.8%; Pred. No. 5.1e-78;
 Matches 144; Conservative 37; Mismatches 67; Indels 15; Gaps 2;
 QY 6 TSHRLSDHYTSAASDYLKPSDLALNLFNRKHTTSLLSLITLFLPSVCGVLFSDS 65
 DB 78 TGVHIDFQVSEVSRDVRMAAEFRKLGFEKNGHVLTYTLAVVAMFLGVLVGVLACTS 137
 QY 66 TGVHLSAALIGFLMTIOSGWIHDSGHVYVMSRLNRAIQILSGNLAGISIGMKWNH 125
 DB 138 VFNHQAALALGLMTIOSATIGHDSGHVYVMSKSTYRPAQLSGNLTGISTAMWMTA 197
 QY 126 NAHHAICNSLDYDPLQHMVFAVSSRFNSITSHXGKKEFDXIAFLICYQHFTYP 185
 DB 198 NAHHAICNSLDYDPLQHMVFAVSSRFNSITSHXGKKEFDXIAFLICYQHFTYP 257
 QY 186 VMCAVAVNLVLTOTILLFSRKVQDRALNIMGLVFTWTFLLALL-----FV--- 234
 DB 258 VMCEGINFLFIQTFLLFSRKVEPRDALNFMGLVFTWTFLLVSCLPNMPERFFVETS 317
 QY 235 -----PIQHQFMNLHAENLYXG 253
 DB 318 FTVTALQHQFTLNHRAADYVVG 340
 RESULT 9
 ID AAU79851 standard; Protein; 452 AA.
 AC AAU79851;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Evening primrose delta6-desaturase.
 XX
 KW delta6-desaturase; sunflower; soybean; maize; tobacco;
 KM peanut; carrot; oil seed rape; gamma linolenic acid; GLA;
 XX chilling tolerance; evening primrose.
 OS Oenothera biennis.
 XX
 PN US635861-B1.
 PD 12-MAR-2002.
 XX
 PF 19-SEP-1997; 97US-0934254.
 XX
 PR 13-OCT-1992; 92US-0959952.
 PR 10-OCT-1991; 91US-0774475.
 PR 08-JAN-1992; 92US-0817919.

PR 14-SEP-1994; 94US-0307382.
 PR 28-JAN-1997; 97US-0789936.
 XX
 PA (RHON) RHONE-POULENC AGROCHIMIE.
 XX
 PI Thomas TL;
 XX
 DR WPI; 2002-380944/41.
 DR N-PSDB; ABK49503.
 XX
 PT Novel nucleic acid encoding evening primrose delta6-desaturase which
 PT converts linoleic acid to gamma linolenic acid useful for producing
 PS gamma linolenic acid in transgenic plant or bacteria
 XX
 PS Claim 3; Column 45-48; 53pp; English.
 XX
 CC The invention describes an isolated nucleic acid encoding an evening
 CC primrose Delta6-desaturase. The nucleic acid and a vector expressing the
 CC nucleic acid are useful for producing a plant such as sunflower, soybean,
 CC maize, tobacco, peanut, carrot or oil seed rape plant, with increased
 CC gamma linolenic acid (GLA) content, and also for inducing or increasing
 CC production of GLA in a bacteria or plant deficient, lacking in or
 CC producing low levels of GLA. The nucleic acid is also useful for inducing
 CC chilling tolerance in plants. This is the amino acid sequence of the
 CC evening primrose delta6 desaturase involved in the production of gamma
 CC linoleic acid.
 CC
 SQ Sequence 452 AA;
 Query Match 57.2%; Score 753.5; DB 23; Length 452;
 Best Local Similarity 53.2%; Pred. No. 3.2e-75;
 Matches 142; Conservative 37; Mismatches 73; Indels 15; Gaps 2;
 QY 2 PASTSHRLSDHYTSAASDYLKPSDLALNLFNRKHTTSLLSLITLFLPSVCGVL 61
 DB 74 PLFTGYTYKDFEVSISIDYRRLNEMERSGIFEEKGHHIMTVEGVVMMAAIYGV 133
 QY 62 FSDSTGVHLSAALIGFLMTIOSGWIHDSGHVYVMSRLNRAIQILSGNLAGISIGMW 121
 DB 134 ASSEVGVHMLCGALLGLMTIOAAVYHDSGHVYVMTREGRNRTQILAGNLTGISTAMW 193
 QY 122 KMNHHAICNSLDYDPLQHMVFAVSSRFNSITSHXGKKEFDXIAFLICYQH 181
 DB 194 KMNHHAICNSLDYDPLQHMVFAVSSRFNSITSHXGKKEFDXIAFLICYQH 253
 QY 182 TFPVNCVAVNLVLTOTILLFSRKVQDRALNIMGLVFTWTFLL-----FV--- 227
 DB 254 TYPVNMIFGRVNLFIQTFLLFSRKVEPRDALNFMGLVFTWTFLLVSCLPNMPERFG 313
 QY 228 -LTLALFVPIQHQFMNLHAENLYXG 253
 DB 314 VLISFAVTALQHQFTLNHRAADYVVG 340
 RESULT 10
 ID ABG73416 standard; Protein; 452 AA.
 AC ABG73416;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Evening primrose delta-6-desaturase #1.
 XX
 KW Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower; soybean;
 KM maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
 KM octadecatetraenoic acid; alpha-linolenic acid; delta-15-desaturase;
 XX evening primrose.
 XX
 OS Oenothera biennis.
 XX
 PN US2002108147-A1.

PD 08-AUG-2002.
 XX
 PF 21-DEC-2001, 2001US-0029756.
 XX
 PR 13-OCT-1992, 92US-0959952.
 PR 19-SEP-1997, 97US-0934454.
 PR 10-OCT-1991, 91US-0774475.
 PR 08-JAN-1992, 92US-0817919.
 PR 14-SEP-1994, 94US-0307382.
 PR 26-JAN-1997, 97US-0789936.
 XX
 PA (THOM/) THOMAS T L.
 XX
 PI Thomas TL;
 XX
 DR WPI: 2003-06659/06.
 DR N-PSDB; ABX15367.
 XX
 XX Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
 PT for producing plant with increased gamma linolenic acid content, and
 PT for inducing octadecatetraenoic acid production in plant
 XX
 PS Claim 3, Fig 10; 55pp; English.
 XX
 CC The invention relates to a nucleic acid encoding an evening primrose
 CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
 CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
 CC for producing a plant (such as sunflower, soybean, maize, tobacco,
 CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
 CC acid (GLA) content by transforming a plant cell with the nucleic acid or
 CC vector and regenerating a plant with increased GLA content from the plant
 CC cell, for inducing or increasing production of GLA in an organism lacking
 CC in or producing low levels of GLA and for inducing production of
 CC octadecatetraenoic acid in at least one of a plant deficient or lacking
 CC in or producing low levels of octadecatetraenoic acid, a bacterium which
 CC produces alpha-linolenic acid or a bacterium which exhibits a
 CC delta-15-desaturase activity on a GLA substrate. This sequence represents
 CC an evening primrose delta-6-desaturase polypeptide.
 XX
 SQ Sequence 452 AA;
 Query Match 57.2%; Score 753.5; DB 24; Length 452;
 Best Local Similarity 53.2%; Pred. No. 3, 2e-75;
 Matches 142; Conservative 37; Mismatches 73; Indels 15; Gaps 2;
 QY 2 PAFSTSHRLSDHTVLAASDDYRKLPSDLSALNLFNRKHTTSLLSLITLPLPVSQGV 61
 DB 74 PLFTGYVYKDFEVSSEISKDYRLNEMSGIFFEKKGHIMWTFGVAVMMALVYGV 133
 QY 62 FSDSTFVHLSAALIGFLWIGSGWIGHDSGHVVMLSRLNRAIQLSGNIIAGISIGW 121
 DB 134 AABSQGVNMLCGALLDLMLIAAIVGHDSGHVQVMPTRGVNRTQLIAGNIIIGSIAWM 193
 QY 122 KNNHNAHIAACNSLDYDPDLOHMPVPAVSSRFNSITSHYGRKXKFXDIAFLICYQHF 181
 DB 194 KMTNHNHIAACNSLDYDPDLOHMPVPAVSSRFNSITSHYGRKXKFXDIAFLICYQHF 253
 QY 182 TTYPVNCAVARNLYLQITILLFSRXXVQDRALNMGILVFTWTF-LF----- 227
 DB 254 TTYPVNCAVARNLYLQITILLFSRXXVQDRALNMGILVFTWTF-LF----- 313
 QY 228 -LLALLFVPIQHIFQFNLNLAENLYXG 253
 DB 314 VLISFAVTAIQHVQFTLNHPSGDTYVG 340

XX
 DE Sphingolipid desaturase protein.
 XX
 KW Sphingolipid desaturase, sld1, sphingobase; ceramide; capnoid;
 KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
 KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KW pharmaceutical; food; chemical raw material.
 XX
 OS Unidentified.
 XX
 PN DE19828850-A1.
 XX
 PD 30-DEC-1999.
 XX
 PF 27-JUN-1998; 98DE-1028850.
 XX
 PR 27-JUN-1998; 98DE-1028850.
 XX
 PA (GVSE-) GVS GRS ERWERB & VERW LANDWIRTSCHAFTLICH.
 XX
 PI Heinz E, Zaehring U, Schmidt H, Sperling P;
 XX
 DR WPI: 2000-127549/12.
 DR N-PSDB; AA244851.
 XX
 PT New sphingolipid desaturase that selectively introduces double bond
 PT into sphingolipid and capnoids -
 XX
 PS Disclosure, Fig 15; 62pp; German.
 XX
 CC This invention describes a novel sphingolipid desaturase that selectively
 CC introduces a double bond into the sphingobase of the ceramide residue of
 CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to
 CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered
 CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
 CC compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 CC materials. This sequence represents a sphingolipid desaturase protein
 CC described in the method of the invention.
 XX
 SQ Sequence 458 AA;
 Query Match 56.7%; Score 747.5; DB 21; Length 458;
 Best Local Similarity 52.8%; Pred. No. 1, 5e-74;
 Matches 140; Conservative 40; Mismatches 66; Indels 19; Gaps 4;
 QY 6 TSHRLSDHTVLAASDDYRKLPSDLSALNLFNRKHTTSLLSLITLPLPVSQ--GVLS 63
 DB 87 TGYHKLQYQVSDISIDYRKLASEFAKGFEEKGH--GVYSLCFVSLLSACVYGVLS 144
 QY 64 DSTFVHLSAALIGFLWIGSGWIGHDSGHVVMLSRLNRAIQLSGNIIAGISIGW 123
 DB 145 GSFVHMLSGAILGLAMQIAYLGHDAHYQMAATRGKMKPGICITGTGSIAMW 204
 QY 124 NENAHIAACNSLDYDPDLOHMPVPAVSSRFNSITSHYGRKXKFXDIAFLICYQHF 183
 DB 205 TNNAHIAACNSLDYDPDLOHMPVPAVSSRFNSITSHYGRKXKFXDIAFLICYQHF 264
 QY 184 YPVNCAVARNLYLQITILLFSRXXVQDRALNMGILVFTWTF-LF-----FV- 234
 DB 265 YPIMCAVARNLYLQITILLFSRXXVQDRALNMGILVFTWTF-LF-----FV- 324
 QY 235 -----PIQHIFQFNLNLAENLYXG 253

DB 325 VSECVTGTGHIQIPLTNHFGSDVYVG 349
RESULT 12
AAG07393
ID AAG07393 standard; Protein; 353 AA.
XX
AC AAG07393;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 4529.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126284.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136382.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139452.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.

PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.

PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151338.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161933.
PR 29-OCT-1999; 99US-0162142.

Query Match 56.2%; Score 741; DB 21; Length 353;
Best Local Similarity 55.2%; Pred. No. 5.7e-74;
Matches 138; Conservative 35; Mismatches 55; Indels 22; Gaps 3;

QY 19 SSDYRKLFDLSALNLFNRKHTTSLILSLTLFPLSYCGVLFSDSTFVHVLASALIGF 78
DB 2 AAEFRK-----LGFENKGGHTLTLYLAFVAMFLRVLYGVLAQSVFAHQIAAALLGL 54
QY 79 LNIQSGWIGHDSGRHYVMLSRLNRAIQIISGNILGIGISGWKKNHNAHHIACNSLDYD 138
DB 55 LNIQSAVIGHDSGRHYVIMSNKSYNRPAQLISGNCILGISIAWMKWNHNAHHIACNSLDYD 114
QY 139 PDLQHMVPFAVSSRFNSITSHYGRKXEPDXLAXFLICQHFTFPVWCVARVNLXLTQ 198

DB 115 PDLQHMVPFAVSTKFPSSILTSRFDYDKLFFDVARFLVSQHFYTPVWCGRINFIQT 174
QY 199 ILLFSRKVQDRAINIMGILVFWTFLELLALL-----FV-----PIQHOPLU 243
DB 175 FLLFSKREVPRALNFAgilVFWTFPLVVSCLPWPBPFVFTGTVTALQHOFTL 234
QY 244 NHLAENTLYXG 253
DB 235 NHFADVYG 244
RESULT 13
AAG53862
ID AAG53862 standard; Protein; 353 AA.
AC AAG53862;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68614.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0128845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
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PR 14-MAY-1999; 99US-0134321.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
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PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
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PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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PR 08-JUN-1999; 99US-0138094.
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PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 17-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139889.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142883.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.

PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149829.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 56.1%; Score 739; DB 21; Length 353;
Best Local Similarity 55.2%; Pred. No. 9, 6e-74;
Matches 138; Conservative 35; Mismatches 55; Indels 22; Gaps 3;

QY	19	SSDRKRLGPSLSALNLFNRKHTTSLLSLTLFLPLSVGVLPFSDSTFVAVLSAALLIGF	78
Db	2	AAERK-----LGLFENKGVTLTYTLAFVAAFLGVLYGVLACTSVFAHOIAAALIGL	54
QY	79	LWISQGNIGHDSGHVYVWLSRRLNRAIQTLSGNITLAGISIGWKNVNAHHIACNSLDYD	138
Db	55	LWISQAVIIGHDSGHVYVWLSRRLNRAIQTLSGNITLAGISIGWKNVNAHHIACNSLDYD	111
QY	139	PDLOHMFVFPVSSRFNSITSHXKYGKKEPDXIAMFLICYQHFTFYPMVCARVNLVLOT	196
Db	115	PDLOHMFVFPVSSRFNSITSHXKYGKKEPDXIAMFLICYQHFTFYPMVCARVNLVLOT	174
QY	199	ILLFSKXKQDADALNIMGLVFWTWFLFLALL-----FV-----PIQHIOFWL	241
Db	175	FLILFSKXKQDADALNIMGLVFWTWFLFLALL-----FV-----PIQHIOFWL	233
QY	244	NHLAENLYXG 253	
Db	235	NHFAADYYVG 244	
RESULT 14			
AA	38455	AAAR98455 standard; Protein; 448 AA.	
XX	AA	AAAR98455;	
XX	AC	AAAR98455;	
XX	DT	15-SEP-1996 (first entry)	
XX	DE	Borage delta-6-desaturase.	
XX	KM	Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;	
XX	KM	polyunsaturated fatty acid; octadecatetraenoic acid;	
XX	OS	chilling resistance; oilseed.	
XX	OS	Borage officinalis.	
XX	FT	Key	Location/Qualifiers
XX	FT	Region	156..163
XX	FT	Region	/label= Lipid_box
XX	FT	Region	196..200
XX	FT	Region	/label= Metal_box-1
XX	FT	Region	372..377
XX	FT	Region	/label= Metal_box-2
XX	PN	WO9621022-A2.	
XX	PD	11-JUL-1996.	
XX	PF	28-DEC-1995; 95WO-1B01167.	
XX	PR	30-DEC-1994; 94US-0366779.	
XX	PA	(RHON) RHONE POULENC AGROCHIMIE.	
XX	PI	Freyssinet GI, Nuccio M, Nunberg AN, Reddy AS, Thomas TL;	
XX	DR	WPI: 1996-333997/33.	
XX	DR	N-PSDB; AAT30395.	
XX	PT	Transgenic plants comprising the borage delta-6-desaturase gene	-
XX	PT	show increased production of gamma linolenic acid and having	
XX	PT	increased resistance to chilling	
XX	PS	Claim 3; Page 52-53; 75pp; English.	
XX	CC	Borage delta-6-desaturase (AAAR98455) catalyses the conversion of	
XX	CC	linoleic acid to gamma-linolenic acid (GLA). Its sequence was	
XX	CC	deduced from that of the delta-6-desaturase gene (AAT30395) isolated	
XX	CC	from a borage membrane-bound polysomal library. The sequence is	
XX	CC	distinct from that of Synecchocystis delta-6-desaturase (AAAR98455).	
XX	CC	Expression of the desaturase in transgenic plants, esp. sunflower,	
XX	CC	soybean, maize, tobacco, peanut, carrot or oilseed rape, results in	

CC	increased GJA prodn. Alteration of the plant membrane lipids as a
CC	result of expression of the desaturase may also result in increased
CC	resistance to chilling.
XX	
XX	
SQ	Sequence 448 AA;
Query Match	55.4%; Score 730.5; DB 17; Length 448;
Best Local Similarity	48.9%; Pred. No. 1.1e-72;
Matches 131; Conservative	50; Mismatches 72; Indels 15; Gaps 2
QY	1 LPAFSSHRSLDHTVSAASDDYRKLFDLSALNLFNRKGHTTSILSLTLPLPSYCGV 60
DB	72 LDFEFYGYLYKXSYSEVSKDYLKVFPEFSKMGLYDKKGHLMFATLCLIALFLFMSVYGV 133
QY	61 LPSDSTFVHVLSAALIGFLMIQSGNIHDSGHYVMLSRLNRAIQLISGNIAGISIGW 120
DB	132 LPCEGVVHLFSGCLMGFLMIQSGNIGHDAGHYVMVDSRLNKKMGIFPAANCISGISIGW 191
QY	121 WKNNHNAHHIACNSLDYDPDLQHMVPAVPSSEFNSISHXGKXKERDXIAXFLICYOH 180
DB	192 WKNNHNAHHIACNSLEYDPDLQYIFPLVAVSKFSGSLTSHFYEKRLTFDLSLRFVSIOH 251
QY	181 FTFEYPMVCARVAVLYLQTLILLFSSXKYQDRAINIMIGLIVFWTFP-----L 226
DB	252 WTFEYPMCAARLNMVYQSILMLTLGRNVSYRAQELGCLGVSTIVYPLLVSCLPWWGERIM 311
QY	227 FLTLALLFVP-IOHIOFWLNHIAENLYXG 253
DB	312 FVIALSLVTGMQOVQFSLNHFSSSYVG 339
RESULT 15	
AAW67471	
ID	AAW67471 standard; Protein; 448 AA.
XX	
XX	AAW67471;
XX	
AC	
XX	
DT	02-MAR-1999 (first entry)
XX	
DE	Borage delta-6 desaturase protein.
XX	
KW	Upstream region; regulatory region; sunflower; albumin; seed; expression.
KM	lipid metabolism; delta-6 desaturase; transgenic plant.
XX	
OS	Borage officinalis.
XX	
PH	Key
FT	Region
FT	Location/Qualifiers
FT	/note= "cytochrome b5 haem-binding motif"
FT	Domain
FT	/note= "His-rich metal binding motif"
FT	Domain
FT	/note= "His-rich metal binding motif"
FT	Domain
FT	/note= "His-rich metal binding motif"
XX	
PN	W09845460-AI.
XX	
PD	15-OCT-1998.
XX	
PF	09-APR-1998; 98WO-US07178.
XX	
PR	09-APR-1997; 97US-0831570.
XX	
PA	(RHON) RHONE-POULENC AGROCHIMIE.
XX	
PL	Beremand PD, Nunberg AN, Thomas TL;
XX	
DR	WPI; 1998-583201/49.
DR	N-PSDB; AAV34398.
XX	
PT	New sunflower albumin 5' regulatory region - useful for directing altered lipid metabolism in plant seeds

Db 266 LSMLOSIFVSGMPTHYDYNTAIYEQ----VGLSLHMAWSLGQLYFLPDMSTRIME 321

Qy 234 VPIQHI--OPWLNHL 246

Db 322 FLVSHLVGFLSHV 336

RESULT 8

H88791

protein T13F2.1 (imported) - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001

C/Accession: H88791

R/Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A/Reference number: A75000; MUID:99069613; PMID:9851916

A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.ele

A/Note: published extrata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A/Accession: H88791

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-454 <STO>

A/Cross-references: GB:chr_IV; PIDN:CAB03352.1; PID:93879828; GSPDB:GN00022; CESP:T13F2.

C/Genetic:

A/Map position: 4

C/Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase

Query Match 14.3%; Score 188; DB 2; Length 454;

Best Local Similarity 24.4%; Pred. No. 2.8e-10;

Matches 64; Conservative 43; Mismatches 101; Indels 54; Gaps 11;

Qy 19 SSDYRKLFSDL-----SALNPNKRGHTTSLILSLILFLPUSVCGULFSDSTFVHLV--- 71

Db 102 SAQINKSFDTLRKVRABGLMD--GSDPLFYRKLETFITF-----ILFAVLYOYHTYLP 154

Qy 72 SALIGFLWIGSGWIGDGHVNVMLSRRLNRAIQLSGNLA-----GISIGWKKM 124

Db 155 SALMGVAMQOLGMLIEFPAHQLFKRYNDLASIVGVFLVSHFNNQFSGCKKEQ 214

Qy 125 HNAHHTACNSLDYDPLQHPVFAVSSRFNSITSHXGKKEFDXIAFLICYHFTFY 184

Db 215 HNVHAAATNVVGRDGLDLPFVATVAEHNNYSQ-----DSVWMLTFRQHVHWT 265

Qy 185 PWCVARVNLVLTITLL-----FSRXKQDQALIMGLVWTFPL---FL-- 228

Db 266 FMLPFLSLWLSIIFVSGMPTHYDYNTAIYEQ----VGLSLHMAWSLGQLYFLPD 321

Qy 229 --LALLFVPIQHI--OPWLNHL 246

Db 322 WSTRIMEFLVSHLVGFLSHV 343

RESULT 9

JG0180

Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000

C/Accession: JG0180

R/Aki, T.; Shimada, Y.; Inagaki, K.; Higashimoto, H.; Kawamoto, S.; Shigeta, S.; Ono, K.

Biochem. Biophys. Res. Commun. 255, 575-579, 1999

A/Title: Molecular cloning and functional characterization of rat delta-6 fatty acid des

A/Reference number: JG0180; MUID:99160394; PMID:10049752

A/Accession: JG0180

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-444 <AKI>

A/Cross-references: DDB:AB021980; NID:94514721; PIDN:BA075496.1; PID:94514722

C/Superfamily: cytochrome b5 core homology

C/Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid biosynthe

F;18-94/Domain: cytochrome b5 core homology <CBS>

F;53,76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 12.9%; Score 170; DB 2; Length 444;

Best Local Similarity 24.9%; Pred. No. 1.4e-08;

Matches 64; Conservative 33; Mismatches 114; Indels 46; Gaps 8;

Qy 16 SAASDYRKLFSDLSALNPNKRGHTTSLILSLITL-----PPLSVCGULFSDSTFVHV 70

Db 107 SQTEDFRALKKTAEDMNLFTKTNHLFFPILLSHIIWESIAPILS-----YFGNGMIPTV 162

Qy 71 LSMALGFLMIGSGWIGDGHVNVMLSRRLNRAIQLSGNLAIGISIGWKKNNAAHNI 130

Db 163 ITAFVILATSOAQAGWLQHDHYGHLISVYKKSIMNIIHVKFVIGHLKGSANWNNRHFOHNA 222

Qy 131 ACSNLDYDPLQHPVFAVSSRFNSITSHXGKKEFDXIAFLICYHFTFYVWCVVA 190

Db 223 KPIHFKDPIKSLAHFVL-----GEMQPEYCKK---KTKLPNNHQHEVFFLGPP 273

Qy 191 RVNLYL--QTILLFSRXKQVORA-----LNIWGLVWTFWFLPLALL 232

Db 274 LIEMVFOYQIMTMRIRRDVLDLWALISYARFITYIPFYGILGALVFLNFRFLSHW 333

Qy 233 FVPIQHIQFW--LNLHL 246

Db 334 FV-----WVTQNMHI 343

RESULT 10

T13155

linoleoyl-CoA desaturase (EC 1.14.19.3) [validated] - human

N/Alternate names: Delta6 fatty acid desaturase; protein DKFZp586C201.1

C/Species: Homo sapiens (man)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 03-Jun-2002

C/Accession: T13155; T08765

R/Cho, H.P.; Nakamura, M.T.; Clarke, S.D.

J. Biol. Chem. 274, 471-477, 1999

A/Title: Cloning, expression, and nutritional regulation of the mammalian Delta-6 desatu

A/Reference number: Z16712; MUID:99085046; PMID:9867867

A/Accession: T13155

A/Status: preliminary; translated from GB/EMBL/DDJ

A/Molecule type: mRNA

A/Residues: 1-444 <CHO>

A/Cross-references: EMBL:AF126799; NID:94406527; PID:94406528; PIDN:AAD20018.1

R/Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, March 1999

A/Reference number: Z16471

A/Accession: T08765

A/Molecule type: mRNA

A/Residues: 'RTRG', 138-428, 'D', 430, 'W', 432-444 <WAM>

A/Cross-references: EMBL:AL050118

A/Experimental source: adult uterus; clone DKFZp586C201

C/Genetic:

A/Gene: GDB:FADS6

A/Residues: GDB:9956652

A/Cross-references: GDB:9956652

A/Note: DKFZp586C201.1

C/Superfamily: cytochrome b5 core homology

C/Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; unsaturated fatty

F;18-94/Domain: cytochrome b5 core homology <CBS>

F;53,76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 12.3%; Score 162; DB 2; Length 444;

Best Local Similarity 23.7%; Pred. No. 8.5e-08;

Matches 60; Conservative 39; Mismatches 116; Indels 38; Gaps 8;

Qy 16 SAASDYRKLFSDLSALNPNKRGHTTSLILSLITLFLPUSVCGULFSDSTFVHLV-SAA 74

Db 107 SKTIEDFRALKKTAEDMNLFTKTNHLFFPILLSHIIWESIAPILS-----YFGNGMIPTV 166

Qy 75 LIQFLMIGSGWIGDGHVNVMLSRRLNRAIQLSGNLAIGISIGWKKNNAAHNIACNS 134

Db 167 VLTATSOAQAGWLQHDHYGHLISVYKKSIMNIIHVKFVIGHLKGSANWNNRHFOHNAKPN 226

Qy 135 LDYDPLQHPVFAVSSRFNSITSHXGKKEFDXIAFLICYHFTFYVWCVARVNL 194

Db 227 FHKDPDVNMLHVFVLSG--WQPI---EYGRK---KIKYLPYNHGHYFPLIGPPLIIPM 277
 QY 195 YL--QTLLLFSSRXKYQDRA-----LNINGILVFWTWFLFLALLFVPI 236
 Db 278 YFQYQIIMTIVIKHWMDLMAVSYIRFTYITPFYIGLALLFLNFIPLFSHWV-- 335
 QY 237 QHIOFW--LNHL 246
 Db 336 -----WYQMNHI 343

RESULT 11
 T36617
 Probable Delta6 fatty acid desaturase (EC 1.14.99.-) SCH35.42c [similarity] - Streptomyces
 C/Species: Streptomyces coelicolor
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
 C/Accession: T36617
 R/Oliver, K.; Hartley, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, June 1999
 A/Reference number: Z21610
 A/Accession: T36617
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-345 <OLI>
 A/Cross-references: EMBL:AL078610; PIDN:CA844385.1; GSPDB:GN00070; SCOEDB:SCH35.42c
 A/Experimental source: strain A3(2)
 C/Genetics:
 A/Gene: SCOEDB:SCH35.42c
 C/Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 11.9%; Score 157; DB 2; Length 345;
 Best Local Similarity 23.7%; Pred. No. 2e-07;
 Matches 55; Conservative 47; Mismatches 104; Indels 26; Gaps 7;

QY 20 SDYRKFSDSLALNFKRHTTISLILTLFPLSVCCVLFSDTFVHLSAALIGFL 79
 Db 15 SDFARLSKRVADAGLGRPGYTLRTAVTGLYAGMAFVLYGASWTLATAAFVAVM 74
 QY 80 WISGWIHGDSGHYNWLSRLRAIQLISGNILA--GISIGMKWNHNAHHIACNSLD 136
 Db 75 YGVALVAMHARQVFRRRRAS---LSGRIGASIGMSYGMWDKTRHHANPTED 130

QY 137 YDDDL-QHMFVAVSSRFNSITSHXGRKKEFDXIXFLICYHFTFVPMCVARVNL 195
 Db 131 LDDPDIIGDLVWSPDQARATGLPRLGR-----WQAFIFFLTLLEGFNHL 177

QY 196 LQITLLLFSSRXKYQDRAINIMGLIVFWTWFLFLALLFV--PIQHIOFWNLH 245
 Db 178 VASGRAMANR-RUKRRALD--GALLLHACAVVLTALFWVLPFGMAIFLAVH 226

RESULT 12
 S35157
 Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - Synecocystis sp.
 C/Species: Synecocystis sp.
 C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
 C/Accession: S35157; S76243
 R/Reddy, A.S.; Nucchio, M.L.; Gross, L.M.; Thomas, T.L.
 Plant Mol. Biol. 22, 293-300, 1993
 A/Title: Isolation of a Delta(6)-desaturase gene from the cyanobacterium Synecocystis
 A/Reference number: S35157; MUID:93283633; PMID:8389613
 A/Accession: S35157
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-359 <RED>
 A/Cross-references: GB:L11421; NID:G349562; PIDN:AAA27286.1; PID:G349563
 R/Kaneke, T.; Sato, S.; Kocani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
 A/Reference number: S74322; MUID:97061201; PMID:8905231
 A/Accession: S76243

A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-359 <KAN>
 A/Cross-references: EMBL:D90914; GB:AB001339; NID:G1653477; PIDN:BAH16502.1; PID:d101923;
 A/Experimental source: PCC 6803
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C/Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 8.6%; Score 114; DB 2; Length 359;
 Best Local Similarity 20.1%; Pred. No. 0.0027;
 Matches 45; Conservative 39; Mismatches 76; Indels 64; Gaps 8;

QY 37 RKCHTTSILSLITLPLSVCG-VLPSDSTF-----VHVSALIGFLMIOGWIHGD 89
 Db 34 QRNPSPMYLKITLIVLMLFSAMAFVFAVIFPVRLGGCVLALAAAF-----SPNVGHD 89

QY 90 SGHYVWLSRLRAIQLISGNILAGISIGWKKWNN-AHHIACNSLDVD----- 138
 Db 90 ANHNAVSSNPHINRVGMTVD--FVGLSSFLMKRYRHYLHHTYTNLIGHDVEIHDGAVR 147

QY 139 --PDQHMVFVAVSSRFNSITSHXGRKKEFDXIXFLICYHFTFVPMCVARVNL 196
 Db 148 MSPEQEHVGIYR-----FQOFYIWGLYLFIPYFWFL 178

QY 197 QTLLLFSSRXKYQDRA-----NINGILVFWTWFLFLALL 231
 Db 179 YDVYLVLNKKGKXHDHKKIPFQPLELASLIGIKLWLGYYFGFLP 222

RESULT 13
 F71969
 hypothetical protein jhp0131 - Helicobacter pylori (strain J99)
 C/Species: Helicobacter pylori
 A/Variety: strain J99
 C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Aug-1999
 R/Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
 Ives, C.; Gibson, R.; Moberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
 Nature 397, 176-180, 1999
 A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
 A/Reference number: A71800; MUID:99120557; PMID:9923682
 A/Accession: F71969
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-482 <ARN>
 A/Cross-references: GB:AE001452; GB:AE001459; NID:G4154639; PIDN:AAD05710.1; PID:G4154643
 A/Experimental source: strain J99
 C/Genetics:
 A/Gene: jhp0131
 C/Superfamily: 2-oxoglutarate/malate translocator

Query Match 8.4%; Score 110.5; DB 2; Length 482;
 Best Local Similarity 25.8%; Pred. No. 0.0081;
 Matches 67; Conservative 36; Mismatches 72; Indels 85; Gaps 15;

QY 28 DSLANLFPNRKHTTISLILTLPLSVCCVLFSDTFVHLSAAL-----GFLWIO 82
 Db 264 ELESWGRFSLKE-----ILMLSTL--LALLGWIFFKSGSLASAVALLVMVMAACKYV 316

QY 83 SGWIGDSGHYNWLSRLRAIQLISGNIL--AGI-SIGWKKWNHNAHHIACNSLDY- 137
 Db 317 S-----YEDITKSKAFNIFLLGSLITMAGLKKVGPANFGNA---AQNLEHA 364

QY 138 --DP--DLQHMVFVAVSSRFNSITSHXGRKKEFDXIXFLICYHFTFVPMCVARV 192
 Db 365 HLDPLIAVFIYALFYLSHPASTAIVASA-----LPALFVIGSSH-----IOGV 410

QY 193 NLYIQITLLLFSSRXKYQDRAINIMGLIV-----PWTW-----FLF 227
 Db 411 NLYQELSLFLMLDS-----LGIMGILTPYGTGSPSTIYVGSYIGSKDPKMGKGFIFGFLY 462

QY 228 LVALFVPIQHIOF-----WL 243

Db 463 LIVL5VCAPEWVFIAYRML 482

RESULT 14

552650 omega-3 fatty acid desaturase (EC 1.14.99.-) - *Synechocystis* sp. (strain PCC6803)

N/Alternate names: delta 15 desaturase

C/Species: *Synechocystis* sp.

A/Variety: PCC 6803

C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C/Accession: S52650; S75843

R/Sakamoto, T.; Los, D.A.; Higashi, S.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.

Plant Mol. Biol. 26, 249-263, 1994

A/Title: Cloning of omega-3 desaturase from cyanobacteria and its use in altering the de

A/Reference number: S52649; MUID:95035996; PMID:7504725

A/Accession: S52650

A/Molecule type: DNA

A/Residues: 1-359 <SAK>

A/Cross-references: GB:D13780; NID:9600596; PIDN:BA02924.1; PID:9600598

A/Note: the authors translated the initiation codon GTG for residue 1 as Val

R/Kaneho, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shino, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A/Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

s.

A/Reference number: S74322; MUID:97061201; PMID:8905231

A/Accession: S75843

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-359 <KAN>

A/Cross-references: EMBL:D90913; GB:AB001339; NID:91653348; PIDN:BA018302.1; PID:9165338

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C/Genetic:

A/Start codon: GTG

C/Superfamily: omega-3 fatty acid desaturase

C/Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 8.1%; Score 107; DB 2; Length 359;

Best Local Similarity 21.9%; Pred. No. 0.013;

Matches 51; Conservative 32; Mismatches 100; Indels 50; Gaps 9;

QY 46 LSILTLFPLPVSQGVLFSDSTFVHLSAALLIGFLWIGSGWIGHDSGHYNMLSRRRLRAI 105

Db 51 VGLIAGFYALAA---YLDWMFYPFIPWLIQGLFMSLFFVGHDCGHSFSKSTLNWI 106

QY 106 QILSGNIIAGISIGWKKMNNNAHIIACNSLDYDPDLQHPVAVSSRFNSITSHXGRK 165

Db 107 GHLSHTPIL-VPYHGMKISHRTHANTGIDTDES-----WYPVSEOKYNQM 152

QY 166 XEFDXIAFX---LICV-----QHFTFYPVMCVARVNLVLTILLFSRXKQDR 211

Db 153 AWTEKLRFLPLAIPIYIFRSPNROSHFMGSPFPRGEKAVLITSTFALAA--- 208

QY 212 ALNIMGILVFWTW---FLFLALLFVPIQHIFW-----LNHLAENTL--YXG 253

Db 209 ---FVGFLGLFTWQFGWLFLKRYVAIVLVFWMLDVLTHHTEDNIPIWYRG 258

RESULT 15

T07687

omega-6 desaturase FAD2-1, microsomal - soybean

C/Species: Glycine max (soybean)

C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-May-2000

C/Accession: T07687

R/Hepard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H.

Plant Physiol. 110, 311-319, 1996

A/Title: Developmental and growth temperature regulation of two different microsomal omeg

A/Reference number: Z16095; MUID:96151506; PMID:8587990

A/Accession: T07687

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Experimental source: seed

C/Genetics:

A/Gene: FAD2-1

C/Function:

A/Description: involved in production of polyunsaturated lipids; plays a major role in c

A/Note: strongly expressed in developing seeds

C/Superfamily: omega-3 fatty acid desaturase

Query Match 7.8%; Score 103; DB 2; Length 387;

Best Local Similarity 20.1%; Pred. No. 0.034;

Matches 52; Conservative 37; Mismatches 88; Indels 82; Gaps 11;

QY 43 SILSLITLFPVSQGVLFSDSTFVHLSA--ALIGF--LWIOSG-----W-IGHDSG 91

Db 53 SLTSTSYVYDLSFAFIFVIATYTHLHPQPSLAWPIYWLQGCCLLTGVVVIHNEG 112

QY 92 HYNVMSRLRLRAIQILSGNIIAGISIGWKKMNNNAHIIACNSLDYDPDLQHPM 145

Db 113 HHAFSKYQWVDVVGTLSTLL-VYPSWKISHRHHNTGSLDRDEVFVPRKSKVAM 171

QY 146 -----VPAVSSRFNSITSHXGRKXERDIAFLICV 178

Db 172 FSKYLNPLGRAVSLVLTITGMPYLAIFNVSGRPYDSPA 213

QY 179 QHFTFYPVMCV---ARVNLVLTILLFSPRXKVDRAINMGILVFWTWFLFLALLFY 234

Db 214 ---YHPAPVYSNRERLLIYSDV-ALPSVYSLRVATIGLV--WLCVGVPLLV 266

QY 235 P-----IQHIFQFWLNH 245

Db 267 NGFLVTITVLOHTHFALPH 285

Search completed: January 1, 2004, 06:39:41

Job time : 10.5223 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 5.5668 Seconds

(without alignments)
2137.240 Million cell updates/sec

Title: US-09-857-524B-6

Perfect score: 1318
Sequence: 1 LPAFSTSHRLSDHTVSASS.....VPIQHIQFWLNLHAENLYXG 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	12.1	444	1	FADS_BRARE
2	114	8.6	359	1	LICD_SYNY3
3	111.5	8.5	400	1	FDI2_MORIS
4	110.5	8.4	400	1	FDI2_MORIS
5	103	7.8	387	1	FDI2_MORIS
6	100.5	7.6	242	1	CRTW_AUCSP
7	99.5	7.5	242	1	CRTW_AUCSP
8	97	7.4	549	1	COX1_LETTA
9	94.5	7.2	334	1	DUFF_MOUSE
10	94	7.1	522	1	NUC7_CABEL
11	89.5	6.8	375	1	D12_GREAL
12	87	6.6	424	1	FDI2_MORIS
13	87	6.6	448	1	FDI2_MORIS
14	86	6.5	500	1	UHPB_ECOLI
15	85.5	6.5	379	1	FDI2_MORIS
16	85	6.4	643	1	NUC7_CABEL
17	84	6.4	302	1	Y195_VIBCH
18	84	6.4	443	1	FDI2_MORIS
19	83.5	6.3	351	1	DESA_SPTL
20	83	6.3	549	1	COX1_TRYBA
21	81	6.1	339	1	RM11_ACACA
22	81	6.1	380	1	FDI2_MORIS
23	81	6.1	500	1	UHPB_ECOLI
24	80.5	6.1	383	1	FDI2_MORIS
25	80	6.1	591	1	COXN_BRAJA
26	79.5	6.0	374	1	Y006_BORBU
27	79.5	6.0	381	1	CYB_NORPE
28	79.5	6.0	446	1	FDI2_MORIS
29	79.5	6.0	802	1	YGN9_YEAST
30	79.5	6.0	1458	1	CUT4_SCHPO
31	79	6.0	380	1	FDI2_MORIS
32	79	6.0	2386	1	RAD3_SCHPO
33	78.5	6.0	447	1	FDI2_MORIS

34	78.5	6.0	505	1	YNN2_CABEL	P54246 caenorhabdi
35	78	5.9	628	1	Y135_MYCTU	O50598 mycobacteri
36	77.5	5.9	382	1	Y135_MYCTU	P47332 mycoplasma
37	77	5.8	382	1	YCAD_ECOLI	P21503 escherichia
38	77	5.8	547	1	NUC7_CABEL	P24884 ascaris suu
39	76.5	5.8	476	1	COX1_PLACH	O99255 plasmodium
40	76.5	5.8	519	1	ACH4_DROME	P25162 drosophila
41	76	5.8	303	1	T2RD_HUMAN	O9YV99 homo sapien
42	76	5.8	404	1	FDI2_MORIS	P48618 braesia na
43	75.5	5.7	359	1	ACOD_HUMAN	O00767 homo sapien
44	75.5	5.7	563	1	ARAB_YERPE	P58543 yerania pe
45	75.5	5.7	902	1	CLC2_CAVPO	O9W445 cavia porce

ALIGNMENTS

RESULT 1	ID	FADS_BRARE	STANDARD	PRT	444 AA
AC	O9DEX7				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Delta-5/delta-6 fatty acid desaturase (EC 1.14.19.-)				
GN	FADS2 OR PADS06				
OS	Brachydanio rerio (Zebrafish) (Danio rerio)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;				
OC	Cyprinidae; Danio				
OX	NCBI_TaxID=7955;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RX	MEDLINE=21592990; PubMed=11724940;				
RA	Hastings N., Agaba M., Tocher D.R., Leaver M.J., Dick J.R.,				
RA	Sargent J.R., Teale A.J.;				
RT	"A vertebrate fatty acid desaturase with delta-5 and delta-6				
RT	activities."				
RL	Proc. Natl. Acad. Sci. U.S.A. 98:14304-14309(2001).				
CC	-1- FUNCTION: Fatty acid desaturase with both delta-5 and delta-6				
CC	activities. May represent a component of the polyunsaturated fatty				
CC	acid biosynthesis pathway.				
CC	-1- PATHWAY: polyunsaturated fatty acid biosynthesis.				
CC	-1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.				
CC	-1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation-				
CC	the European Bioinformatics Institute. There are no restrictions on its				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
DR	EMBL: AR309556; ANG25710.1; -				
DR	HSSP: P00173; JUEX.				
DR	ZFIN: ZDB-GENE-011212-1; fads2.				
DR	InterPro: IPR001199; Cyt B5.				
DR	InterPro: IPR005804; FA desat fam.				
DR	Pfam: PF00487; FA desaturase; 1.				
DR	Pfam: PF00173; heme_1; 1.				
DR	ProDom: PD000612; Cyt B5; 1.				
DR	ProDom: PD001081; FA desat fam; 2.				
DR	PROSITE: PS00191; CYTOCHROME B5_1; FALSE_NEG.				
DR	PROSITE: PS02055; CYTOCHROME B5_2; 1.				
KW	Fatty acid biosynthesis; Oxidoreductase; Heme.				
FT	DOMAIN 18 95				
FT	FT				
FT	METAL 53 53				
FT	METAL 76 76				
SQ	SEQUENCE 444 AA; 52032 MW; 6AA25A1DC1DC0F65 CRC64;				
Query Match	12.1%; Score 159; DB 1; Length 444;				

Best Local Similarity 22.1%; Pred. No. 2.6e-07;
Matches 58; Conservative 42; Mismatches 118; Indels 44; Gaps 7;

QY 16 SAASDVRKLPFSDLSALNLRKQHTSILSLITLFPISVGVCSFSDSTFPAVLSAL 75
D 107 AAVEPFRALRELEAGCEKCTOPLPFALHGHILLLEAIPMMVWFYFGINTLLVAV 166
QY 76 I-GFLMISGIMIGDGHVYVMSRLNRAIQLISGNIAGISIGWKNNHNAHICNS 134
D 167 ILATAGSQAGMLQHDHGLSVFKTSGNNHLYHKVIGHLKGASAGMNNHNFQHHAKPN 226
QY 135 LDVDPDLQHPVFAVSSRFNSITSHYGRKKEPFIAXFLICYHFTFYVNCVAVNL 194
D 227 FKQDPVNMNANAFV-----GNQPVVEYGVK-----KIKHLPVNHQHKYFFIGPILLIPV 277
QY 195 YLQTLILFESRKKVQDAALIMGIL-----VFPT-----WEL 226
D 278 YFQ--FOIFNNMISHGMVVLMLWCISYVRYFLCYTQYGVFAAILFNFVREMSHFV 335
QY 227 FLTALFVPI-----QHIQFWLN 244
D 336 WVTQMSHIFPNWIDYKQDMIS 357

RESULT 2

LCSD_SYNY3 STANDARD; PRT: 359 AA.

AC Q08871;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Linoicoyl-CoA desaturase (EC 1.14.19.3) (Delta(6)-desaturase).
GN DSS6 OR SL120262.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93283633; PubMed=8389613;
RA Reddy A.S., Nuccio M.L., Gross L.M., Thomas T.L.;
RT "Isolation of a delta 6-desaturase gene from the cyanobacterium
RT Synechocystis sp. strain PCC 6803 by gain-of-function expression in
RT Arabidopsis sp. strain PCC 7120."
RL Plant Mol. Biol. 22:293-300(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugitara M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
CC -1- CATALYTIC ACTIVITY: linoicoyl-CoA + AH(2) + O(2) = gamma-
CC linoenoyl-CoA + A + 2 H(2)O.
CC -1- COFACTOR: IRON.
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CC -----
CC EMBL, L11421; AAA27286.1; -
CC DR EMBL, D90914; BAA1502.1; -
CC DR InterPro, IPR005804; FA desat fam.
CC Pfam, PF00487; FA desaturase_1.
CC ProDom, PD001081; FA_desat_fam; 1.

KM Oxidoreductase; Iron; Complete proteome.
SQ SEQUENCE 359 AA; 41425 MW; 33FB165AB98C05F CRC64;

Query Match 8.6%; Score 114; DB 1; Length 359;
Best Local Similarity 20.1%; Pred. No. 0.0028;
Matches 45; Conservative 39; Mismatches 76; Indels 64; Gaps 8;

QY 37 RKCHTSSILSLITLFPISVCG-VLPSDSTF-----VHVSALIGFLMISGIMIGHD 89
D 34 QRDNPSEMYLKTLLIYVLFESANAFVLPFAVIFPVRLGCGVLAIALAF-----SFVGH 89
QY 90 SGHYVMSRLNRAIQLISGNIAGISIGWKNNHNAHICNSLDVD----- 138
D 90 ANHNNAVSNPHINRVLGMTYD--FVGLSSFLMRRYRNNLHHTVTNLIGHDVEIHGDGAVR 147
QY 139 --PDLOHMPVFAVSSRFNSITSHYGRKKEPFIAXFLICYHFTFYVNCVAVNL 196
D 148 MSPBOEHVGIYR-----FQGFYIWLGLYLFIPYWEFL 178
QY 197 QTLILFESRKKVQDAALIMGIL-----NIMGILVFWTFLPLAL 231
D 179 YDYLVLANKKTHDKIPPEPPLSLGLIKLMIGYFGPL 222

RESULT 3

FD12_MORAP STANDARD; PRT: 400 AA.

AC Q918H5; Q96TH3; Q9UVV4;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Delta-12 fatty acid desaturase (EC 1.14.99.-).
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;
OC Mortierellaceae; Mortierella.
OX NCBI_TaxID=64518;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RX STRAIN=1S-4;
RX MEDLINE=99234062; PubMed=10215899;
RA Sakurada B., Kobayashi M., Ashikari T., Shimizu S.;
RT "Identification of delta12-fatty acid desaturase from arachidonic
RT acid-producing Mortierella fungus by heterologous expression in the
RT yeast Saccharomyces cerevisiae and the fungus Aspergillus oryzae."
RL Eur. J. Biochem. 261:812-820(1999).
RN [2]
RP SEQUENCE FROM N.A., AND FUNCTION.
RX STRAIN=ATCC 32221;
RX MEDLINE=99406036; PubMed=10478922;
RA Huang Y.-S., Chaudhary S., Thurmond J.M., Bobik E.G. Jr., Yuan L.,
RA Chan G.M., Kirchner S.J., McKerji P., Knutson D.S.;
RT "Cloning of delta12- and delta6-desaturases from Mortierella alpina
RT and recombinant production of gamma-linolenic acid in Saccharomyces
RT cerevisiae."
RL Lipids 34:649-659(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 16266;
RA Liu L., Li M., Xing L., Hu G.;
RT "Delta 12 fatty acid desaturase gene of Mortierella alpina."
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ database.
CC -1- FUNCTION: Catalyzes the desaturation of oleic acid (delta9-18:1)
CC to linoleic acid (delta9, delta12-18:2).
CC -1- PATHWAY: C20 polyunsaturated fatty acid biosynthesis.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- DOMAIN: The histidine box domains may contain the active site
CC and/or be involved in metal ion binding.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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DR EMBL: AB020033; BAAB1754.1; -
 DR EMBL: AF110509; AAF08684.1; -
 DR EMBL: AF117244; AAL13301.1; -
 DR GO: GO:0016491; F:oxidoreductase; IDA.
 DR GO: GO:0006633; P:fatty acid biosynthesis; IDA.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; Transmembrane; Repeat.
 FT TRANSMEM 91 111 POTENTIAL.
 FT TRANSMEM 199 219 POTENTIAL.
 FT TRANSMEM 245 265 POTENTIAL.
 FT TRANSMEM 277 297 POTENTIAL.
 FT DOMAIN 112 116 HISTIDINE BOX-1.
 FT DOMAIN 148 152 HISTIDINE BOX-2.
 FT DOMAIN 339 343 HISTIDINE BOX-3.
 FT CONFLICT 17 19 STS -> TTT (IN REF. 3).
 FT CONFLICT 21 23 APT -> PN (IN REF. 2).
 FT CONFLICT 95 95 A -> V (IN REF. 2).
 FT CONFLICT 107 107 I -> V (IN REF. 2).
 FT CONFLICT 179 179 N -> S (IN REF. 3).
 FT CONFLICT 180 182 AAA -> VAV (IN REF. 1).
 FT CONFLICT 261 261 A -> T (IN REF. 1).
 FT CONFLICT 280 280 V -> I (IN REF. 3).
 FT CONFLICT 358 358 Y -> Q (IN REF. 1).
 FT CONFLICT 392 392 H -> Q (IN REF. 2).
 SQ SEQUENCE 400 AA; 46001 MW; 40B2PC1C1E01F93F CRC64;

Query Match 8.5%; Score 111.5; DB 1; Length 400;
 Best Local Similarity 19.5%; Pred. No. 0.0053;
 Matches 58; Conservative 40; Mismatches 109; Indels 91; Gaps 13;

QY 2 PAESTHRLSDHTVSAASDYKRLPSDSLALNLFNRKHTTSLSLTLPLPSVGV 61
 DB 27 PAFERNYQLPEPTI-----KEIRICIPAHCEGSG-----LRGCHVAIDLTASLL 73
 QY 62 FSDSTFVHLVSAALIGFL-----WIOSG-----WI-GHDSGHVYVLSRLNRAIQILS 109
 DB 74 FLAATQIDKFNPLIRYLAMPAYWIMQIVCTGIVLWLAHECHGQSFTSKTLNN----- 127
 QY 110 GNLAGISIGW-----WKNNHNAHHIACNSLDYDPLQHPVFAVSSRF----- 153
 DB 128 -----TVGMILHSMVLVPHYSWRISHSKHKHATGHTKD-----QVFVPRKTSQVGL 174
 QY 154 -----FNSITSHXYGKKEFDXIAKFLICYQHTFTFPVVCV-----ARVNL 194
 DB 175 PKENAAAANVOEDMSVHL---DEEAPIVTLFPMVVOFLFGWPAYVLIIMNASGODYGRWTS 231
 QY 195 YIQTILLFSRXKQVDRALNIMGI-----LVFWTWFLFLAL---LVFPIQHIOFWL 243
 DB 232 HFTTSPIFEPNPFDIITSDGLVALGALIVASMQSLTLTKYTYIIVPLVFNFWL 289

RESULT 4
 FD12 MORIS
 ID FD12 MORIS STANDARD; PRT; 400 AA.
 AC P59668;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DE Delta-12 fatty acid desaturase (EC 1.14.99.-)
 OS Mortierella isabellina (Unbelonging to isabellina).
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
 OC Mucorales incertae sedis; Umbelopsis.
 NC NCBI_TaxID=91625;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=M6-22;
 RA Liu L., Li M., Xing L., Hu G.;

RT "Delta 12 fatty acid desaturase mRNA of Mortierella isabellina."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Catalyzes the desaturation of oleic acid (delta9-18:1)
 CC to linoleic acid (delta9, delta12-18:2) (By similarity).
 CC -1- PATHWAY: C20 polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- DOMAIN: The histidine box domains may contain the active site
 CC and/or be involved in metal ion binding.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

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DR EMBL: AF117245; AAL13301.1; -
 DR GO: GO:0016491; F:oxidoreductase; IDA.
 DR GO: GO:0006633; P:fatty acid biosynthesis; IDA.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; Transmembrane; Repeat.
 FT TRANSMEM 91 111 POTENTIAL.
 FT TRANSMEM 199 219 POTENTIAL.
 FT TRANSMEM 245 265 POTENTIAL.
 FT TRANSMEM 277 297 POTENTIAL.
 FT DOMAIN 112 116 HISTIDINE BOX-1.
 FT DOMAIN 148 152 HISTIDINE BOX-2.
 FT DOMAIN 339 343 HISTIDINE BOX-3.
 SQ SEQUENCE 400 AA; 46016 MW; F5512DP8210BBD2 CRC64;

Query Match 8.4%; Score 110.5; DB 1; Length 400;
 Best Local Similarity 19.1%; Pred. No. 0.0066;
 Matches 57; Conservative 41; Mismatches 109; Indels 91; Gaps 13;

QY 2 PAESTHRLSDHTVSAASDYKRLPSDSLALNLFNRKHTTSLSLTLPLPSVGV 61
 DB 27 PAFERNYQLPEPTI-----KEIRICIPAHCEGSG-----LRGCHVAIDLTASLL 73
 QY 62 FSDSTFVHLVSAALIGFL-----WIOSG-----WI-GHDSGHVYVLSRLNRAIQILS 109
 DB 74 FLAATQIDKFNPLIRYLAMPAYWIMQIVCTGIVLWLAHECHGQSFTSKTLNN----- 127
 QY 110 GNLAGISIGW-----WKNNHNAHHIACNSLDYDPLQHPVFAVSSRF----- 153
 DB 128 -----TVGMILHSMVLVPHYSWRISHSKHKHATGHTKD-----QVFVPRKTSQVGL 174
 QY 154 -----FNSITSHXYGKKEFDXIAKFLICYQHTFTFPVVCV-----ARVNL 194
 DB 175 PKENAAAANVOEDMSVHL---DEEAPIVTLFPMVVOFLFGWPAYVLIIMNASGODYGRWTS 231
 QY 195 YIQTILLFSRXKQVDRALNIMGI-----LVFWTWFLFLAL---LVFPIQHIOFWL 243
 DB 232 HFTTSPIFEPNPFDIITSDGLVALGALIVASMQSLTLTKYTYIIVPLVFNFWL 289

RESULT 5
 FD61 SOYBN
 ID FD61 SOYBN STANDARD; PRT; 387 AA.
 AC P48650;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DE Omega-6 fatty acid desaturase, endoplasmic reticulum isoform 1
 DE (EC 1.14.19.-).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

NCBI_TaxID=3847;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Seed;
 RX MEDLINE=96151506; PubMed=8587990;
 RA Hoppard E.P., Kinney A.J., Stecca K.L., Mao G.H.;
 RT "Developmental and growth temperature regulation of two different
 RT microosomal omega-6 desaturase genes in soybeans";
 RL Plant Physiol. 110:311-319(1996).
 CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
 CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS;
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
 CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN DEVELOPING SEEDS.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/ OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; L43920; AAB00859.1; -
 DR PIR; T07687; T07687.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR ProDom; PD001081; FA_desat_fam; 2.
 KM Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
 KW Transmembrane.
 FT TRANSMEM 54 74 POTENTIAL.
 FT TRANSMEM 87 107 POTENTIAL.
 FT TRANSMEM 121 141 POTENTIAL.
 FT TRANSMEM 183 203 POTENTIAL.
 FT TRANSMEM 227 247 POTENTIAL.
 FT TRANSMEM 251 271 POTENTIAL.
 FT DOMAIN 109 113 HISTIDINE BOX-1.
 FT DOMAIN 145 149 HISTIDINE BOX-2.
 FT DOMAIN 319 323 HISTIDINE BOX-3.
 FT DOMAIN
 SQ SEQUENCE 387 AA; 44662 MW; 49068805C21A1C31 CRC64;
 Query Match 7.8%; Score 103; DB 1; Length 387;
 Best Local Similarity 20.1%; Pred. No. 0.031;
 Matches 52; Conservative 37; Mismatches 88; Indels 82; Gaps 11;
 QY 43 SLLSLILTLFPLPSVCGVLFSDSTFVAVLSA--ALIGF--LWIOGQ-----W-IGHDSG 91
 DB 53 SLTFSFVVYVYDLSFAFIYATYFLLPQPSFLIMPIYVWVQGLGANGVIAIECG 112
 QY 92 HYVWMLSRRLRAQIISGNILAGISIGWKMNNNAHHIACNSLDYDPDQHM----- 145
 DB 113 HHAEKYQWDDVGLTLHSTLL--VPYFSWKISHRHHSNTGSLDRDEVFVPRKSKVAV 171
 QY 146 -----VFAVSRFFNSITSHXGXGRKXEPDIXFLICY 178
 DB 172 FSKYLNPLGRAVSLVLTITGMPMYLAFVNSGPRYSFASH----- 213
 QY 179 QHFTFVPMCV---ARVNLVLOTILLFSRXKQVDRALNMGILVFWTFLALLLFV 234
 DB 214 ---YHYPAPYISNRERLLIYSDV-ALFSVTYSLYNAVATLKGV--WLLCVGVPLLIIV 266
 QY 235 P-----IQHIGFNLNH 245
 DB 267 NGFLVITTYLOHTHFALPH 285

RESULT 6
 CRTW_ALCSP
 ID CRTW_ALCSP STANDARD; PRT; 242 AA.
 AC Q44261;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Beta-carotene ketolase (EC 1.13.--) (Beta-carotene oxygenase).
 OS Alcalligenes sp.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcalligenaceae; Alcalligenes.
 OX NCBI_TaxID=512;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95251715; PubMed=7733978;
 RA Misawa N., Kajiwara S., Kondo K., Yokoyama A., Satomi Y., Saito T.,
 RA Miki W., Ohnari T.;
 RT "Canthaxanthin biosynthesis by the conversion of methylene to keto
 RT groups in a hydrocarbon beta-carotene by a single gene";
 RL Biochem. Biophys. Res. Commun. 209:867-876(1995).
 CC -1- FUNCTION: CONVERTS BETA-CAROTENE TO CANTHAXANTHIN VIA ECHINENONE.
 CC -1- PATHWAY: CAROTENOID BIOSYNTHESIS. INVOLVED IN ASTAXANTHIN
 CC BIOSYNTHETIC PATHWAY.
 CC -----
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 CC -----
 DR EMBL; D58423; BAA09596.1; -
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR ProDom; PD001081; FA_desat_fam; 1.
 KM Carotenoid biosynthesis; Oxidoreductase.
 SQ SEQUENCE 242 AA; 26939 MW; 077DA83F4AAD14B4 CRC64;
 Query Match 7.6%; Score 100.5; DB 1; Length 242;
 Best Local Similarity 28.6%; Pred. No. 0.032;
 Matches 58; Conservative 19; Mismatches 71; Indels 55; Gaps 13;
 QY 39 GHTTSLLS-LITLPLPSVCGVLFSDSTFVAVLSA--ALIGFLWIOGQW--IGHDSGHY 93
 DB 17 GLTAAILLCVLAHATLWML-----DAAHPLVLAVLCLAGTMTLSVGLFIADHMMG 70
 QY 94 NVMLSR-RUNRAIOIISGNILAGISIGWKM--NHNNAHHIACNSLDYDPDQHM-MPVAV 149
 DB 71 SVVPRGRPRANNAIIGQALMLVYAGFS--WPKLIAKHTTHRHAGT--DNDDPFGHGV--- 124
 QY 150 SSRFFNSITSHXGXGRKXEPDIXFLICY-----QHFTFVPMCVARVNLVLOTILL 201
 DB 125 --RWYGSFVSTYVGWR-EGILLFVITVYVALIGDRMVMYVIEFVPVAV----- 169
 QY 202 LFSRXKQVDRALNMGILVFWTW 224
 DB 170 -----LSTIOIFVFGTW 181
 RESULT 7
 CRTW_AGRAU
 ID CRTW_AGRAU STANDARD; PRT; 242 AA.
 AC P54972;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Beta-carotene ketolase (EC 1.13.--) (Beta-carotene oxygenase).
 GN CRTW.
 OS Agrobacterium aurantiacum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 OX NCBI_TaxID=44155;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96062243; PubMed=7592436;
 RA Misawa N., Satomi Y., Kondo K., Yokoyama A., Kajiwara S., Saito T.,
 RA Ohnami T., Miki W.;
 RT "Structure and functional analysis of a marine bacterial carotenoid
 biosynthesis gene cluster and astaxanthin biosynthetic pathway
 proposed at the gene level."
 RL J. Bacteriol. 177:6575-6584 (1995).
 CC -1- FUNCTION: CONVERTS BETA-CAROTENE TO CANTHAXANTHIN VIA ECHINENONE.
 CC -1- PATHWAY: CAROTENOID BIOSYNTHESIS. INVOLVED IN ASTAXANTHIN
 CC BIOSYNTHETIC PATHWAY.
 CC -----
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 CC -----
 CC EMBL, D58420; BAA09591.1; -
 CC InterPro: IPR005804; PA_desat_fam.
 CC Pfam: PF00487; PA_desaturase; 1.
 CC ProDom: PD001081; PA_desat_fam; 1.
 CC Carotenoid biosynthesis; Oxidoreductase.
 KM SEQUENCE 242 AA; 27128 MW; 6AEB5BF60BE3D8 CRC64;
 SQ
 Query Match 7.5%; Score 99.5; DB 1; Length 242;
 Best Local Similarity 25.8%; Pred. No. 0.039;
 Matches 59; Conservative 30; Mismatches 77; Indels 63; Gaps 14;
 QY 27 SDLSANLFRKRGHTTSILS--LILPLPLSCGVFSDSTFVHLSAA-LIGFLMIQS 83
 DB 9 ADLTA-----TSLIVSGGIIAAMALHVAALFDDAAHPILAIANFGLTSLV 58
 QY 84 GM---IGHDSGHVWMLSR-RLNRAIQLSGNLAGISIGMKM--NHNAAHICNSLDYD 138
 DB 59 GLPIAHDAHGSVPRPANAAMGQVLMLVNGFS--WRKQIVKMAHRIAGT-DDD 115
 QY 139 PDLQHPFVAVSSRFNSITSHYXGKKEPDIXAFLICYOHTFYVPMCVARVNYLQT 198
 DB 116 PFDHGGPVMVYARFIST-----YFGW-----REGLLPV 145
 QY 199 LILFSKXKQDRAINMGLVPTWTFLLALLFPVQIHF--WLNH 245
 DB 146 IVTVYALI-LGDRWYV---VFWP-----LPSILASIQLFVGTWLP 184
 RESULT 8
 COXI_LEITA
 ID COXI_LEITA STANDARD; PRT; 549 AA.
 AC P14544;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Cytochrome c oxidase polypeptide I (EC 1.9.3.1).
 GN COI.
 OS Leishmania tarentolae (Saurioleishmania tarentolae).
 OG Mitochondrion.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85079995; PubMed=6096360;
 RA de la Cruz V.F., Neckelmann N., Simpson L.;
 RT "Sequences of six genes and several open reading frames in the
 RT kinetoplast maxicircle DNA of Leishmania tarentolae."
 RL J. Biol. Chem. 259:15136-15147 (1984).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE
 CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN

CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 CC AND COPPER B
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -1- PATHWAY: Respiratory chain; terminal step.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE. CONTAINS 12 POTENTIAL TRANSMEMBRANE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR PIR; D30010; D30010.
 DR HSSP; P18401; 1FFT.
 DR InterPro; IPR000883; COX1.
 DR Pfam; PF00115; COX1; 1.
 DR PRINTS; PR00165; CYCOXIDASE1.
 DR PROSITE; PS00077; COX1; 1.
 KW Oxidoreductase; Heme; Copper; Mitochondrion; Transmembrane;
 KW Respiratory chain; Inner membrane; Kinetoplast.
 FT METAL 243 243
 FT METAL 247 247
 FT METAL 292 292
 FT METAL 293 293
 FT METAL 378 378
 FT METAL 380 380
 FT CROSSLINK 243 247
 SQ SEQUENCE 549 AA; 63271 MW; F6DD04815A4917C2 CRC64;
 Query Match 7.4%; Score 97; DB 1; Length 549;
 Best Local Similarity 24.1%; Pred. No. 0.16;
 Matches 64; Conservative 40; Mismatches 108; Indels 54; Gaps 14;
 QY 23 RKLPSDLALNLFNRKHTTSILSLTLF---PLSCGVLPDSSTFVHLSAALIGF 78
 DB 176 RKFSEFLS-WSLPIAALITALLITLTPVLAVGVTLLCDNPNFSFDVVGGLILF 234
 QY 79 ---LWIOSGIGHDSGHVWML-----RLNRAIQLSGNLAGISIGMW 121
 DB 235 QHIFP---FPGHPE-VYIILPVGLISTIVYVGFRCVFSTVAMITYMILLAI-LGMF 288
 QY 122 KWNHNAHICNSLDYDPD-----LQHPFVAVSSRFNSITSHYXGKKEPDIXA 173
 DB 289 VM---AHMFVVGMDVDSRAVFGVSILGLPTCV---KLFWMIYSFLY---TDMIT 337
 QY 174 FLICYOHTFYVPMCVARVNYLQTI---LILFSKXKQDRA--ALNMGILVPTWTF 227
 DB 338 FEYVFIPIFIMFLIGAVTGLSLVNGIDIMLDYTFVGVGHVYLSLGAVVGFTGFIH 397
 QY 228 LIALFPVQIHFMLNHLAENLYXG 253
 DB 398 FLA-KWPIELLYLFWMFYISTLFTIG 422
 RESULT 9
 DUFF_MOUSE
 ID DUFF_MOUSE STANDARD; PRT; 334 AA.
 AC Q90U16; Q35970; Q91YB6; Q920X0; Q920X1; Q920X2; Q920X3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Duff antigen/chemokine receptor.
 GN FY OR DRY OR DARC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97458170; PubMed=9314499;
 RA Luo H., Chaudhuri A., Johnson K.R., Neote K., Zbrzezna V., He Y.,
 RA Pogo A.O.;
 RT "Cloning, characterization, and mapping of a murine promiscuous
 RT chemokine receptor gene: homolog of the human Duff gene."
 RL Genome Res. 7:932-941 (1997).

[2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA Touramille C., Colin Y.;
 RT "Murine skeletal muscle diffy antigen/receptor for chemokine
 RT glycoprotein (DARC).";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99449053; PubMed=10520743;
 RA Tang T., Owen U.D., Du Y., Walker C.L., Richmond A.;
 RT "Molecular cloning and characterization of a mouse gene with homology
 RT to the Duffy antigen receptor for chemokines.";
 RL DNA Seq. 9:129-143(1998).
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=BL/6J, B6W/2msf, C57BL/10SnJ, CAST/Ei, HMI/Msf, MSM/Msf,
 RC NUL/Msf, Pgn2, and SMN/Msf;
 RA Liu Y., Kitano T., Koide T., Shiotschi T., Moriaki K., Saitou N.;
 RT "Conspicuous differences among gene genealogies of 21 nuclear genes of
 RT five Mus musculus subspecies.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Krausner R.D., Collins F.S., Wagner L.H., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Cannini P., Prange C.,
 RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Vallajon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schmechel A., Schein J.E., Jones S.J.M., Matra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN
 RP FUNCTION: Non-specific receptor for many chemokines (By
 RP similarity).
 CC
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in liver and brain.
 CC
 CC -1- SIMILARITY: BELONGS TO FAMILY DUPLY OF G-PROTEIN COUPLED
 CC RECEPTORS.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: AF016697; AAC53360.1; -
 DR EMBL: AF016584; AAC53354.1; -
 DR EMBL: AF109159; AAF14225.1; -
 DR EMBL: U88431; AAF08328.1; -
 DR EMBL: AB039074; BAB68598.1; -
 DR EMBL: AB039075; BAB68599.1; -
 DR EMBL: AB039076; BAB68600.1; -
 DR EMBL: AB039077; BAB68601.1; -
 DR EMBL: AB039078; BAB68602.1; -
 DR EMBL: AB039079; BAB68603.1; -
 DR EMBL: AB039080; BAB68604.1; -
 DR EMBL: AB039081; BAB68605.1; -
 DR EMBL: AB039082; BAB68606.1; -

DR EMBL: BC005583; AAH05583.1; -
 DR MGD: MG1:1097689; DfY.
 DR GO: GO:0006954; P:inflammatory response; IMP.
 DR InterPro: IPR005384; Duffantigen.
 DR PRINTS: PR01559; DUFFYANTIGEN.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
 DR
 FT DOMAIN 1 61
 FT TRANSMEM 62 82
 FT DOMAIN 83 93
 FT TRANSMEM 94 114
 FT DOMAIN 115 124
 FT TRANSMEM 125 145
 FT DOMAIN 146 164
 FT TRANSMEM 165 185
 FT DOMAIN 186 205
 FT TRANSMEM 206 226
 FT DOMAIN 227 242
 FT TRANSMEM 243 263
 FT DOMAIN 264 285
 FT TRANSMEM 286 306
 FT DOMAIN 307 334
 FT CARBOHYD 16 16
 FT CARBOHYD 26 26
 FT CARBOHYD 32 32
 FT CARBOHYD 285 285
 FT VARIANT 10 10
 FT VARIANT 56 56
 FT VARIANT 61 61
 FT VARIANT 76 76
 FT VARIANT 178 178
 FT VARIANT 188 188
 FT VARIANT 194 194
 FT VARIANT 207 207
 FT VARIANT 221 221
 FT VARIANT 256 256
 FT VARIANT 268 268
 SQ SEQUENCE 334 AA; 36693 MW; 21AC4B6147D840C8 CRC64;
 Query Match 7.2%; Score 94.5; DB 1; Length 334;
 Best Local Similarity 21.7%; Pred. No. 0.16; 86; Indels 77; Gaps 12;
 Matches 55; Conservative 35; Mismatches 86; Indels 77; Gaps 12;
 QY 11 SDHTVNASSDYKRLFSDSLALNLFNRKG-----HTSILSLILTLFPLSV-----58
 DB 39 SDVSLTPAACVSCNLDRLSLEPMLTSLVGLMAGSLIFALRPFHMQICSPPIIA 98
 QY 59 -----GVLFSDSTFV-----HVLSAALIGFLWIOSGWTIGDGHYVM-----LS 98
 DB 99 ELAVGSLFSAIVPIIAPLPGLSHSHSTALCNIGY-----WVWYTSAPQAALLIGCYACLN 152
 QY 99 RLRLRAIQLISGIIAGISIGMKKNNHNAHICNSLDYDPLQIHMPVPVAVSSRFRNSIT 158
 DB 153 PRLN--IGQIRGFTL-GLSLVGLNG-----AAALSGLPV-ALADVYNGFC 193
 QY 159 SHXYGRKXEPDXIAXFLICVQHTFFYPVVCVAVNLYLTITLLFSRXKQVDAALNMG- 217
 DB 194 TPSSRDMEALKTHYALCTITFTVPLTILAAKGLKI-----ALS-KGP 237
 QY 218 ---ILVFWTWLFP 227
 DB 238 GPMVSVLMWIF 250

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RESULT 10
ID UNCT CAEBL STANDARD; PRT; 522 AA.
AC 003412;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inexin unc-7.
GN UNC-7 OR R07D5.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peleoderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN 11
RC SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=93202469; PubMed=7681023;
RA Starich T.A., Herman R.K., Shaw J.E.;
RT "Molecular and genetic analysis of unc-7, a Caenorhabditis elegans
RT gene required for coordinated locomotion.";
RL Genetics 133:527-541(1993).
RN 12
RC SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Smve R.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: STRUCTURAL COMPONENTS OF THE GAP JUNCTIONS. REQUIRED FOR
CC COORDINATED LOCOMOTION.
CC -1- SUBUNIT: HETEROOLIGOMER OF UNC-7 AND UNC-9 (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DEVELOPMENTAL STAGE: PRESENT IN ALL DEVELOPMENTAL STAGES BUT MOST
CC ABUNDANT IN L1-L3 LARVAE.
CC -1- SIMILARITY: Belongs to the innoxin family.
CC -----
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CC -----
DR EMBL; Z19123; CA979529.1; -
DR EMBL; Z70685; CA994607.1; -
DR F.R.; T24027; T24027.
DR WormPep; R07D5.1; CE06279.
DR InterPro; IPR000990; Innoxin.
DR Pfam; PF00876; Innoxin.1.
DR PRINTS; PR01262; INNOXIN.
KM Gap junction; Transmembrane.
FT DOMAIN 20 25
FT TRANSMEM 151 171 POTENTIAL.
FT TRANSMEM 221 241 POTENTIAL.
FT TRANSMEM 320 340 POTENTIAL.
FT TRANSMEM 405 425 POTENTIAL.
SQ SEQUENCE 522 AA; 60120 MW; 950D7AFBA961120 CRC64;
Query Match 7.1%; Score 94; DB 1; Length 522;
Best Local Similarity 18.0%; Pred. No. 0.29;
Matches 66; Conservative 52; Mismatches 117; Indels 140; Gaps 17;
QY 1 LPAFST-----SH--RLSDHTVSA-----SSDYRKLFSDL 29
DB 78 LPYQAKLDGSHQIDSHHVGSAHGAGQGCHKEKRPAMILYLLASAFRALYPRLL 137
QY 30 -----SALNLFNKRGHSTSLILSLTL-----PLSLVCGVLFSTSTVHLSALIG 77
DB 138 DDDPEVDEKLANLY-----YTTTLASPALVLSAKOYVGPIQ-CWV---PATTDAMEQYTEN 189
QY 78 FLWIQSG-WIGHDGSHYVNLRLRN-----AIQLISGNIILAGISIGWKKWN 124

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DB 190 YCWQNTYVWPMQEDIPREIYSRR-NROIGYQWVPFLIALLEALFYVPCILRGLLYWH 248
QY 125 HNAH-----HIACNSLDYDPPDLOHMPFAVSSRFNSISHXGRKE-----FDXIAXFL 175
DB 249 SGINLQGLVQMACDALMDSIEIKRTVTYTMARMODEVOLTINIDRGHSRSCFSNLQIGA 308
QY 176 ICYHFFTFYPMVCVAV-----NLVLTILL----- 201
DB 309 NCRHRCGCYVMTLYIGIKVLVSANVLLQFPLNLHLSGNDLVAGFSLDLMAHAIEMEQ 368
QY 202 -LFSRXKVDPRALINWG-----ILVFTWPL-----FLI 229
DB 369 GMEPRVTLCDPEVRVAVGNHRTVQCULMINMENEXIFLFMEWFLTCGIVTCNTMYMT 428
QY 230 ALLFVPIQHIOFWLNL 246
DB 429 LIMEIPSGMSFVRKYL 445
RESULT 11
ID D12 CREAL STANDARD; PRT; 375 AA.
AC 081931;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Delta(12) fatty acid dehydrogenase (EC 1.14.99.33) (Crepennate
DE synthase) (Delta-12 fatty acid acetylase).
OS Crepis alpina.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Asterales; Asteraceae; Cichorioideae;
OC Cichoriaceae; Crepis.
OX NCBI_Taxid=72610;
RN 11
RC SEQUENCE FROM N.A.
RX MEDLINE=98239771; PubMed=9572738;
RA Lee M., Lemman M., Banas A., Bafor M., Singh S., Schweizer M.,
RA Nilsson R., Liljenberg C., Dahlqvist A., Gunneron P.O., Sjoedahl S.,
RA Green A., Stymne S.;
RT "Identification of non-heme diron proteins that catalyze triple bond
RT and epoxy group formation.";
RL Science 280:915-918(1998).
CC -1- FUNCTION: CHANGES THE DELTA-12 DOUBLE BOND OF LINOLEIC ACID INTO A
CC TRIPLE BOND IN THE BIOSYNTHESIS OF CREPENYNIC ACID.
CC -1- CATALYTIC ACTIVITY: Linoleate + AH(2) + O(2) = crepenynate + A +
CC H(2)O.
CC -1- COFACTOR: Iron.
CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- TISSUE SPECIFICITY: Seed.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE AND/
CC OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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CC -----
DR EMBL; Y16285; CA976158.2; -
DR InterPro; IPR005804; FA desat. fam.
DR Pfam; PF00487; FA desaturase; 1.
DR ProDom; PD001081; FA desat. fam; 2.
KM Oxidoreductase; Fatty acid biosynthesis; Transmembrane; Iron.
FT TRANSMEM 54 74 POTENTIAL.
FT TRANSMEM 77 97 POTENTIAL.
FT TRANSMEM 110 130 POTENTIAL.
FT TRANSMEM 172 192 POTENTIAL.
FT TRANSMEM 218 238 POTENTIAL.

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FT TRANSNM 242 262 POTENTIAL.
 FT DOMAIN 98 102 HISTIDINE BOX-1.
 FT DOMAIN 134 138 HISTIDINE BOX-2.
 FT DOMAIN 308 312 HISTIDINE BOX-3.
 SQ SEQUENCE 375 AA; 43382 MW; B31F5A64DDC2926 CRC64;
 Query Match 6.8%; Score 89.5; DB 1; Length 375;
 Best Local Similarity 25.2%; Pred. No. 0.53;
 Matches 32; Conservative 21; Mismatches 49; Indels 25; Gaps 6;
 QY 73 AALIGFMIQSGMIGHSGHYNWLRLRAIOLISGNILAGISGMKNNNAHIAC 132
 DB ASITGLTMV-----IGHGCGHIAFSDYQWVDYTFILHSFIMTPYFS-WKXSHNNHANT 141
 QY 133 NSLDYDLDLOHMPVFAVSSRFNSITSHXGRKKXEPDIXAFILCYQHFE-VPVNCVAR 191
 DB 142 NSLNDL--VYIFSKAKVALYKVLNHPER-----LLMFTFTLIGFP----- 184
 QY 192 VNLVLTQT 198
 DB 185 --LVLTFT 189
 RESULT 12
 PD6C SOYBN STANDARD; PRT; 424 AA.
 AC P48628;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Omega-6 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).
 OS Glycine max (soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 NC NCB1_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Seed;
 RX MEDLINE=94345008; PubMed=8066133;
 RA Hiltz W.D., Carlson T.J., Booth J.R. Jr., Kinney A.J., Stecca K.L.,
 RA Yedav N.S.;
 RT "Cloning of a higher-plant plastid omega-6 fatty acid desaturase cDNA
 RT and its expression in a cyanobacterium.";
 RL Plant Physiol. 105:635-641(1994).
 CC -1- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES
 CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
 CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/ OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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 CC
 DR EMBL, L29215; AA050158.1; -
 DR PIR, T07742; T07742.
 DR InterPro, IPR005804; FA_desat_fam.
 DR Pfam, PF00487; FA_desaturase_1.
 DR ProDom, PD001081; FA_desat_fam; 2.
 KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
 KW Transf. peptide.
 FT TRANSIT 1 63 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 64 424 OMEGA-6 FATTY ACID DESATURASE.

FT DOMAIN 165 169 HISTIDINE BOX-1.
 FT DOMAIN 201 205 HISTIDINE BOX-2.
 FT DOMAIN 361 365 HISTIDINE BOX-3.
 SQ SEQUENCE 424 AA; 49641 MW; 4F3D552D4B1A2009 CRC64;
 Query Match 6.8%; Score 87; DB 1; Length 424;
 Best Local Similarity 21.7%; Pred. No. 1;
 Matches 58; Conservative 42; Mismatches 97; Indels 70; Gaps 15;
 QY 19 SSDYRK-LFSDLSALNLFNRKHTTS--ILSLILFLPLSYC-----GYLPSDST 66
 DB 75 SAERYQLADYD-----FRQVGEPLDDVTLKQVINPLPKVEPEIDDVKAMKSVLSVTS 130
 QY 67 F---VHVLAA---LLGLFLIOSGM-----IGHSGHYNWLRLRAIOLISGNIL 113
 DB 131 YALGLFMISKAPRYLPLAWMTGTATITGFPVGHGCAH---RSTSSKLVEDYGT-L 185
 QY 114 AGISIGM---WKNNNAHHIACNSLDYDLDLOHMPFA---VSSRFNSITSHXGRKX 166
 DB 186 AFMPILYYPPEPWFKQDRIHAKTNML--REDTAMHVPWVWDEPSTPLRKALITGYGPR 243
 QY 167 EPDIXAFILCYQHFFPYPMCVARNVLIQTI-----LLLSRKXVQDALNIG 217
 DB 244 CMMSIAMHLMWHPDLKKFRPSEVPRVKISLACVFAFATGWPILYK-----TGIMG 295
 QY 218 ILVFWTWFLPLALLFPPIQHIFWLN 244
 DB 296 WIKFW-----LMPWLGTHFMS 312
 RESULT 13
 PD6C ARATH STANDARD; PRT; 448 AA.
 AC P46312; Q9M094;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Omega-6 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopses.
 NC NCB1_TaxID=3702;
 RN [1]
 RP SEQUENCE OF 1-418 FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=95148736; PubMed=7846158;
 RA Falcone D.L., Gibson S., Lemieux B., Somerville C.R.;
 RT "Identification of a gene that complements an Arabidopsis mutant
 RT deficient in chloroplast omega 6 desaturase activity.";
 RL Plant Physiol. 106:1453-1459(1994).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=cv. Columbia;
 CC MEDLINE=20083488; PubMed=10617198;
 RA Meyer K.F.X., Schneller C., Mandut R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
 RA Harris B., Ansgore W., Brandt P., Grievell L., Rieger W.,
 RA Weichselgartner M., de Simone V., Obermaier B., Maché R., Mueller M.,
 RA Kreis M., Dalseny M., Puigdomenech P., Watson M., Schmidtheini T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hohisel J., Zimmermann W., Medler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Biham L., Robben J.,
 RA Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandenbusche F.,
 RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Weitenegger T., Bothé G., Ramsperger U., Hilbert H., Braun M.,
 RA Holzner E., Brandt A., Peters S., van Staveren M., Dirke P.,
 RA Woolfman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Bernier S., Hempel S., Feldpausch W., Lambertz S., Van den Daele H.,
 RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIay K., Mayes R.,

RA Patzelt A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
 RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.H.,
 RA Dose S., de Haan M., Maarse A., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fattmann B., Granderath K., Dauner D., Herzl A.,
 RA Neumann S., Argiriotou A., Vitale D., Ligouri K., Piravandi E.,
 RA Messeret O., Quigley F., Clabaud G., Mwendileh A., Felber R.,
 RA Schindl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Cheffor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandendol M., Bargeux M., Terol J., Torres A.,
 RA Perez-Perez A., Punnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Frances P., Bietke C.,
 RA Frisman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 RA Seshon K., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stonking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton L., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Spiehl J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Cotton M., Joseph C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shukher M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Grant S., Shandy N., Hasegawa A., Hameed A., Lochi M., Johnson A.,
 RA Chen E., Marra M., Mathiesen R., McCombie W.R.,
 RT "sequence and analysis of chromosome 4 of the plant Arabidopsis
 RT thaliana";
 RL Nature 402:769-777(1999).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 RT SFP Consortium (Salk/Stanford/PGECC).";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES
 CC THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
 CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
 CC -1- DEVELOPMENTAL STAGE: HIGHEST LEVELS FOUND IN EXPANDING LEAVES.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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 CC -----
 CC EMBL: U09503; AAA92800.1; -;
 DR EMBL: AL022198; CA18198.1; -;
 DR EMBL: AL161578; CAB79813.1; -;
 DR EMBL: AY045621; AKK73979.1; -;
 DR EMBL: AY058078; AAL24186.1; -;
 DR EMBL: AY058852; AAL24240.1; -;
 DR PIR: D83562; D83562.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desat_fam; 2.
 DR ProDom: PD001081; FA_desat_fam; 2.
 KM Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
 KM Transist peptide.
 FT TRANSIT 1 69 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 70 448 OMEGA-6 FATTY ACID DESATURASE.
 FT DOMAIN 171 175 HISTIDINE BOX-1.
 FT DOMAIN 207 211 HISTIDINE BOX-2.
 FT DOMAIN 367 371 HISTIDINE BOX-3.

SQ SEQUENCE 448 AA; 51225 MW; C3AC72FB28FBF287 CRC64;
 Query Match 6.6%; Score 87; DB 1; Length 448;
 Best Local Similarity 20.3%; Pred. No. 1.1; Indels 74; Gaps 11;
 Matches 55; Conservative 39; Mismatches 103;
 QY 12 DHTVSAASDPRKLFSDLSANLNFNRKHTSTLSLILTLPLPLSGVLFSD-----ST 66
 DB 84 DRQGLAESYGFRIIGDL-----PENVTLNDIMTLTKPEFEI--DDKLKLSV 130
 QY 67 FVHLSAALIGFLWISGW-----IGHSGHYVMLSRLNRAIQI 107
 DB 131 LISVTSYTLGLFPIAKSPWTLPLAMWGTATITGPFVIGHDCAH-----KSFKNKLVED 186
 QY 108 LSGNIILAGISIGW-----WKNNHNAHIIACNSLDYDDDLQMPVFAV--SSRPFSSISHX 162
 DB 187 IVGT-LAFPLVPLVYPPWRKDRHNAKTMTLVDHAWOPVPEPESSVPMKAIIFGY 245
 QY 163 GRKCEPDIXAFPLICQHFYFVPMCVARNVLYQTI-----LLFSRXKVDRL 213
 DB 246 GPRFPLSLAHWVNMHFNKLKFRASEVKNVKISLACVFAFMVGVPLIVK-----V 297
 QY 214 NINGILVFWTWFLFLALLFVPIQHIQFWLN 244
 DB 298 GILGWKFW-----LMPWLGYHFWMS 318
 RESULT 14
 ID UHPB_ECOLI STANDARD; PRT; 500 AA.
 AC P09835; P76729;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sensor protein uhpB (EC 2.7.3.-).
 GN UHPB OR B3668.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87279903; PubMed=3301805;
 RA Friedrich M.J., Kadner R.J.;
 RT "Nucleotide sequence of the uhp region of Escherichia coli.";
 RL J. Bacteriol. 169:3556-3563(1987).
 RN [2]
 RP REVISIONS.
 RA Kadner R.J.;
 RL Submitted (AUG-1990) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92234930; PubMed=1569007;
 RA Ireland M.D., Wei B.-Y., Kadner R.J.;
 RT "Structure and function of the uhp genes for the sugar phosphate
 RT transport system in Escherichia coli and Salmonella typhimurium.";
 RL J. Bacteriol. 174:2754-2762(1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=93315143; PubMed=7686887;
 RA Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
 RT "DNA sequence and analysis of 136 kilobases of the Escherichia coli
 RT genome: organizational symmetry around the origin of replication.";
 RL Genome 16:551-561(1993).
 CC -1- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM UHPB/UHPA
 CC INVOLVED IN THE REGULATION OF THE UPTAKE OF HEXOSE PHOSPHATES.
 CC UHPB FUNCTIONS AS A MEMBRANE-ASSOCIATED PROTEIN KINASE THAT
 CC PHOSPHORYLATES UHPA IN RESPONSE TO ENVIRONMENTAL SIGNALS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC -1- SIMILARITY: Contains 1 histidine kinase domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).

 DR EMBL: M17102; AAA24721.1; ALT_SEQ.
 DR EMBL: M94479; AAA24725.1; ALT_INIT.
 DR EMBL: L10328; AAA62020.1; ALT_INIT.
 DR EMBL: AE000444; AAC76691.1; ALT_INIT.
 DR PIR: E65168; RGEUB.
 DR EcoGene; EG11052; unbp.
 DR InterPro: IPR003594; ATPbind_ATPase.
 DR InterPro: IPR005467; His_kinase.
 DR Pfam; PF02518; HATPase_c1.
 DR SMART; SM00387; HATPase_c1.
 DR PROSITE; PS50109; HIS_KIN_1.
 KM Sensory transduction; Transferrase; Kinase; Phosphorylation;
 KM Transmembrane; Inner membrane; Sugar transport; Complete proteome.

FT TRANSMEM 8 28 POTENTIAL.
 FT TRANSMEM 78 98 POTENTIAL.
 FT TRANSMEM 112 132 POTENTIAL.
 FT TRANSMEM 140 160 POTENTIAL.
 FT TRANSMEM 185 205 POTENTIAL.
 FT TRANSMEM 213 233 POTENTIAL.
 FT TRANSMEM 253 273 POTENTIAL.
 FT DOMAIN 311 499 HISTIDINE KINASE.
 FT MOD RES 313 313 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 500 AA; 56305 MW; A7353FC1FD53152 CRC64;

Query Match 6.5%; Score 86; DB 1; Length 500;
 Best Local Similarity 23.3%; Pred. No. 1.5; Indels 62; Gaps 11;
 Matches 51; Conservative 33; Mismatches 73;

40 HTTSILSLITLTFPLSCVLSFSDSTFVH-----VLSALIGFLMIGS-GWIGHDS 90
 Db HFLPLMIGSLTLTLPVALI-----SNRRHQBDKRTLLGALTAALQSLPWLHCK 135

Qy 91 GHNVMISRLNRAIQILSGNIIAGISIGWKNHNAHIAACS-LDYDPDLOHMPVFAV 149
 Db ESNMALI-----LTLTGTLTAPICLVFW-----HYLANNTWPLGSPVLSQPI--- 179

Qy 150 SSRFFNSITSHXGKKEPFIXAKFLCYOHFFTFYPCVAVNLVYQITLL-LFSXKV 208
 Db 180 -----NMGR-----HLWYLLFV--ISLWQLGLPELSRFTP 212

Qy 209 QDBALNMGILVFTWFLFLALFLVPIQH--QFWLNH 245
 Db 213 FCLALPIALAMHYGMOGALITLMAIALIASQTRWDH 251

RESULT 15
 FD3E TOBAC STANDARD; PRT; 379 AA.
 AC P48626;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-).
 GN PAD3.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
 OC NCBI_TaxID=4097;
 RN [1]
 RC SEQUENCE FROM N. A.
 RC STRAIN=cv. SRI, TISSUE=leaf;
 RX MEDLINE=95011632; PubMed=7926817;
 RA Hamada T., Kodama H., Nishimura M., Iba K.;
 RT "Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase";
 RL Gene 147:293-294(1994).

CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEDOWN IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

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 CC use by non-profit institutions as long as its content is in no way
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 DR EMBL: D26509; BA05515.1; -.
 DR PIR: JC2555; JC2555.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase_1.
 DR ProDom; PD001081; FA_desat_fam; 2.
 KM Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
 KM Transmembrane

FT TRANSMEM 52 72 POTENTIAL.
 FT TRANSMEM 213 233 POTENTIAL.
 FT TRANSMEM 236 256 POTENTIAL.
 FT DOMAIN 97 101 HISTIDINE BOX-1.
 FT DOMAIN 133 137 HISTIDINE BOX-2.
 FT DOMAIN 300 304 HISTIDINE BOX-3.
 SQ SEQUENCE 379 AA; 44149 MW; 87221A21AB02E1B2 CRC64;

Query Match 6.5%; Score 85.5; DB 1; Length 379;
 Best Local Similarity 22.2%; Pred. No. 1.2;
 Matches 47; Conservative 29; Mismatches 89; Indels 47; Gaps 9;

Qy 52 LPLPSCGV-LRSDSTFVAVLSALIGFLMIGSGHSGHNWLSRLNRAI-QILS 109
 Db 60 IFVATLIGIAIHDSWLFPLWYALIGQTMFWALFVYGHGCGSGFSDSLNNVGHILH 119

Qy 110 GNLAGISIGWKNHNAHIAACS-LDYDPDLOHMPVFAVSSRFFNSITSHXGKKEPD 169
 Db 120 SAIL--VPTHGMRISKTHQNHGNETDESNVMP-----EKLYKV--GYSTFLAY 169

Qy 170 XIAXFLICY-----QHFTFY-----PVMC---VARNLYLOIT 199
 Db 170 KIPFPLAVPMYLMKRSPOKSGSHFNPYSDLPQPHKRYVVTSLCWTMAALLVYLCTA 229

Qy 200 LLLFSRXKQDRAALNMGILVFTWFLFLAL 231
 Db 230 FGSLQMFKIYGA-----YLIFWMLDFVYTL 256

Search completed: January 1, 2004, 06:30:56
 Job time : 7.56688 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 22.707 Seconds
(without alignments)
2875.205 Million cell updates/sec

Title: US-09-857-524B-6
Sequence: 1 LPAGSTSHRLSDHTVSAASS.....VPIOHIOFWINHLAENLYXG 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	822	62.4	446	10	Q92TY9
2	780.5	59.2	449	10	Q81B96
3	780.5	59.2	449	10	Q81B96
4	778.5	59.1	449	10	Q81B96
5	768.5	58.3	446	10	Q81B96
6	765.5	58.1	446	10	Q81B96
7	747.5	56.7	458	10	Q81B96
8	740.5	56.2	448	10	Q81B96
9	735.5	55.8	448	10	Q81B96
10	730.5	55.4	448	10	Q81B96
11	729.5	55.3	448	10	Q81B96
12	686.5	52.1	469	10	Q81B96
13	678.5	51.5	448	10	Q81B96
14	377.5	28.6	523	3	Q9HDE8
15	342.5	26.0	573	3	Q8NKG8
16	317	24.1	568	3	Q8NKG9

17	263	20.0	467	3	Q96VC3	Q96VC3 mucor circi
18	251.5	19.1	457	3	Q9HEV4	Q9HEV4 mortierella
19	249.5	18.9	457	3	Q8X173	Q8X173 mortierella
20	247.5	18.8	457	3	Q9UVY3	Q9UVY3 mortierella
21	247.5	18.8	457	3	Q9UVY3	Q9UVY3 mortierella
22	244.5	18.6	483	10	Q9LENO	Q9LENO ceratodon p
23	244	18.5	477	10	Q8RXB0	Q8RXB0 phaeodactyl
24	234.5	17.8	357	3	Q9HDP4	Q9HDP4 mortierella
25	234.5	17.8	457	3	Q9HEV1	Q9HEV1 mortierella
26	234.5	17.8	457	3	Q8X174	Q8X174 mortierella
27	232	17.6	419	10	Q9SMO9	Q9SMO9 euglena gra
28	227	17.2	459	10	Q944W4	Q944W4 pythium lit
29	224.5	17.0	443	5	Q61388	Q61388 caenorhabdi
30	224.5	17.0	443	5	Q23221	Q23221 caenorhabdi
31	212.5	16.1	520	10	Q9LEW9	Q9LEW9 ceratodon p
32	204	15.5	525	10	Q9ZNM2	Q9ZNM2 physcomittr
33	201.5	15.3	447	5	Q9XTB7	Q9XTB7 caenorhabdi
34	197	14.9	350	16	Q9F2M3	Q9F2M3 streptomyce
35	172	13.1	444	11	Q9ZOR9	Q9ZOR9 mus musculi
36	170	12.9	444	11	Q9Z122	Q9Z122 rattus norv
37	164	12.4	347	16	Q9FC35	Q9FC35 streptomyce
38	162	12.3	386	4	Q9EH07	Q9EH07 homo sapien
39	162	12.3	422	4	Q9H3G3	Q9H3G3 homo sapien
40	162	12.3	444	4	Q95864	Q95864 homo sapien
41	160.5	12.2	444	4	Q96139	Q96139 homo sapien
42	160.5	12.2	444	4	Q9VYX1	Q9VYX1 homo sapien
43	160.5	12.2	444	4	Q96T10	Q96T10 homo sapien
44	160.5	12.2	444	4	Q60427	Q60427 homo sapien
45	160.5	12.2	501	4	Q8NCC7	Q8NCC7 homo sapien

ALIGNMENTS

RESULT 1
ID Q92TY9 PRELIMINARY; PRT; 446 AA.
AC Q92TY9;
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Desaturase/cytochrome b5 protein.
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotyledons; Euphorbiales; Euphorbiaceae; Ricinus.
OX NCBI_TaxID=3968;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed endosperm;
RX MEDLINE=97268723; PubMed=910811;
RA Sayanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,
RA Christie W.W., Shewry P.R., Napier J.A.;
RT "Expression of a borage desaturase cDNA containing an N-terminal
RT cytochrome b5 domain results in the accumulation of high levels of
RT delta6-desaturated fatty acids in transgenic tobacco.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
RL -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC EMBL; AF005096; AAD01240.1; -.
DR HSSP; P00171; IISU.
DR InterPro; IPR001199; Cyt B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt B5; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
DR PROSITE; PSS0255; CYTOCHROME_B5_2; 1.
KW Heme
SQ SEQUENCE 446 AA; 51418 MW; A1954FDB2DB600F CRC64;
Query Match 62.4%; Score 822; DB 10; Length 446;
Best Local Similarity 57.5%; Pred. No. 5.6e-70;
Matches 154; Conservative 38; Mismatches 60; Indels 16; Gaps 3;

```

QY 1 LPAFSTSHRLSDHTVSAASDVRKLFSDLSALNLFNRKHTTSLILSLITLFPPLSVCGV 60
DB 71 LDFEFGYHKLKXSVSETSDYRLVAEFKLG-FEKGKIAITLVSWMMLALSTYGV 129
QY 61 LPSDSTFVHVALIGFLMTIGSGWIGSHYVNLSPRLNRAIQILSGNIIAGISIGW 120
DB 130 LGSNSTWVHLISGLGFMWIGWIGSHYVNMSSRRFNRLAQILSGNCLAGISIAW 189
QY 121 WKNNHNAHIAACNSLDVDPDQHPVFAVSSRFNSITSHYGRKKEFDXIAFLICYH 180
DB 190 WKNNHNAHIAACNSLDVDPDQHPVFAVSSRFNSITSHYGRKKEFDXIAFLICYH 249
QY 181 FFEPYMCVAVNYLYQTILLFSRKKVODRALNMGILVFTWFLFLA-----LL 232
DB 250 LTFYPMCARILFPAOSISLILSKRVANRGOEILGVLVFWLWYPLVSLCENWGERVW 309
QY 233 FVP-----IOHIOFWNLHLENLYXG 253
DB 310 FVAASFSVTRIGHVQFCNLHNFSSSVYL 337

RESULT 2
Q8LB96 PRELIMINARY; PRT; 449 AA.
AC Q8LB96;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 23, Last sequence update)
DE Delta-8 sphingolipid desaturase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volkovskiy N., Town C.D., Troupkan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troupkan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AY087345; AAM64895.1; -.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KM Heme.
SQ SEQUENCE 449 AA; 51744 MW; A1EB557B8CE03B18 CRC64;

Query Match 59.2%; Score 780.5; DB 10; Length 449;
Best Local Similarity 54.8%; Pred. No. 5e-66;
Matches 144; Conservative 37; Mismatches 67; Indels 15; Gaps 2;
QY 6 TSHRLSDHTVSAASDVRKLFSDLSALNLFNRKHTTSLILSLITLFPPLSVCGV 65
DB 78 TSHRLSDHTVSAASDVRKLFSDLSALNLFNRKHTTSLILSLITLFPPLSVCGV 137
QY 66 TSHRLSDHTVSAASDVRKLFSDLSALNLFNRKHTTSLILSLITLFPPLSVCGV 125
DB 138 TSHRLSDHTVSAASDVRKLFSDLSALNLFNRKHTTSLILSLITLFPPLSVCGV 197
QY 126 NAHIAACNSLDVDPDQHPVFAVSSRFNSITSHYGRKKEFDXIAFLICYH 185

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DB 198 NAHIAACNSLDVDPDQHPVFAVSSRFNSITSHYGRKKEFDXIAFLICYH 257
QY 186 VMCVAVNYLYQTILLFSRKKVODRALNMGILVFTWFLFLA-----LV--- 234
DB 258 VMCVAVNYLYQTILLFSRKKVODRALNMGILVFTWFLFLA-----LV--- 317
QY 235 ---PIOHIOFWNLHLENLYXG 253
DB 318 FVTAALQHTLNLHFAADVYTG 340

RESULT 3
Q9ZRP8 PRELIMINARY; PRT; 449 AA.
AC Q9ZRP8;
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DE Delta-8 sphingolipid desaturase.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxId=3708;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Drakkar; TISSUE=ripening embryos;
RC MEDLINE=99003197; PubMed=976850;
RA Sperling P., Zaehring U., Heinz E.;
RT "A sphingolipid desaturase from Higher Plants Identification of a New
RT Cytochrome b5 Fusion Protein.";
RL J. Biol. Chem. 273:28590-28596(1998).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AJ224160; CA11857.1; -.
DR HSP; P82291; ICXY.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KM Heme.
SQ SEQUENCE 449 AA; 51490 MW; FEEB37AF9D390C1 CRC64;

Query Match 59.2%; Score 780.5; DB 10; Length 449;
Best Local Similarity 54.0%; Pred. No. 5e-66;
Matches 141; Conservative 44; Mismatches 61; Indels 15; Gaps 2;
QY 8 HRLSDHTVSAASDVRKLFSDLSALNLFNRKHTTSLILSLITLFPPLSVCGV 67
DB 80 HRLSDHTVSAASDVRKLFSDLSALNLFNRKHTTSLILSLITLFPPLSVCGV 139
QY 68 HRLSDHTVSAASDVRKLFSDLSALNLFNRKHTTSLILSLITLFPPLSVCGV 127
DB 140 HRLSDHTVSAASDVRKLFSDLSALNLFNRKHTTSLILSLITLFPPLSVCGV 199
QY 128 HRLSDHTVSAASDVRKLFSDLSALNLFNRKHTTSLILSLITLFPPLSVCGV 187
DB 200 HRLSDHTVSAASDVRKLFSDLSALNLFNRKHTTSLILSLITLFPPLSVCGV 259
QY 188 HRLSDHTVSAASDVRKLFSDLSALNLFNRKHTTSLILSLITLFPPLSVCGV 234
DB 260 HRLSDHTVSAASDVRKLFSDLSALNLFNRKHTTSLILSLITLFPPLSVCGV 319
QY 235 ---PIOHIOFWNLHLENLYXG 253
DB 320 VTAALQHTLNLHFAADVYTG 340

RESULT 4

```

Q9ZRP7 PRELIMINARY; PRT; 449 AA.

AC Q9ZRP7;

DT 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DE Delta-8 sphingolipid desaturase (ATG61580/P2A19_180).

GN SLD1 OR F2A19.180 OR ATG61580.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucosids II; Brassicales; Brassicaceae; Arabidopsis.

OC NCBI_Taxid=3702;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ccv Columbia; TISSUE=flower; MAINLY GREEN PARTS, and Root;

RX MEDLINE=99003197; PubMed=9786850;

RT Speirling P., Zaehlinger U., Heinz E.;

RT "A sphingolipid desaturase from higher plants. Identification of a new cytochrome b5 fusion protein."

RT J. Biol. Chem. 273:28590-28596(1998).

RL [2]

RN SEQUENCE FROM N.A.

RP De Haan M., Maarse A.C., Grivell L.A., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;

RA Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RL [3]

RN SEQUENCE FROM N.A.

RP EU Arabidopsis sequencing project;

RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RL [4]

RN SEQUENCE FROM N.A.

RP Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bower L., Carrinci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen J., Onda C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;

RA "Arabidopsis cDNA clones."

RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

RL [5]

RN SEQUENCE FROM N.A.

RP Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T., Carrinci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A., Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M., Seki M., Shinn P., Tang C.C., Toriumi M., Wallender B.K., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Shinzaki K., Ecker J., Theologis A., Davis R.W.;

RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

RL -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

CC EMBL: AJ224161; CA11858.1; -

DR EMBL: AL132962; CAB71088.1; -

DR EMBL: AF428420; AAL16189.1; -

DR EMBL: BF000442; AAN17419.1; -

DR HSP; P00171; I15U.

DR InterPro; IPR001199; Cyt B5.

DR InterPro; IPR005804; FA_desat_fam.

DR Pfam; PF00487; FA_desaturase; 1.

DR Pfam; PF00173; heme_1; 1.

DR ProDom; PD000612; Cyt B5; 1.

DR ProDom; PD001081; FA_desat_fam; 1.

DR PROSITE; PSS0255; CYTOCHROME_B5_2; 1.

DR Heme.

SC SEQUENCE 449 AA; 51675 MW; 145048F9FD35964 CRC64;

Query Match 59.1%; Score 778.5; DB 10; Length 449;

Best Local Similarity 54.8%; Pred. No. 7.7e-66;

Matches 144; Conservative 37; Mismatches 67; Indels 15; Gaps 2;

QY 6 TSHRLSDHTVSAASDYRKLFSDLGALNLFNRKGGTTTSLILTLPLPLSLVGVLFSDS 65

DB 78 TGYHIRDQVSEVSRDYRRMALEFRKLGLENKGGHTVLTFLAFVAMFGLVGYVLACTS 137

QY 66 TTVHVLGALIGFLMIGOSGCHDSGHVVMLSRRLNRAIQLSGNIIAGISIGMKKMH 125

DB 138 VFAHDIALLGLMLIQSAVIGHDGSHVYVSKNKNRPAQLSGNGLGISIAMKKMTH 197

QY 126 NAHHLACSLDVPDPLQHPVAVSSRPFNSITSHXGKXEFDXIAXFLICYQHFTFYP 185

DB 198 NAHHLACSLDVPDPLQHPVAVSTKFFSSITSRFYDKLTFDPVAPRLVSYQHFTTYP 257

QY 196 VMCVARVNLVYQITILLFSRKKVODRALNIMGILVFWTFLLALL-----FV--- 234

DB 258 VMCGRINLFIQITFLFSKREVPDRALNFAGILVFWTFPLVSCLPWMPERFFVFTS 317

QY 235 ----FIQHGFNLNLAENLYXG 253

DB 318 FTVTALQHIQFTLNHPADVVG 340

RESULT 5

Q9FR82 PRELIMINARY; PRT; 446 AA.

AC Q9FR82;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Delta 8-sphingolipid desaturase.

GN SLD1.

OS Borago officinalis (Bourrache).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; OC Asteridae; Lamiales; Boraginaceae; Borago.

OX NCBI_Taxid=13363;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21092516; PubMed=11162428;

RA Libisch B., Michelson L.V., Lewis M.J., Shewry P.R., Napier J.A.;

RT "Chimers of Delta6-fatty acid and Delta8-sphingolipid desaturases."

RT Biochem. Biophys. Res. Commun. 279:779-785(2000).

RL [2]

RN SEQUENCE FROM N.A.

RX MEDLINE=2160464; PubMed=11368168;

RA Speirling P., Libisch B., Zaehlinger U., Napier J.A., Heinz E.;

RT "Functional identification of a delta 8-sphingolipid desaturase from Borago officinalis."

RL Arch. Biochem. Biophys. 388:293-298(2001).

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

DR EMBL: AF133728; AAG43277.1; -

DR HSP; P00171; I15U.

DR InterPro; IPR001199; Cyt B5.

DR InterPro; IPR005804; FA_desat_fam.

DR Pfam; PF00487; FA_desaturase; 1.

DR Pfam; PF00173; heme_1; 1.

DR ProDom; PD000612; Cyt B5; 1.

DR ProDom; PD001081; FA_desat_fam; 1.

DR PROSITE; PSS0255; CYTOCHROME_B5_2; 1.

DR Heme.

SC SEQUENCE 446 AA; 50926 MW; EBD579F03A3AFOC CRC64;

Query Match 58.3%; Score 768.5; DB 10; Length 446;

Best Local Similarity 55.9%; Pred. No. 6.9e-65;

Matches 147; Conservative 35; Mismatches 66; Indels 15; Gaps 2;

QY 6 TSHRLSDHTVSAASDYRKLFSDLGALNLFNRKGGTTTSLILTLPLPLSLVGVLFSDS 65

DB 76 TGYHLEDVLSISIDYRKLASEFSEKAGLFEKKGHTVTCISFIALLLCGCYGVLCNS 135

QY 66 TTVHVLGALIGFLMIGOSGCHDSGHVVMLSRRLNRAIQLSGNIIAGISIGMKKMH 125

DB 136 LNVHMLGAMLCMCIQAVLIGHDGSHVYVSKNKNRPAQVANGNCLGISIAMKKMTH 195

QY 126 NAHHLACSLDVPDPLQHPVAVSSRPFNSITSHXGKXEFDXIAXFLICYQHFTFYP 185

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DB 196 NAHIIICNSLDYDPDLOHLPFAVPSSFFKSLSRFGRLTGDGSRFLVSQHHTIYI 255
QY 186 VMCVAVNLYLQTLILLFSRXKQVDRALNMGILVFTWFLFLA-----LFRV--- 234
DB 256 VMIFGINLVQVQFLLFFSRKVPDRALNIGILVYTWTPVYLSCLPNNBRVFLVLC 315
QY 235 -----PIOHIOFWNLHLENLXG 253
DB 316 FSVALOHIOFTLNHFAADYVVG 338

RESULT 6
Q8LUD7 PRELIMINARY; PRT; 446 AA.
AC Q8LUD7;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Sphingolipid long chain base delta 8 desaturase.
OS Aquilegia vulgaris.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
OC Ranunculaceae; Aquilegia.
OC NCBI_TaxID=3451;
RN [1]
RA SEQUENCE FROM N.A.
RA Longman A.V., Michaelson L.V., Napier J.A.;
RT "Isolation and characterization of a cDNA encoding a delta 8
RT sphingolipid desaturase from Aquilegia vulgaris.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL: AF406816; AAN03619.1; -.
DR InterPro: IPR001199; Cyt_B5.
DR InterPro: IPR005804; FA_desat_fam.
DR Pfam: PF00487; FA_desaturase; 1.
DR Pfam: PF00173; heme_1; 1.
DR PRINTS: PR00363; CYTOCHROME_B5.
DR ProDom: PD000612; Cyt_B5; 1.
DR ProDom: PD001081; FA_desat_fam; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 446 AA; 51273 MW; 76366DB0EB956D09 CRC64;

Query Match 58.1%; Score 765.5; DB 10; Length 446;
Best Local Similarity 54.1%; Pred. No. 1.3e-64;
Matches 140; Conservative 43; Mismatches 61; Indels 15; Gaps 2;
QY 10 LSDHTVAASSDYRKLFSDLSALNLFNRKGTTSILSLITLPLSVCGVLFSDFSTFVH 69
DB 79 LKQYITSEVSKDRKLVAFESKAGLYDKGHILFSLFTYILMAISVKGVLCSDKTMAH 138
QY 70 VLSAALIGFLWIOSGWTGHDGSHYVNLRLNRAIQILSGNLAGISIGMKMKNNAHH 129
DB 139 LAAVAALVGLIMMOIGFVGHDSGHYNTLTKLNRFMOIFGNCITGISIGMKMKNNAHH 198
QY 130 IACNSLDYDPDLOHMPFAVSSRFPNSITSHXGKKEPFXIXFLICYGHFTFPMCV 189
DB 199 IAVNSLDYDPDLOHIFPLAVSSDI FSSLTSKFGKKTTPDIRFLISFOHMTFYPVMAI 258
QY 190 ARVNLVQTLILLFSRXKQVDRALNMGILVFTWFLFLALL-----FVPI----- 236
DB 259 ARINLPAQSTILLISKRPVTDRLAEILGLVFWCMWISLLACLPMWGERAMTVAMSPAVS 318
QY 237 -----OHIOFWNLHLENLXG 253
DB 319 GYQHIOFCUNHFSAHYVVG 337

RESULT 7
Q43469 PRELIMINARY; PRT; 458 AA.
AC Q43469;

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DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Delta-8 sphingolipid desaturase.
GN SLD1.
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Campanulidae; Asterales; Asteroceae; Asteroideae;
OC Heliantheae; Helianthus.
OC NCBI_TaxID=4232;
OX [1]
RN [1]
RA SEQUENCE FROM N.A.
RA STRAIN=cv. Indred line HA89;
RC TISSUE=Cotyledons of developing sunflower fruits;
RX MEDLINE=96028121; PubMed=7588718;
RA Sperling P., Schmidt H., Heinz E.;
RT "A cytochrome b5-containing fusion protein similar to plant acyl lipid
RT desaturases.";
RL Eur. J. Biochem. 232:798-805 (1995).
RN [2]
RA SEQUENCE FROM N.A.
RC STRAIN=cv. Indred line HA89;
RC TISSUE=Cotyledons of developing sunflower fruits;
RX MEDLINE=21116801; PubMed=1171153;
RA "Further characterization of delta 8-sphingolipid desaturases from
RT higher plants.";
RL Biochem. Soc. Trans. 28:638-641 (2000).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL: X87143; CA60621.1; -.
DR HSSP: P00171; 1F03.
DR InterPro: IPR001199; Cyt_B5.
DR InterPro: IPR005804; FA_desat_fam.
DR Pfam: PF00487; FA_desaturase; 1.
DR Pfam: PF00173; heme_1; 1.
DR ProDom: PD000612; Cyt_B5; 1.
DR ProDom: PD001081; FA_desat_fam; 1.
DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 458 AA; 52231 MW; D182287AB0E99245 CRC64;

Query Match 56.7%; Score 747.5; DB 10; Length 458;
Best Local Similarity 52.8%; Pred. No. 7e-63;
Matches 140; Conservative 40; Mismatches 66; Indels 19; Gaps 4;
QY 6 TSHRLSDHTVAASSDYRKLFSDLSALNLFNRKGTTSILSLITLPLSVCGVLFS 63
DB 87 TGVHLKDYDVSDISRDYRKLASBFAKAGFEKKGH--GVYSLCFVSLLSACVYGLVS 144
QY 64 DSTFVNLVSAALIGFLWIOSGWTGHDGSHYVNLRLNRAIQILSGNLAGISIGMKMKN 123
DB 145 GSEFWHMLSGALIGLAWMOIAYLGHDAGHYQWATGKMKFAGIFGNCITGISIAMMKM 204
QY 124 NNAHHIACNSLDYDPDLOHMPFAVSSRFPNSITSHXGKKEPFXIXFLICYGHFTF 183
DB 205 TNAHHIACNSLDYDPDLOHMPFAVSSRFPNSITSHXGKKEPFXIXFLICYGHFTF 264
QY 184 YPMVCVAVNLYLQTLILLFSRXKQVDRALNMGILVFTWFLFLALL-----FV- 234
DB 265 YPIMCVARVNLVQTLILLISKRKIPDRGLNIGTLIFWTWFLVSRPLPNNPERVAVFL 324
QY 235 -----PIOHIOFWNLHLENLXG 253
DB 325 VSECVTQIOHIOFTLNHFSGDYVVG 349

RESULT 8
Q8VZ22 PRELIMINARY; PRT; 448 AA.
AC Q8VZ22;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

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DT 01-OCT-2002 (TREMBlrel. 22, last annotation update)
 DE Delta-6-desaturase.
 GN D6DS.
 OS Echinum gentianoides.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Boraginaceae; Echinum.
 NCBI_TaxId=173991;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maroto F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz J.R.;
 RT "Cloning and Molecular Expression of the D6-Desaturase from
 Echinum: Functional Expression in Yeast and Tobacco."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AY055117; AL23580.1; --
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 DR Heme.
 KW SEQUENCE 448 AA; 51428 MW; C2A937951E87C183 CRC64;
 SQ
 Query Match 56.2%; Score 740.5; DB 10; Length 448;
 Best Local Similarity 48.5%; Pred. No. 3,2e-62;
 Matches 130; Conservative 59; Mismatches 64; Indels 15; Gaps 2;
 QY 1 LPAFSTSHRLSDHTVSAASDVRKLFSDLSALNLFNRKHTTSLILTLTLPPLSVCGV 60
 DB 72 LDSFPTGYLKDYSVEVSKDRIKLVFERNKGLFKKHGYLVTVVFFIAMPFAMSVGV 131
 QY 61 LFSSTFVVLAAALIGFLMIQSGWIGHDSGHYNWLSRLNRAIQILSGNIIAGISIGM 120
 DB 132 LFCBGVVLHLAGLGMFWIOWGIGHAGHYIVMPNPLNLMGIVASNCISGISIGM 191
 QY 121 WKNNNAHHIACNSLDYDPDLQHPFVAVSSRFNSITSHYGRKKEPDIXAPLICYOH 180
 DB 192 WKNNNAHHIACNSLDYDPDLQHPFVAVSSRFNSITSHYGRKKEPDIXAPLICYOH 251
 QY 181 FFYFVPMCVARNVLYQTILLFSSRXKQDRAINIGLIVFTWF-----L 226
 DB 252 WFFYPMCVARNVLYQTILLFSSRXKQDRAINIGLIVFTWF-----L 226
 QY 227 FLALLFVP-IOHIOFWNLHLENLYXG 253
 DB 312 FVVASLSTVGTGQVQPSLNHFAASYVG 339
 RESULT 9
 ID Q8VZ21 PRELIMINARY; PRT; 448 AA.
 AC Q8VZ21;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta-6-desaturase.
 GN D6DS.
 OS Echinum pitardii var. pitardii.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Boraginaceae; Echinum.
 NCBI_TaxId=174255;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maroto F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz J.R.;
 RT "Cloning and Molecular Characterization of the D6-Desaturase from
 Echinum: Functional Expression in Yeast and Tobacco."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AY055116; AL23581.1; --

DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 DR Heme.
 KW SEQUENCE 448 AA; 51394 MW; 4B6D6EA4905DE263 CRC64;
 SQ
 Query Match 55.8%; Score 735.5; DB 10; Length 448;
 Best Local Similarity 48.1%; Pred. No. 9,5e-62;
 Matches 129; Conservative 59; Mismatches 65; Indels 15; Gaps 2;
 QY 1 LPAFSTSHRLSDHTVSAASDVRKLFSDLSALNLFNRKHTTSLILTLTLPPLSVCGV 60
 DB 72 LDSFPTGYLKDYSVEVSKDRIKLVFERNKGLFKKHGYLVTVVFFIAMPFAMSVGV 131
 QY 61 LFSSTFVVLAAALIGFLMIQSGWIGHDSGHYNWLSRLNRAIQILSGNIIAGISIGM 120
 DB 132 LFCBGVVLHLAGLGMFWIOWGIGHAGHYIVMPNPLNLMGIVASNCISGISIGM 191
 QY 121 WKNNNAHHIACNSLDYDPDLQHPFVAVSSRFNSITSHYGRKKEPDIXAPLICYOH 180
 DB 192 WKNNNAHHIACNSLDYDPDLQHPFVAVSSRFNSITSHYGRKKEPDIXAPLICYOH 251
 QY 181 FFYFVPMCVARNVLYQTILLFSSRXKQDRAINIGLIVFTWF-----L 226
 DB 252 WFFYPMCVARNVLYQTILLFSSRXKQDRAINIGLIVFTWF-----L 226
 QY 227 FLALLFVP-IOHIOFWNLHLENLYXG 253
 DB 312 FVVASLSTVGTGQVQPSLNHFAASYVG 339
 RESULT 10
 ID Q9SAU5 PRELIMINARY; PRT; 448 AA.
 AC Q9SAU5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta-6-desaturase.
 OS Borago officinalis (Borraghe) (Borage).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Boraginaceae; Borago.
 NCBI_TaxId=13363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Seed;
 RA Numborg A.N., Beremand P.D., Thomas T.L.;
 RT "Engineering of Plant Seed Oils to Produce Gamma Linolenic Acid
 (GLA)."
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AF007561; AA001410.1; --
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 DR Heme.
 KW SEQUENCE 448 AA; 51626 MW; EAC3F0BF22E0DE00 CRC64;
 SQ
 Query Match 55.4%; Score 730.5; DB 10; Length 448;
 Best Local Similarity 48.9%; Pred. No. 2,9e-61;
 Matches 131; Conservative 50; Mismatches 72; Indels 15; Gaps 2;
 QY 1 LPAFSTSHRLSDHTVSAASDVRKLFSDLSALNLFNRKHTTSLILTLTLPPLSVCGV 60
 DB 72 LDSFPTGYLKDYSVEVSKDRIKLVFERNKGLFKKHGYLVTVVFFIAMPFAMSVGV 131

Db 72 LDKFTGYLKDYVSSEVSKDYRKLYVEFSKMGLYDKKGMHIMPATLCFIAMLPAMSVYGV 131
 QY 61 LFDSTFVHYLSAALIGFLWIOSGMIGHDSGHYVNMISRLNRAIOISGNIIAGISIGM 120
 Db 132 LFCGCVLHFLFSCGLMGFLWIOSGMIGHDSGHYVNMISRLNRAIOISGNIIAGISIGM 191
 QY 121 WKNHNAHNIACNSLDYDPDLOHMPVAVSSRFNSITSHXGRKKEFDXIAFLICYQH 180
 Db 192 WKNHNAHNIACNSLEVDPLQYIPLVYSSKFFGSLTSHFYERKRLTFDSLSRFVSYQH 251
 QY 181 FTFYPMCVARVNLVYQITILLFSRXXVQDRAINIMGILVFWTF-----L 226
 Db 252 WTFYPMCAARLNMVYQSLIMLTILKRVNSYRAQELLGLVFSIWIYPLVSCLPNMBERIM 311
 QY 227 FLTALLFVP-IOHIOFNLHLENLXYG 253
 Db 312 FVIALSLVTGMQOVQSLNHFSSSVYGV 339

RESULT 11

004353 PRELIMINARY; PRT; 448 AA.
 AC 004353;
 DT 01-JUL-1997 (TEMBLrel. 04, Created)
 DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)
 DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
 DE Delta 6 desaturase
 OS Borago officinalis (Borragace) (Borage).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Boraginaceae; Borago.
 NC NCB1_TaxId=13363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97268723; PubMed=9108131;
 RA Sayanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,
 RA Christie W.W., Shewry P.R., Napier J.A.;
 RT "Expression of a borage desaturase cDNA containing an N-terminal
 RT cytochrome b5 domain results in the accumulation of high levels of
 RT delta6-desaturated fatty acids in transgenic tobacco."
 RT Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; U79010; AAC49700.1; -.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00467; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 448 AA; 51635 MW; B62EE701680909F CRC64;

Query Match 55.3%; Score 729.5; DB 10; Length 448;

Best Local Similarity 48.9%; Pred. No. 3.5e-61;
 Matches 131; Conservative 50; Mismatches 72; Indels 15; Gaps 2;

QY 1 LPPFSTSHRLSDTVSAASDYRLKFSDSLALNPNKGGTTSLILTLPLSYGV 60
 Db 72 LDFEFGYLYKDYVSSEVSKDYRKLYVEFSKMGLYDKKGMHIMPATLCFIAMLPAMSVYGV 131
 QY 61 LFDSTFVHYLSAALIGFLWIOSGMIGHDSGHYVNMISRLNRAIOISGNIIAGISIGM 120
 Db 132 LFCGCVLHFLFSCGLMGFLWIOSGMIGHDSGHYVNMISRLNRAIOISGNIIAGISIGM 191
 QY 121 WKNHNAHNIACNSLDYDPDLOHMPVAVSSRFNSITSHXGRKKEFDXIAFLICYQH 180
 Db 192 WKNHNAHNIACNSLEVDPLQYIPLVYSSKFFGSLTSHFYERKRLTFDSLSRFVSYQH 251
 QY 181 FTFYPMCVARVNLVYQITILLFSRXXVQDRAINIMGILVFWTF-----L 226
 Db 252 WTFYPMCAARLNMVYQSLIMLTILKRVNSYRAQELLGLVFSIWIYPLVSCLPNMBERIM 311

QY 227 FLTALLFVP-IOHIOFNLHLENLXYG 253
 Db 312 FVIALSLVTGMQOVQSLNHFSSSVYGV 339

RESULT 12

092UT8 PRELIMINARY; PRT; 469 AA.
 AC 092UT8;
 DT 01-MAY-1999 (TEMBLrel. 10, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE S276.
 GN S276.
 OS Triticum aestivum (wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Triticum.
 NC NCB1_TaxId=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. ET3;
 RA Delhaize E., Hebb D.M., Gardner R.C., Richards K.D.;
 RT "Aluminum tolerance in yeast conferred by over-expression of wheat
 RT gene.";
 RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AF031194; AAD10250.1; -.
 DR HSP; P00171; 115U.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR InterPro; IPR001092; H4H_basit.
 DR Pfam; PF00467; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR PRINTS; PR00363; CYTOCHROME_B5.
 DR ProDom; PD000612; Cyt B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 469 AA; 52617 MW; 16F223C01F79740D CRC64;

Query Match 52.1%; Score 686.5; DB 10; Length 469;

Best Local Similarity 48.1%; Pred. No. 4.6e-57;
 Matches 125; Conservative 46; Mismatches 74; Indels 15; Gaps 1;

QY 9 RLSDDTVSAASDYRLKFSDSLALNPNKGGTTSLILTLPLSYGV 68
 Db 100 RLTDYTVPPASADFRLALQSSAGLFEVGHTPKFLVAMSVLFCIALYCVLACSTGA 159
 QY 69 HVLSAALIGFLWIOSGMIGHDSGHYVNMISRLNRAIOISGNIIAGISIGMKNHNAH 128
 Db 160 HMFAGLIGFLWIOSGMIGHDSGHYVNMISRLNRAIOISGNIIAGISIGMKNHNAH 219
 QY 129 HICNSLDYDPDLOHMPVAVSSRFNSITSHXGRKKEFDXIAFLICYQHFTFYVNC 188
 Db 220 HICNSLDYDPDLOHMPVAVSSRFNSITSHXGRKKEFDXIAFLICYQHFTFYVNC 279
 QY 189 VARVNLVYQITILLFSRXXVQDRAINIMGILVFWTF-----F 233
 Db 280 FARINLVQSIYVFLIQKQRQWLEIAGVAAFWVYPLVSCLPNMBERVAVLASFYI 339
 QY 234 VPIQHIOFNLHLENLXYG 253
 Db 340 TGIQHVQFLNHFSSSVYGV 359
 RESULT 13
 ID 08L717 PRELIMINARY; PRT; 448 AA.
 AC 08L717;
 DT 01-OCT-2002 (TEMBLrel. 22, Created)
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
 DE Delta-6-desaturase.
 OS Argania spinosa.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridales; Ericales; Sapotaceae; Argania.
 RN NCB1_TaxID=85884;
 RP SEQUENCE FROM N.A.
 RA El Filali A., Anderson M., Abbas K.;
 RT "Characterization and cloning of delta-6-desaturase in Argania spinosa
 fruit.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AY131238; AAM94345.1; -
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme 1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 448 AA; 51304 MW; 0B46F81B7DEE29EF CRC64;
 Query Match 51.5%; Score 678.5; DB 10; Length 448;
 Best Local Similarity 46.6%; Pred. No. 2.5e-56;
 Matches 125; Conservative 49; Mismatches 79; Indels 15; Gaps 2;
 QY 1 LPAFSTSHRLSDHTVSAASDYKRLPSDLALNLFNKGHTTSLILSLTLFPLSVGV 60
 DB 72 LDFEFGYVLYKDYVSSEVSKDYKLVPEFSKMGLYDKAGHMFATLCFIMLFAMSYGV 111
 QY 61 LPEDSFVYVLSAALIGFLMIOGSGHDSGHYVWMLSRNLNLAIOQLSGNIAGSIGW 120
 DB 132 LRCEGVLYHLSQCLMGFLMIOGSGHDSGHYVWMLSRNLNLAIOQLSGNIAGSIGW 191
 QY 121 WKNHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAH 180
 DB 192 SKNNHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAHNAH 251
 QY 181 FTFYVWCARVNLVLTQTLILFSSRXKVDNALINMGLVFWTF-----L 226
 DB 252 WTFYTIMCARLNMVYQSLIMLTGRNVSYRAHEHLCGLVFSIWPPLVSCLPNGERIM 311
 QY 227 FLIALLFVP-IGHIQFNLNLAENLYXG 253
 DB 312 FVIASLSVTGMQOVFSLNHFSSSVYVG 339
 RESULT 14
 Q9HDG8 PRELIMINARY; PRT; 523 AA.
 AC Q9HDG8;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
 DE Delta-6 desaturase.
 OS Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
 OC Mucor.
 RN NCB1_TaxID=29923;
 RP SEQUENCE FROM N.A.
 RA STRAIN=ATCC 24905;
 RC MEDLINE=20563795; Pubmed=11112411;
 RA Laoteng K., Mannontarat R., Tanticharoen M., Cheevadhanarak S.;
 RT "Delta(6)-desaturase of Mucor rouxii with high similarity to plant
 delta(6)-desaturase and its heterologous expression in Saccharomyces
 cerevisiae.";
 RL Biochem. Biophys. Res. Commun. 279:17-22(2000).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AF296076; AAG36960.1; -

DR EMBL: AF296083; AAG36959.1; -
 DR HSP; P00173; 1EX.
 DR InterPro: IPR001525; C5_DNA_mech.
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme 1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS00095; C5_MTASE_2; 1.
 DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 523 AA; 60622 MW; A03727AF39EB7857 CRC64;
 Query Match 28.6%; Score 377.5; DB 3; Length 523;
 Best Local Similarity 32.5%; Pred. No. 1.3e-27;
 Matches 81; Conservative 46; Mismatches 87; Indels 35; Gaps 5;
 QY 22 YRLLFSDLSALNLFN-----RKG--HTTSLILSLTLFPLSVGVLSFSDTFVYVLS 72
 DB 167 YRLLFSDLSALNLFN-----RKG--HTTSLILSLTLFPLSVGVLSFSDTFVYVLS 217
 QY 73 AALIGFLMIOGSGHDSGHYVWMLSRNLNLAIOQLSGNIAGSIGWKMNNHNAHNAHNAH 132
 DB 218 AAFMAFMHQLVPTADAGHNETGKSEIDHVGIVIANPISGLSGWMDNNHNAHNAHNAH 277
 QY 133 NSLDYDPLQHPVAVSSRFNSITSHYGRKEDXIAFLICYQHPFVWCVARV 192
 DB 278 NHEHDPDIOHVFMAITTKFPNNIYSTYKRLPFDASRFVRQHYLYLISFGRF 337
 QY 193 NLYLQTLILFSSRXKVDNALINMGLVFWTFPLLA-----LFLVPI 236
 DB 338 NLRRLSFAYLLTCNVKRLTLVLTGLTFPFWGSLSTLPTNIRIAYIMSYMLTFPL 397
 QY 237 OHIQFWLNH 245
 DB 398 -HQVITLSH 405
 RESULT 15
 Q8NKG8 PRELIMINARY; PRT; 573 AA.
 AC Q8NKG8;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 23, last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
 DE Putative delta 8-sphingolipid desaturase.
 OS Kluyveromyces fragilis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 RN NCB1_TaxID=28985;
 RP SEQUENCE FROM N.A.
 RA STRAIN=IFO 1090;
 RA Takakuwa N., Kinoshita M., Oda Y., Ohnishi M.;
 RT "Isolation and characterization of the genes encoding delta 8-
 sphingolipid desaturase from Saccharomyces kluyveri and Kluyveromyces
 fragilis.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AB085690; BAB93118.1; -
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme 1; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 573 AA; 67065 MW; 9383EBA4333F1A57 CRC64;
 Query Match 26.0%; Score 342.5; DB 3; Length 573;
 Best Local Similarity 29.2%; Pred. No. 3.1e-24;

Matches 75; Conservative 53; Mismatches 92; Indels 37; Gaps 5;

QY 19 SSDYRKLFDLSALNLFNRKGHTTSILSLILFLPLSVGVLPSDSTFY-----HYLSA 73
 Db 195 ASEYRKLHGRTYAGLYQ-----CNVRYRLREFLRIGTLFGISFYLLSLKWPALSA 245

QY 74 ALIGFLWIOSGWIQHDGSHYVNLRLRAIOILSGNLAGISIGWKNHNAHHIACN 133
 Db 246 ICLGFAMQQLVFLAHADGHISITHNYQVDNIGMTVASWIGSLGSKWKRKHVDVHLLVTN 305

QY 134 SLDDYDPLQMPVPAVSSRFNSITSHXGKCKEFDXIAFLICYQHTFYPMCVARVN 193
 Db 306 DPVHDDPDICHTLPEFAVSTRLFHNVTSTYDCKFLMFDKFAQKVVPICQHYLYPILCFGRFN 365

QY 194 LY-LQTIILLFSRXKVQDRA-----ININGILVFWTWELFLALLFVP----- 235
 Db 366 LYRLSMWHVLLGGGPRGRKAMFRYYELAEISFPNYWFFYLITYKQMPINAERPKYVMIS 425

QY 236 -----IQHIQFWLNHLA 247
 Db 426 HIATMTIVHQITLSHFA 442

Search completed: January 1, 2004, 06:33:55
 Job time : 23.907 secs

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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 8.78981 Seconds
(without alignments)
1217.848 Million cell updates/sec

Title: US-09-857-524B-6
Perfect score: 1318
Sequence: 1 LPFSTSHRLSDHTVSAASS.....VPQHIFWNLHLENLYXG 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/2/1aa/6CTOS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	753.5	57.2	452	4	US-08-934-254-27 Sequence 27, Appl
2	730.5	55.4	448	1	US-08-366-779-5 Sequence 5, Appl
3	730.5	55.4	448	1	US-08-789-936-5 Sequence 5, Appl
4	730.5	55.4	448	2	US-08-934-254-5 Sequence 5, Appl
5	721.5	54.7	446	2	US-08-833-610-5 Sequence 5, Appl
6	721.5	54.7	446	3	US-08-834-033A-15 Sequence 15, Appl
7	682.5	51.8	252	2	US-08-834-655-7 Sequence 7, Appl
8	682.5	51.8	252	3	US-08-834-033A-8 Sequence 8, Appl
9	682.5	51.8	252	4	US-09-363-574-7 Sequence 7, Appl
10	682.5	51.8	252	4	US-09-363-574-7 Sequence 7, Appl
11	291	22.1	104	2	US-08-834-655-6 Sequence 6, Appl
12	291	22.1	104	3	US-08-834-033A-7 Sequence 7, Appl
13	291	22.1	104	3	US-09-363-574-6 Sequence 6, Appl
14	291	22.1	104	4	US-09-363-574-6 Sequence 6, Appl
15	247.5	18.8	457	2	US-08-834-655-2 Sequence 2, Appl
16	247.5	18.8	457	3	US-08-834-033A-2 Sequence 2, Appl
17	247.5	18.8	457	4	US-09-363-574-2 Sequence 2, Appl
18	247.5	18.8	457	4	US-09-363-574-2 Sequence 2, Appl
19	247.5	18.8	457	4	US-09-330-235-18 Sequence 18, Appl
20	247.5	18.8	458	4	US-09-439-261-10 Sequence 10, Appl
21	247.5	18.8	458	4	US-09-439-261-44 Sequence 44, Appl
22	247.5	18.8	458	4	US-09-227-613-11 Sequence 11, Appl
23	247.5	18.8	458	4	US-09-227-613-11 Sequence 11, Appl
24	245.5	18.6	355	2	US-08-834-655-5 Sequence 5, Appl
25	245.5	18.6	355	3	US-08-834-033A-6 Sequence 6, Appl
26	245.5	18.6	355	3	US-09-363-574-5 Sequence 5, Appl
27	245.5	18.6	355	4	US-09-363-574-5 Sequence 5, Appl

28	245.5	18.6	457	2	US-08-833-610-4 Sequence 4, Appl
29	245.5	18.6	457	3	US-08-834-033A-14 Sequence 14, Appl
30	241.5	18.3	323	4	US-09-439-261-17 Sequence 17, Appl
31	241.5	18.3	323	4	US-09-227-613-17 Sequence 17, Appl
32	160.5	12.2	360	4	US-09-439-261-41 Sequence 41, Appl
33	160.5	12.2	360	4	US-09-227-613-39 Sequence 39, Appl
34	160.5	12.2	444	4	US-09-439-261-11 Sequence 11, Appl
35	160.5	12.2	444	4	US-09-227-613-12 Sequence 12, Appl
36	160.5	12.2	445	4	US-09-439-261-39 Sequence 39, Appl
37	160.5	12.2	445	4	US-09-439-261-45 Sequence 45, Appl
38	158	12.0	432	4	US-09-439-261-9 Sequence 9, Appl
39	158	12.0	432	4	US-09-227-613-9 Sequence 9, Appl
40	158	12.0	465	4	US-09-439-261-40 Sequence 40, Appl
41	158	12.0	465	4	US-09-227-613-38 Sequence 38, Appl
42	156.5	11.9	444	4	US-09-048-888-3 Sequence 3, Appl
43	153.5	11.6	444	4	US-09-439-261-43 Sequence 43, Appl
44	153.5	11.6	444	4	US-09-227-613-42 Sequence 42, Appl
45	150.5	11.4	445	4	US-09-048-888-1 Sequence 1, Appl

ALIGNMENTS

```
RESULT 1
US-08-934-254-27
; Sequence 27, Application US/08934254
; Patent No. 6355861
;
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESS: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,254
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 83832XXWVU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-934-254-27
;
; Query Match 57.2%; Score 753.5; DB 4; Length 452;
; Best Local Similarity 53.2%; Pred. No. 1e-76;
; Matches 142; Conservative 37; Mismatches 73; Indels 15; Gaps 2;
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; QY 2 PAFSTSHRLSDHTVSAASSDYRKLPDSIALNLNFKGHTTSLISLTLPPLSVCCVL 61
; DB 74 PLFCGYVYVLAALIGFLMIQSGWIGHDSGHYNNWLSRLRAIQLISGNIAGISIGMW 121
; QY 62 FSDSTFVYVLAALIGFLMIQSGWIGHDSGHYNNWLSRLRAIQLISGNIAGISIGMW 121
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Db 134 ASBVGVMHLCGALLGLWIAQAVYGHDSGHYQVMPFRGVNRTQILAGNITLGISIAM 193
 Qy 122 KKNHNAHHIACNSLDYDPPDIQMPVAVSRFRNSITSHXGKKEPDIXALFLICYOH 181
 Db 194 KMTNHHHACNSLDYDPPDIQMPVAVSRFRNSITSHXGKKEPDIXALFLICYOH 253
 Qy 182 TFPVAVCVARVNLVYQITLLFSRXKQODRALNMGILVFWTWL-F- 227
 Db 254 TFPVAVCVARVNLVYQITLLFSRXKQODRALNMGILVFWTWL-F- 313
 Qy 228 -LLALLFVPIQIHFVNLHLENLXXG 253
 Db 314 VLISFAVTAIQHVQFTLNHFSGDTYVG 340

RESULT 2
 US-08-366-779-5
 ; Sequence 5, Application US/08366779
 ; Patent No. 5614393
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; APPLICANT: Reddy, Avutu S.
 ; APPLICANT: Nuccio, Michael
 ; APPLICANT: Freysinet, Georges L.
 ; APPLICANT: Nunberg, Andrew N.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; TITLE OF INVENTION: DELTA 6-DESATURASE
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/366,779
 ; FILING DATE: 30-DEC-1994
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 83832YXX
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 448 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-366-779-5

Query Match 55.4%; Score 730.5; DB 1; Length 448;
 Best Local Similarity 48.9%; Pred. No. 4e-74;
 Matches 11; Conservative 50; Mismatches 72; Indels 15; Gaps 2;
 Qy 1 LPAFSTSHSLDHTVSAASDVRKLFSDLSALNLFNRKGGHTTSILSLITLTPPLSVCGV 60
 Db 72 LDKFPGYVILKXSVSEVSKDVRKLVFERSKMGLYDKKGIMFATLCFIAMLPAMSVYGV 131
 Qy 61 LPSDSTFVHLSAALIGFLMIQSGWIGHDSGHYVNLSSRLNRAIQLISGNILAGISIGW 120
 Db 132 LFCBGLVHLFGSGLMGFLMIQSGWIGHDSGHYVNLSSRLNRAIQLISGNILAGISIGW 191

Qy 121 KKNHNAHHIACNSLDYDPPDIQMPVAVSRFRNSITSHXGKKEPDIXALFLICYOH 180
 Db 192 KKNHNAHHIACNSLDYDPPDIQMPVAVSRFRNSITSHXGKKEPDIXALFLICYOH 251
 Qy 181 TFPVAVCVARVNLVYQITLLFSRXKQODRALNMGILVFWTWL-F- 226
 Db 252 TFPVAVCVARVNLVYQITLLFSRXKQODRALNMGILVFWTWL-F- 311
 Qy 227 FLALLFVPIQIHFVNLHLENLXXG 253
 Db 312 VLISFAVTAIQHVQFTLNHFSGDTYVG 339

RESULT 3
 US-08-789-936-5
 ; Sequence 5, Application US/08789936
 ; Patent No. 5789220
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; APPLICANT: Reddy, Avutu S.
 ; APPLICANT: Nuccio, Michael
 ; APPLICANT: Freysinet, Georges L.
 ; APPLICANT: Nunberg, Andrew N.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; TITLE OF INVENTION: DELTA 6-DESATURASE
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/789,936
 ; FILING DATE: 28-JAN-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/366,779
 ; FILING DATE: 30-DEC-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 83832YXX
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 448 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE:
 ; US-08-789-936-5

Query Match 55.4%; Score 730.5; DB 1; Length 448;
 Best Local Similarity 48.9%; Pred. No. 4e-74;
 Matches 11; Conservative 50; Mismatches 72; Indels 15; Gaps 2;
 Qy 1 LPAFSTSHSLDHTVSAASDVRKLFSDLSALNLFNRKGGHTTSILSLITLTPPLSVCGV 60
 Db 72 LDKFPGYVILKXSVSEVSKDVRKLVFERSKMGLYDKKGIMFATLCFIAMLPAMSVYGV 131
 Qy 61 LPSDSTFVHLSAALIGFLMIQSGWIGHDSGHYVNLSSRLNRAIQLISGNILAGISIGW 120
 Db 132 LFCBGLVHLFGSGLMGFLMIQSGWIGHDSGHYVNLSSRLNRAIQLISGNILAGISIGW 191

QY 121 WKNNHNAHHIACNSLDYDLDQMPVFAVSSRFNSITSHXGRKKEFDXIAFLICYOH 180
 DB 192 WKNNHNAHHIACNSLEYDLDQYIPFLVSSKFFGSLTSHFEKRLTFPSLSRFPVSYOH 251
 QY 181 FTFYPMCAARVNLVYQITILLFSSKXKQDRALNIGILVFWTF-----L 226
 DB 252 WTFYPMCAARLNMVYQSLIMLTTRKRVSYRAOELGLCVFSIWYPLVSCLPNMBERIM 311
 QY 227 FLTALLFVP-IOHIOFWLNHLAENLYXG 253
 DB 312 FVIAISLVTGMQOVQPSLNHFSSSVYVG 339
 RESULT 4
 US-08-934-254-5
 ; Sequence 5, Application US/08934254
 ; Patent No. 6355861
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Releasee #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/934,254
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 83832ZYXWVU
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4356
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 448 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Protein
 ; US-08-934-254-5
 Query Match 55.4%; Score 730.5; DB 4; Length 448;
 Best local Similarity 48.9%; Pred. No. 4e-74;
 Matches 111; Conservative 50; Mismatches 72; Indels 15; Gaps 2;
 QY 1 LPAFSTSHRLSDHTVSAASSDYRKLFSDLSALNLFNRKGGHTTISLILTLTFLPPLSVCGV 60
 DB 72 LDKFFGYVLYKDYSEVSKDYRKLVFEFSKMGLYDKGHIMFATLCFIAMLFAMSVYGV 131
 QY 61 LPSDSFFVAVLSAALIGFLMIOGWTGHDGSHYNNWLSRLNRAIQILSGNIIAGISIGW 120
 DB 132 LFCBGLVHLFSCCLMGFLMIOGWTGHDGSHYNNWLSRLNRAIQILSGNIIAGISIGW 191
 QY 121 WKNNHNAHHIACNSLDYDLDQMPVFAVSSRFNSITSHXGRKKEFDXIAFLICYOH 180
 DB 192 WKNNHNAHHIACNSLEYDLDQYIPFLVSSKFFGSLTSHFEKRLTFPSLSRFPVSYOH 251
 QY 181 FTFYPMCAARVNLVYQITILLFSSKXKQDRALNIGILVFWTF-----L 226
 DB 252 WTFYPMCAARLNMVYQSLIMLTTRKRVSYRAOELGLCVFSIWYPLVSCLPNMBERIM 311

QY 227 FLTALLFVP-IOHIOFWLNHLAENLYXG 253
 DB 312 FVIAISLVTGMQOVQPSLNHFSSSVYVG 339
 RESULT 5
 US-08-833-610-5
 ; Sequence 5, Application US/08833610
 ; Patent No. 5972664
 ; GENERAL INFORMATION:
 ; APPLICANT: KNOTZON, DEBORAH
 ; APPLICANT: MURKERJI, PRADIP
 ; APPLICANT: HUANG, YUNG-SHENG
 ; APPLICANT: THURMOND, JENNIFER
 ; APPLICANT: CHAUDHARY, SUNITA
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
 ; STREET: 260 SHERIDAN AVE, P.O. BOX 60039
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Releasee #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/833,610
 ; FILING DATE: 11-APR-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RAE-VENTER, BARBARA
 ; REGISTRATION NUMBER: 32,750
 ; REFERENCE/DOCKET NUMBER: CGNE.123.000S
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 328-4400
 ; TELEFAX: (650) 328-4477
 ; TELEX: N/A
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 446 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-833-610-5
 Query Match 54.7%; Score 721.5; DB 2; Length 446;
 Best local Similarity 48.5%; Pred. No. 4.1e-73;
 Matches 130; Conservative 50; Mismatches 73; Indels 15; Gaps 2;
 QY 1 LPAFSTSHRLSDHTVSAASSDYRKLFSDLSALNLFNRKGGHTTISLILTLTFLPPLSVCGV 60
 DB 72 LDKFFGYVLYKDYSEVSKDYRKLVFEFSKMGLYDKGHIMFATLCFIAMLFAMSVYGV 131
 QY 61 LPSDSFFVAVLSAALIGFLMIOGWTGHDGSHYNNWLSRLNRAIQILSGNIIAGISIGW 120
 DB 132 LFCBGLVHLFSCCLMGFLMIOGWTGHDGSHYNNWLSRLNRAIQILSGNIIAGISIGW 191
 QY 121 WKNNHNAHHIACNSLDYDLDQMPVFAVSSRFNSITSHXGRKKEFDXIAFLICYOH 180
 DB 192 WKNNHNAHHIACNSLEYDLDQYIPFLVSSKFFGSLTSHFEKRLTFPSLSRFPVSYOH 251
 QY 181 FTFYPMCAARVNLVYQITILLFSSKXKQDRALNIGILVFWTF-----L 226
 DB 252 WTFYPMCAARLNMVYQSLIMLTTRKRVSYRAOELGLCVFSIWYPLVSCLPNMBERIM 311
 QY 227 FLTALLFVP-IOHIOFWLNHLAENLYXG 253

Db 312 FVIASLSVTGMQOVQFSLNHFSSSVYVG 339

RESULT 6

US-08-834-033A-15

Sequence 15, Application US/08834033A

Patent No. 6075183

GENERAL INFORMATION:

APPLICANT: KNOTZON, DEBORAH

APPLICANT: MURKERT, PRADIP

APPLICANT: HUANG, YUNG-SHENG

APPLICANT: THURMOND, JENNIFER

APPLICANT: CHAUDHARY, SUNITA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.

STREET: 2001 FERRY BUILDING

CITY: SAN FRANCISCO

STATE: CA

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/834,033A

FILING DATE: 11-Apr-1997

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: WARD, MICHAEL R.

REGISTRATION NUMBER: 38,651

REFERENCE/DOCKET NUMBER: CGAB-300, USA

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 433-4150

TELEFAX: (415) 433-8716

TELEX: N/A

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 446 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-834-033A-15

Query Match

Best Local Similarity 54.7%; Score 721.5; DB 3; Length 446;

Matches 130; Conservative 50; Mismatches 73; Indels 15; Gaps 2;

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

RESULT 7

US-08-834-655-7

Sequence 7, Application US/08834655

Patent No. 5968809

GENERAL INFORMATION:

APPLICANT: KNOTZON, DEBORAH

APPLICANT: MURKERT, PRADIP

APPLICANT: HUANG, YUNG-SHENG

APPLICANT: THURMOND, JENNIFER

APPLICANT: CHAUDHARY, SUNITA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: RAE-VENTER LAW GROUP, P.C.

STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039

CITY: PALO ALTO

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/834,655

FILING DATE: 11-Apr-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: RAE-VENTER, BARBARA

REGISTRATION NUMBER: 32,750

REFERENCE/DOCKET NUMBER: CGNE.124.0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 328-4400

TELEFAX: (650) 328-4477

TELEX: N/A

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 252 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-834-655-7

Query Match

Best Local Similarity 51.8%; Score 682.5; DB 2; Length 252;

Matches 125; Conservative 27; Mismatches 43; Indels 15; Gaps 2;

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

RESULT 8

US-08-834-033A-8

Sequence 8, Application US/08834033A

Patent No. 6075183

GENERAL INFORMATION:

APPLICANT: KNOTZON, DEBORAH

APPLICANT: MURKERT, PRADIP

APPLICANT: HUANG, YUNG-SHENG

APPLICANT: THURMOND, JENNIFER

APPLICANT: CHAUDHARY, SUNITA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: RAE-VENTER LAW GROUP, P.C.

STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039

CITY: PALO ALTO

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/834,655

FILING DATE: 11-Apr-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: RAE-VENTER, BARBARA

REGISTRATION NUMBER: 32,750

REFERENCE/DOCKET NUMBER: CGNE.124.0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 328-4400

TELEFAX: (650) 328-4477

TELEX: N/A

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 252 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-834-655-7

Query Match

Best Local Similarity 59.5%; Score 682.5; DB 2; Length 252;

Matches 125; Conservative 27; Mismatches 43; Indels 15; Gaps 2;

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

```

GENERAL INFORMATION:
APPLICANT: KUTZON, DEBORAH
APPLICANT: MURKERT, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300, USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-8

Query Match
Best local Similarity 51.8%; Score 682.5; DB 3; Length 252;
Matches 125; Conservative 27; Mismatches 43; Indels 15; Gaps 2;

QY 59 GVLFSSTFVHVAALIGFLWIOGMIHDSGHVYVMSRLNRAIQILSGNLAGIST 118
DB 5 GVLACTSVFAHQIAAALLGLMIQSAVIGHDSGHVYVMSKSYNRFQQLSGNCLGIST 64
QY 119 GAWKMNHNAHIAACNSLDYDPDLOHMPVAVSSRFNSITSHYKXKEDXIAFLICY 178
DB 65 AAWKMTNNAHIAACNSLDYDPDLOHMPVAVSSRFNSITSHYKXKEDXIAFLICY 124
QY 179 QHFTFVPMCVARVNLVYLOTITLLFSRXKYODRALNIMGLVFWTWFLFLLALL----- 232
DB 125 QHFTFVPMCVARVNLVYLOTITLLFSRXKYODRALNIMGLVFWTWFLFLLALL----- 232
QY 233 --FV-----PIQHIOFWLNLAEMLYXG 253
DB 185 FFEVFTSFVTALQHIOFTLNFPAADVYVG 214

RESULT 9
US-09-363-574-7
Sequence 7, Application US/09363574
Patent No. 6136574
GENERAL INFORMATION:
APPLICANT: KUTZON, DEBORAH
APPLICANT: MURKERT, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA

```

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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-574-7

Query Match
Best local Similarity 51.8%; Score 682.5; DB 3; Length 252;
Matches 125; Conservative 27; Mismatches 43; Indels 15; Gaps 2;

QY 59 GVLFSSTFVHVAALIGFLWIOGMIHDSGHVYVMSRLNRAIQILSGNLAGIST 118
DB 5 GVLACTSVFAHQIAAALLGLMIQSAVIGHDSGHVYVMSKSYNRFQQLSGNCLGIST 64
QY 119 GAWKMNHNAHIAACNSLDYDPDLOHMPVAVSSRFNSITSHYKXKEDXIAFLICY 178
DB 65 AAWKMTNNAHIAACNSLDYDPDLOHMPVAVSSRFNSITSHYKXKEDXIAFLICY 124
QY 179 QHFTFVPMCVARVNLVYLOTITLLFSRXKYODRALNIMGLVFWTWFLFLLALL----- 232
DB 125 QHFTFVPMCVARVNLVYLOTITLLFSRXKYODRALNIMGLVFWTWFLFLLALL----- 232
QY 233 --FV-----PIQHIOFWLNLAEMLYXG 253
DB 185 FFEVFTSFVTALQHIOFTLNFPAADVYVG 214

RESULT 10
US-09-363-526-7
Sequence 7, Application US/09363526
Patent No. 6410288
GENERAL INFORMATION:
APPLICANT: KUTZON, DEBORAH
APPLICANT: MURKERT, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING

```

CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,526
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-201 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-526-7

Query Match 51.8%; Score 682.5; DB 4; Length 252;
Best Local Similarity 59.5%; Pred. No. 4,7e-69;
Matches 125; Conservative 27; Mismatches 43; Indels 15; Gaps 2;

QY 59 GVLPSTFVHVLSAALIGFLMIGSGHSGHYNMLSRLNRAIQIISGNIAGISL 118
DB 5 GVLACTSVFPAHQIAALIGLMLTOSAYIGHDSGHVYMSNKSXNRFQALISGNCITGISI 64

QY 119 GWMKMNHNHHIACNSLDYDPDLOHMPVFVSSRFPSISHXYYGRXEPDITAXFLICY 178
DB 65 AMKMKWTHNHHIACNSLDYDPDLOHMPVFVSSRFPSISHXYYGRXEPDITAXFLICY 124

QY 179 QHFTFVPMCVARVNLVLTILLFSRXKVQDRALNIMGILVFWTFELFLALL----- 232
DB 125 QHFTFVPMCVARVNLVLTILLFSRXKVQDRALNIMGILVFWTFELFLALL----- 232

QY 233 --FV-----PIQHIOFWNLHIAENLYXG 253
DB 185 FFEVFTSFVTALQHIQFIHHPADVYVG 214

RESULT 11
US-08-834-655-6
Sequence 6, Application US/08834655
Patent No. 5968809
GENERAL INFORMATION:
APPLICANT: KUNTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGAB-300 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-655-6

Query Match 22.1%; Score 291; DB 2; Length 104;
Best Local Similarity 52.4%; Pred. No. 2.3e-25;
Matches 55; Conservative 15; Mismatches 25; Indels 10; Gaps 2;

QY 50 LTLPLPS-----VCCVLPDSSTFVHVLSAALIGFLMIGSGHSGHYNMLSRL 100
DB 1 VTLVTLAPVANSIGLVGLVACPSVPHQIAAGLGLMIGSAYIGXSGHYNMKS 60

QY 101 LNRALQISGNIAGISIGMWMKMNHNHHIACNSLDYDPDLOHMP 145
DB 61 NNXFAQLISGNCITGI-1AMKMKWTHNHHIACNSLDYGPVLCITP 104

RESULT 12
US-08-834-033A-7
Sequence 7, Application US/08834033A
Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KUNTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716

TELEX: N/A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-7

Query Match 22.1%; Score 291; DB 3; Length 104;
Best Local Similarity 52.4%; Pred. No. 2.3e-25;
Matches 55; Conservative 15; Mismatches 25; Indels 10; Gaps 2;

QY 50 LTLFPLS-----VCGVLFSDSTFVHLSAALIGFLMIOGWI GHDGHNWLSRR 100
DB 1 VTLVTLAFPAANSLSGLVGLVACPSVXPHQIAAGLGLMIOGSAVIGXDSGHVIMSNKS 60
QY 101 LNRATQILSGNITLACISIGWKKNNNAHHIACNSLDYDPDLQHP 145
DB 61 NNXPQQLLSGNCLTGI-IAMWKTHNAHHLACNSLDYGNLQHIP 104

RESULT 13
US-09-363-574-6
Sequence 6, Application US/09363574
Patent No. 6136574

GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 PERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-574-6

Query Match 22.1%; Score 291; DB 3; Length 104;
Best Local Similarity 52.4%; Pred. No. 2.3e-25;
Matches 55; Conservative 15; Mismatches 25; Indels 10; Gaps 2;

QY 50 LTLFPLS-----VCGVLFSDSTFVHLSAALIGFLMIOGWI GHDGHNWLSRR 100
DB 1 VTLVTLAFPAANSLSGLVGLVACPSVXPHQIAAGLGLMIOGSAVIGXDSGHVIMSNKS 60
QY 101 LNRATQILSGNITLACISIGWKKNNNAHHIACNSLDYDPDLQHP 145
DB 61 NNXPQQLLSGNCLTGI-IAMWKTHNAHHLACNSLDYGNLQHIP 104

RESULT 14
US-09-363-526-6
Sequence 6, Application US/09363526
Patent No. 6410288

GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 PERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,526
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-201 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-526-6

Query Match 22.1%; Score 291; DB 4; Length 104;
Best Local Similarity 52.4%; Pred. No. 2.3e-25;
Matches 55; Conservative 15; Mismatches 25; Indels 10; Gaps 2;

QY 50 LTLFPLS-----VCGVLFSDSTFVHLSAALIGFLMIOGWI GHDGHNWLSRR 100
DB 1 VTLVTLAFPAANSLSGLVGLVACPSVXPHQIAAGLGLMIOGSAVIGXDSGHVIMSNKS 60
QY 101 LNRATQILSGNITLACISIGWKKNNNAHHIACNSLDYDPDLQHP 145
DB 61 NNXPQQLLSGNCLTGI-IAMWKTHNAHHLACNSLDYGNLQHIP 104

RESULT 15
US-08-834-655-2
Sequence 2, Application US/08834655
Patent No. 5968809
GENERAL INFORMATION:

APPLICANT: KNUITZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A.
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-655-2

Query Match 18.8%; Score 247.5; DB 2; Length 457;
Best Local Similarity 26.7%; Pred. No. 1.5e-19;
Matches 64; Conservative 45; Mismatches 110; Indels 21; Gaps 6;
QY 19 SSDYRKLFSDLSALNLFNRKHTTSLILTLFPLS--VCGVLESDSTFVHLSAALI 76
DB 101 AAEVRKRLTFLFQSLGYDSSKAYAFVFSNLCIWTGISTVIYAKWGQSTLANVLSAALL 160
QY 77 GFLMIOGWIIGHDSGHYVWMLSRRLNRAIQILSGNIIAGISIGWKKNNHNAHHIACNSLD 136
DB 161 GLFWQCGWLAHDFLHQVQDFRFGDLFGAFLGVCQGSSSWKKDKNTHHAAPVHVG 220
QY 137 YDPLQHPVPAVSS--REFNSITSHXYGRKKEFDXIAAFELICYHFTFYVWCVARVN 193
DB 221 EDDPDIDTHPLTWSEHALMEFSDVDPDEBLTRMW----SRFVNLNQTWFFYFPLISFARLS 275
QY 194 LVIQTILLF-----SRXKVQDRALNTMGILVFTWTFLLALLFV--PIQHIOFNL 243
DB 276 WCLQSILFVLPNGOAKRPAGARVPISLVEQLSLAMHTWYIATM-FLFIKDPVNMIVYFL 334

Search completed: January 1, 2004, 06:38:14
Job time: 9.98981 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:37:05 ; Search time 48.1975 Seconds
(without alignments)
1053.214 Million cell updates/sec

Title: US-09-857-524b-6
Perfect score: 1338
Sequence: 1 IFAFSTSHRLSDHTVSAASS.....VPQHIOFWLHIAEVLTXG 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 733937 seqs, 200641211 residues

Total number of hits satisfying chosen parameters: 733937

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Published Applications AA.*
2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	753.5	57.2	452	US-10-029-756-27	Sequence 27, Appl
2	747.5	56.7	458	US-10-340-779A-11	Sequence 11, Appl
3	730.5	55.4	448	US-10-029-756-5	Sequence 5, Appl
4	729.5	55.3	448	US-10-340-779A-13	Sequence 13, Appl
5	352.5	26.7	366	US-10-369-493-4137	Sequence 4137, Ap
6	258.5	19.6	453	US-09-769-863-14	Sequence 14, Appl
7	258.5	19.6	453	US-10-054-534B-14	Sequence 14, Appl
8	258.5	19.6	453	US-10-431-952-14	Sequence 14, Appl
9	247.5	18.8	457	US-10-278-391-4	Sequence 4, Appl
10	247.5	18.8	458	US-10-191-513A-11	Sequence 11, Appl
11	247.5	18.8	458	US-10-191-513A-41	Sequence 41, Appl
12	241.5	18.3	323	US-10-191-513A-17	Sequence 17, Appl
13	225.5	17.1	443	US-09-967-477B-8	Sequence 8, Appl
14	225.5	17.1	443	US-10-340-779A-20	Sequence 20, Appl
15	224.5	17.0	473	US-10-369-493-6108	Sequence 6108, Ap

16	198.5	15.1	448	US-10-340-779A-4	Sequence 4, Appl
17	188	14.3	454	US-10-369-493-6107	Sequence 6107, Ap
18	176	13.4	365	US-10-156-761-9835	Sequence 9835, Ap
19	175	13.3	353	US-10-156-761-9130	Sequence 9130, Ap
20	160.5	12.2	360	US-10-191-513A-39	Sequence 39, Appl
21	160.5	12.2	444	US-10-191-513A-12	Sequence 12, Appl
22	158	12.0	432	US-10-191-513A-9	Sequence 9, Appl
23	158	12.0	465	US-10-191-513A-38	Sequence 38, Appl
24	157	11.9	439	US-09-769-863-29	Sequence 29, Appl
25	157	11.9	439	US-10-054-534B-29	Sequence 29, Appl
26	157	11.9	439	US-10-431-952-29	Sequence 29, Appl
27	156.5	11.9	444	US-10-262-617-3	Sequence 31, Appl
28	154	11.7	439	US-10-054-534B-31	Sequence 31, Appl
29	153.5	11.6	444	US-10-191-513A-42	Sequence 42, Appl
30	150.5	11.4	445	US-10-262-617-1	Sequence 1, Appl
31	147	11.2	430	US-10-120-637A-69	Sequence 69, Appl
32	147	11.2	433	US-10-120-637A-55	Sequence 55, Appl
33	144	10.9	442	US-10-054-534B-35	Sequence 35, Appl
34	143	10.8	456	US-10-054-534B-33	Sequence 33, Appl
35	141.5	10.7	182	US-10-191-513A-20	Sequence 20, Appl
36	141	10.7	356	US-10-191-513A-18	Sequence 18, Appl
37	140	10.6	347	US-10-191-513A-40	Sequence 40, Appl
38	139.5	10.6	439	US-09-967-477B-4	Sequence 4, Appl
39	138	10.5	219	US-10-191-513A-19	Sequence 19, Appl
40	138	10.5	287	US-10-191-513A-14	Sequence 14, Appl
41	138	10.5	288	US-10-191-513A-15	Sequence 15, Appl
42	137.5	10.4	266	US-10-102-806-650	Sequence 650, App
43	136	10.3	261	US-10-104-047-2586	Sequence 2586, Ap
44	114	8.6	359	US-10-340-779A-12	Sequence 12, Appl
45	114	8.6	359	US-10-369-493-2766	Sequence 2766, Ap

ALIGNMENTS

RESULT 1
US-10-029-756-27
Sequence 27, Application US/10029756
Publication No. US20020108147A1
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/029, 756
FILING DATE: 21-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/934, 254
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19, 827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:

LENGTH: 452 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 27:
 US-10-029-756-27

Query Match 57.2%; Score 753.5; DB 14; Length 452;
 Best Local Similarity 53.2%; Pred. No. 1.2e-69;
 Matches 142; Conservative 37; Mismatches 73; Indels 15; Gaps 2;

QY 2 PAFSTSHRLSDHTVSAASDYRKLFSDSLALNLFNRKHTTSLILSLTLFPLSVGCVL 61
 DB 74 PLFTGYLYLKDPEVSEISKYRRLNEMSRSGIFKKGHIMWTFVAVMAAIVGV 133
 QY 62 FDSSTFVHVSALLGLFMIOGMIHDSGHYVWMLSRNLRAIQLISGNIAGISIGW 121
 DB 134 ASSESVHMLCGALLGLMIOAAVGHDSGHYVWMPTRGYNRTITQLIAGNITLGI 193
 QY 122 KMNHNAAHIACNSLDYDPLDQHPVFAVSSRPFNSITSHXGRKXEPDIXAFLLICQHF 181
 DB 194 KTHNAAHIACNSLDYDPLDQHPVFAVSTRLENSTSVYGRVLFKDEVARFLVSYQW 253
 QY 182 TFPVNCVAVRNLYQTILLFGRKKVQDRALNIMGLVFWTF-LF----- 227
 DB 254 TYPVNMIFGRVNLFIQTFLLLTRRDVDRALNMGIAVFWTFPLFVSCLPNMPERFGF 313
 QY 228 -LLALLFVPIQHIOFWNLNLAENLYXG 253
 DB 314 VLISFAVTAIQHVQFTLNHPSGDTYVG 340

RESULT 2

US-10-340-779a-11
 ; Sequence 11, Application US/10340779A
 ; Publication No.: US20030152983A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Napier, Johnathan A.
 ; APPLICANT: Michaelson, Louise
 ; APPLICANT: Stobart, Keith
 ; TITLE OF INVENTION: Desaturase
 ; FILE REFERENCE: 005407.00004
 ; CURRENT APPLICATION NUMBER: US/10/340, 779A
 ; PRIOR FILING DATE: 2003-03-24
 ; PRIOR APPLICATION NUMBER: US 09/582, 034
 ; PRIOR FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: PCT/GB98/03895
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: UK 9814034.6
 ; PRIOR FILING DATE: 1998-06-29
 ; PRIOR APPLICATION NUMBER: UK 9727256.1
 ; PRIOR FILING DATE: 1997-12-23
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 11
 ; LENGTH: 458
 ; TYPE: PRT
 ; ORGANISM: Helianthus annuus
 ; US-10-340-779a-11

Query Match 56.7%; Score 747.5; DB 12; Length 458;
 Best Local Similarity 52.8%; Pred. No. 1.2e-69;
 Matches 140; Conservative 40; Mismatches 66; Indels 19; Gaps 4;

QY 6 TSHRLSDHTVSAASDYRKLFSDSLALNLFNRKHTTSLILSLTLFPLSVGCVL 63
 DB 87 TGYHLKDQYSDISRDKLASERAKGMEKKGH--GVYSLCFVSLLSACVGVLYS 144
 QY 64 DSFFVHVSALLGLFMIOGMIHDSGHYVWMLSRNLRAIQLISGNIAGISIGW 123
 DB 145 GSFVHMLSGALLGLMIOAAVGHDSGHYVWMPTRGYNRTITQLIAGNITLGI 204
 QY 124 KMNHNAAHIACNSLDYDPLDQHPVFAVSSRPFNSITSHXGRKXEPDIXAFLLICQHF 183

DB 205 THNAAHIACNSLDYDPLDQHPVFAVSSKLFNSITSVFGRQLTFPDLARFVSQHYLY 264
 QY 184 YPNCVAVRNLYQTILLFGRKKVQDRALNIMGLVFWTFPLFALLL-----FV- 234
 DB 265 YPNCVAVRNLYQTILLFGRKKVQDRALNIMGLVFWTFPLFALLL-----FV- 324
 QY 235 -----PIQHIOFWNLNLAENLYXG 253
 DB 325 VSFVYGIQHIOFTLNHPSGDTYVG 349

RESULT 3

US-10-029-756-5
 ; Sequence 5, Application US/10029756
 ; Publication No.: US20020108147A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; DELTA 6-DESATURASE
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA: US/10/029, 756
 ; APPLICATION NUMBER: US/10/029, 756
 ; FILING DATE: 21-Dec-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/934,254
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 83832YXWVU
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 448 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 ; US-10-029-756-5

Query Match 55.4%; Score 730.5; DB 14; Length 448;
 Best Local Similarity 48.9%; Pred. No. 6.9e-68;
 Matches 131; Conservative 50; Mismatches 72; Indels 15; Gaps 2;

QY 1 LPAFSTSHRLSDHTVSAASDYRKLFSDSLALNLFNRKHTTSLILSLTLFPLSVGCVL 60
 DB 72 LDFEFTGYLYKDYSEVSKDYRKLVEFSKGLYDKGHIMWTFVAVMAAIVGV 131
 QY 61 LFSSTFVHVSALLGLFMIOGMIHDSGHYVWMLSRNLRAIQLISGNIAGISIGW 120
 DB 132 LDFEFTGYLYKDYSEVSKDYRKLVEFSKGLYDKGHIMWTFVAVMAAIVGV 191
 QY 121 KMNHNAAHIACNSLDYDPLDQHPVFAVSSRPFNSITSHXGRKXEPDIXAFLLICQHF 180
 DB 192 KMNHNAAHIACNSLDYDPLDQHPVFAVSSRPFNSITSHXGRKXEPDIXAFLLICQHF 251

QY 181 FFEYPMCVARNLYQITILLFSRXXKQDRAININGILVFWTF-----L 226
 Db 252 WFEYPMCAARLAMYQSILMLTKGNVSRQAGELLCGLVSIWYPLVSLCPNMGERRIM 311
 QY 227 FLIALLFVP-IGHIQFWLNLHLENLYXG 253
 Db 312 FVIASLSVTGMQOVQFSLNHFSSSVYVG 339

RESULT 4

US-10-340-779A-13
 ; Sequence 13, Application US/10340779A
 ; Publication No. US20030152983A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Napier, Jonathan A.
 ; APPLICANT: Michelson, Louise
 ; APPLICANT: Stobart, Keith
 ; TITLE OF INVENTION: Desaturase
 ; FILE REFERENCE: 005407.00004
 ; CURRENT APPLICATION NUMBER: US/10/340,779A
 ; CURRENT FILING DATE: 2003-03-24
 ; PRIOR APPLICATION NUMBER: US 09/582,034
 ; PRIOR FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: PCT/GB98/03895
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: UK 9814034.6
 ; PRIOR FILING DATE: 1998-06-29
 ; PRIOR APPLICATION NUMBER: UK 9727256.1
 ; PRIOR FILING DATE: 1997-12-23
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 448
 ; TYPE: PRT
 ; ORGANISM: Borago officinalis
 ; US-10-340-779A-13

Query Match 55.3%; Score 729.5; DB 12; Length 448;
 Best Local Similarity 48.9%; Pred. No. 8.8e-68;

Matches 131; Conservative 50; Mismatches 72; Indels 15; Gaps 2;

QY 1 LPAFSTSHRLSDHTVSAASDVRKLFPSDSLALNLFNRKGGHTSILSLITLPLPLSVCGV 60
 Db 72 LDFEFGYVLKDVSEBVSVDYRKLVFEFSKMGLYDKKGIMFATLCFLAMLVG 131
 QY 61 LFSDFTFVHLSALIGFLWTQSGWIGHDSGHYVNLMSRLNRAIQLSGNIIAGISIGW 120
 Db 132 LFCEGVLVHLSFSGCLMGFLWTQSGWIGHDAGHYMVVSDSLNKFMGIFANCLSGISIGW 191
 QY 121 WKNHNAHHIACNSLDYDPLQMPVPAVSSRFNSITSHXGRKKEFDXIAFLICYOH 180
 Db 192 WKNHNAHHIACNSLEDPDLYIPLVSSKFFSGTSHFYERKRLTFDSLRFVSYOH 251
 QY 181 FFEYPMCVARNLYQITILLFSRXXKQDRAININGILVFWTF-----L 226
 Db 252 WFEYPMCAARLAMYQSILMLTKGNVSRQAGELLCGLVSIWYPLVSLCPNMGERRIM 311
 QY 227 FLIALLFVP-IGHIQFWLNLHLENLYXG 253
 Db 312 FVIASLSVTGMQOVQFSLNHFSSSVYVG 339

RESULT 5

US-10-369-493-4137
 ; Sequence 4137, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 4137
 ; LENGTH: 366
 ; TYPE: PRT
 ; ORGANISM: Neurospora crassa

US-10-369-493-4137

Query Match 26.7%; Score 352.5; DB 12; Length 366;
 Best Local Similarity 31.3%; Pred. No. 1.7e-28;

Matches 78; Conservative 43; Mismatches 101; Indels 27; Gaps 4;

QY 22 YRKLFSDSLALNLFNRKGGHTSILSLITLPLPLSVCGVFSDFSTFVHLSAALIGFLWT 81
 Db 7 YRELNRIRAKGLYD-----CNYVAVAIEGFRYTLFCGCLLFLKMGVYVSAFCLGSPWH 62
 QY 82 QSGWIGHDSGHYVNLMSRLNRAIQLSGNIIAGISIGWKNHNAHHIACNSLDYDPL 141
 Db 63 QLVFTADAGHMGIHTHFHVDVYIGIILADFIGLSLGMKKNHNVHIIITNSPERDPDI 122
 QY 142 OHMPVPAVSSRFNSITSHXGRKKEFDXIAFLICYOFTFYPMCVARNLY-LQITL 200
 Db 123 EHLFFAISHREFTNLRSTYIDRWNEYDILFAKFFVSLQHYLYIIMFARLNIRLSWEY 182
 QY 201 LFSRXXKQ-----DRAININGILVFWTF-----LPLALLFVPLOH 238
 Db 183 LKGAQAPKRGAPAMWHRHLELVGVFWFCWFGYIMYKALDGMNRFVFMISHAVSPH 242
 QY 239 IQFWNLHLA 247
 Db 243 VOITLSHFA 251

RESULT 6

US-09-769-863-14
 ; Sequence 14, Application US/09769863
 ; Publication No. US20030157144A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pradip
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Das, Tapas
 ; APPLICANT: Thurmond, Jennifer
 ; APPLICANT: Pereira, Suzette L.
 ; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
 ; FILE REFERENCE: 6763 US 01
 ; CURRENT APPLICATION NUMBER: US/09/769,863
 ; CURRENT FILING DATE: 2001-01-25
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 453
 ; TYPE: PRT
 ; ORGANISM: Saprolegnia diclina
 ; US-09-769-863-14

Query Match 19.6%; Score 258.5; DB 12; Length 453;
 Best Local Similarity 26.3%; Pred. No. 1.5e-18;

Matches 69; Conservative 52; Mismatches 98; Indels 43; Gaps 9;

QY 3 AFSTSHRLSDHTVSAAS---SDYRKLFSDSLALNLF--NRKGGHTSILSLITLPLPLSV 57
 Db 85 AYDTS--ISDEVYKSGSDPIASRYKRLVYKGLVDSKLYLVYKCASTLSIALVSAI 142
 QY 58 CGVLFSDFTFVHLSAALIGFLWTQSGWIGHDSGHYVNLMSRLNRAIQLSGNIIAGIS 117
 Db 143 C--LHFDSTAMVVAIVILGLFYQCGGMLAHDFLHHQVFENHLFGDLVGVVGNLWQGS 200

QY 118 IGMWKNHNAHIAAC-----SLDYPDLQMPVFAVSSRPFNSITSHYGRKKKEFX 170
 DB 201 VQWKKKNTHTAIPHLHATPEIAFHGDIDIMPLANSK-----MACHAVD-----SP 251
 QY 171 IAXFLICYOHEFTFYPVPCARVNLVLOTILLF-----SRKKVODRALINIGILVFWT 223
 DB 252 VGLFEMRYOAYLYPFLILFARISWVIOQAMVAFYVNGPGCTDKVOYPLLEBRAGLLIYG 311
 QY 224 WFLFL-----ALLFV 234
 DB 312 WNLGLVYAANMSLQAAAFV 333

RESULT 7
 US-10-054-534B-14

Sequence 14, Application US/10054534B
 Publication No. US20030167525A1
 GENERAL INFORMATION:
 APPLICANT: Abbott Laboratories
 APPLICANT: Mukerji, Pradip
 APPLICANT: Huang, Yung-Sheng
 APPLICANT: Das, Tapas
 APPLICANT: Thurmond, Jennifer M.
 APPLICANT: Pereira, Suzette L.
 TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
 FILE REFERENCE: 6763 US, P1
 CURRENT APPLICATION NUMBER: US/10/054, 534B
 CURRENT FILING DATE: 2002-01-22
 PRIOR APPLICATION NUMBER: US 09/769, 863
 PRIOR FILING DATE: 2001-01-25
 NUMBER OF SEQ ID NOS: 55
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 14
 LENGTH: 453
 TYPE: PRT
 ORGANISM: Saprolegnia diclina
 US-10-054-534B-14

Query Match 19.6%; Score 258.5; DB 12; Length 453;
 Best Local Similarity 26.3%; Pred. No. 1.5e-18;
 Matches 69; Conservative 52; Mismatches 98; Indels 43; Gaps 9;

QY 3 AFSTSHRLSDHTVSAAS---SDYRKLPDLSALNLF--NRKGHTTSILSLITLFPPLSV 57
 DB 85 AVDTG--ISDEVKKSQSDPIASRYKRLVKKLGYDSKLYLYKCASTLSIALVSAAI 142
 QY 58 CGVLPDSSTFVAVLSAALIGFLMIQSGWIGHDSGHYVNLSSRLNRAIOILSGNIIAGIS 117
 DB 143 C--LHFDSTAMVMAVAILGLFYQCGWLAHDFLHQVEFNHLFGDLVGVWGNLMQGPS 200
 QY 118 IGMWKNHNAHIAAC-----SLDYPDLQMPVFAVSSRPFNSITSHYGRKKKEFX 170
 DB 201 VQWKKKNTHTAIPHLHATPEIAFHGDIDIMPLANSK-----MACHAVD-----SP 251
 QY 171 IAXFLICYOHEFTFYPVPCARVNLVLOTILLF-----SRKKVODRALINIGILVFWT 223
 DB 252 VGLFEMRYOAYLYPFLILFARISWVIOQAMVAFYVNGPGCTDKVOYPLLEBRAGLLIYG 311
 QY 224 WFLFL-----ALLFV 234
 DB 312 WNLGLVYAANMSLQAAAFV 333

RESULT 8
 US-10-431-952-14
 Sequence 14, Application US/10431952
 Publication No. US20030190733A1
 GENERAL INFORMATION:
 APPLICANT: Abbott Laboratories
 APPLICANT: Mukerji, Pradip
 APPLICANT: Huang, Yung-Sheng
 APPLICANT: Das, Tapas
 APPLICANT: Thurmond, Jennifer

APPLICANT: Pereira, Suzette L.
 TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
 FILE REFERENCE: 6763 US, O1
 CURRENT APPLICATION NUMBER: US/10/431, 952
 CURRENT FILING DATE: 2003-05-08
 PRIOR APPLICATION NUMBER: US/09/769, 863
 PRIOR FILING DATE: 2001-01-25
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 14
 LENGTH: 453
 TYPE: PRT
 ORGANISM: Saprolegnia diclina
 US-10-431-952-14

Query Match 19.6%; Score 258.5; DB 12; Length 453;
 Best Local Similarity 26.3%; Pred. No. 1.5e-18;
 Matches 69; Conservative 52; Mismatches 98; Indels 43; Gaps 9;

QY 3 AFSTSHRLSDHTVSAAS---SDYRKLPDLSALNLF--NRKGHTTSILSLITLFPPLSV 57
 DB 85 AVDTG--ISDEVKKSQSDPIASRYKRLVKKLGYDSKLYLYKCASTLSIALVSAAI 142
 QY 58 CGVLPDSSTFVAVLSAALIGFLMIQSGWIGHDSGHYVNLSSRLNRAIOILSGNIIAGIS 117
 DB 143 C--LHFDSTAMVMAVAILGLFYQCGWLAHDFLHQVEFNHLFGDLVGVWGNLMQGPS 200
 QY 118 IGMWKNHNAHIAAC-----SLDYPDLQMPVFAVSSRPFNSITSHYGRKKKEFX 170
 DB 201 VQWKKKNTHTAIPHLHATPEIAFHGDIDIMPLANSK-----MACHAVD-----SP 251
 QY 171 IAXFLICYOHEFTFYPVPCARVNLVLOTILLF-----SRKKVODRALINIGILVFWT 223
 DB 252 VGLFEMRYOAYLYPFLILFARISWVIOQAMVAFYVNGPGCTDKVOYPLLEBRAGLLIYG 311
 QY 224 WFLFL-----ALLFV 234
 DB 312 WNLGLVYAANMSLQAAAFV 333

RESULT 9
 US-10-278-391-4
 Sequence 4, Application US/10278391
 Publication No. US20030159164A1
 GENERAL INFORMATION:
 APPLICANT: KOPCHIK, JOHN J.
 KELLER, BRUCE
 HUANG, YUNG-SHENG
 KIRCHNER, STEPHEN J.
 MUKERJI, PRADIP
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM
 PRODUCTS
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MEDLEN & CARROLL, LLP
 STREET: 220 MONTGOMERY STREET, SUITE 2200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Releasee #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/278,391
 FILING DATE: 23-Oct-2002
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/087,578
 FILING DATE: 29-MAY-1998

```

1 ATTORNEY/AGENT INFORMATION:
2 NAME: CARROLL, PETER G.
3 REGISTRATION NUMBER: 32,837
4 REFERENCE/DOCKET NUMBER: OHU-03348
5 TELECOMMUNICATION INFORMATION:
6 TELEPHONE: (415) 705-8410
7 TELEFAX: (415) 397-8338
8 INFORMATION FOR SEQ ID NO: 4:
9 SEQUENCE CHARACTERISTICS:
10 LENGTH: 457 amino acids
11 TYPE: amino acid
12 STRANDNESS: NO. US20030159164A1 Relevant
13 TOPOLOGY: NO. US20030159164A1 Relevant
14 MOLECULE TYPE: protein
15 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
16 US-10-278-391-4

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Best Local Similarity	26.7%	Pred. No. 2.1e-17		
Matches 64	Conservative 45	Mismatches 110	Indels 21	Gaps 6

[illegible]

RESULT 10
US-10-191-513A-11

Sequence 11, Application US/10191513A
Publication No. US20030104596A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pardeep
APPLICANT: Leonard, Amanda E.
APPLICANT: Huang, Yung-Sheng
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF

```

1 CURRENT APPLICATION NUMBER: US/10/191,513A
2 CURRENT FILING DATE: 2002-09-25
3
4 PRIOR APPLICATION NUMBER: US 09/227,613
5
6 PRIOR FILING DATE: 1999-01-08
7
8 PRIOR APPLICATION NUMBER: PCT/US98/07422
9
10 PRIOR FILING DATE: 1998-04-10
11
12 PRIOR APPLICATION NUMBER: US 08/833,610
13
14 PRIOR FILING DATE: 1997-04-11
15
16 NUMBER OF SEQ ID NOS: 54
17
18 SOFTWARE: PasteSeq for Windows Version 4.0
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20 SEQ ID NO 11
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22 LENGTH: 458
23
24 TYPE: PRT
25
26 ORGANISM: Homo sapiens
27
28 FEATURE:
29
30 NAME/KEY: VARIANT
31
32 LOCATION: (458)...(458)
33
34 OTHER INFORMATION: Xaa = Unknown or other at position 458
35
36 US-10-191-513A-11

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Query Match	18.8%	Score 247.5	DB 15	Length 458
Best Local Similarity	26.7%	Pred. NO. 2.1e-17		
Matches 64; Conservative	45;	Mismatches 110;	Indels 21;	Gaps 6

[illegible]

\vdots

RESULT 11
US-10-191-513A-41

Publication No. US20030104596A1
 GENERAL INFORMATION:
 APPLICANT: Abbott Laboratories
 APPLICANT: Mukerji, Paridip
 APPLICANT: Leonard, Amanda E.
 APPLICANT: Huang, Yung-Sheng
 APPLICANT: Tapas, Das
 TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
 FILE REFERENCE: 6295.US.D3
 CURRENT APPLICATION NUMBER: US/10/191,513A
 CURRENT FILING DATE: 2002-09-25
 PRIOR APPLICATION NUMBER: US 09/227,613
 PRIOR FILING DATE: 1998-01-08
 PRIOR APPLICATION NUMBER: PCT/US98/07422
 PRIOR FILING DATE: 1998-04-10

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; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0

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? ORGANISM: Homo sapiens
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? LOCATION: (458)...(458)
? OTHER INFORMATION: Xaa = Unknown or other at position 458
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[illegible]

RESULT 12
US-10-191-513A-17

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QY 230 ALLEFV-PIQHIOFWLNHLAENL 250
Db 309 FLLEPTWPLRVAVYFIISQMGGL 330

RESULT 15

US-10-369-493-6108
; Sequence 6108, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6108
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6108

Query Match 17.0%; Score 224.5; DB 12; Length 473;

Best local Similarity 26.7%; Pred. No. 5.5e-15;

Matches 70; Conservative 36; Mismatches 115; Indels 41; Gaps 8;

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Db 119 VSAAYDVSAQEKWVESFEKLRLQKLDHDDLM--KANETVFLFKAIISTLSIMAFAYLQYL 176
QY 59 GVLFSDSTFVHVLSALIGFLWIGSGWIGHDSGHVWMLSRRLNRAIQIUSGNIAGIST 118
Db 177 G-----WYITSACLALAWQFGWLTPECHQOPTKNRPLNDTISLFFGNFLOGFSR 228
QY 119 GWWKKNHNAHHCNSLDYDPLQHMVFAVSSRFNSITSHXGGRKXEPDXIAXFLICY 178
Db 229 DMWKDKNTHHAATNVIHDGDIIDLAFLFAF-----IPGDLCKTKASFKAALKIVPY 281
QY 179 QHFTFYVWCVARVNLVLTQITILLFSRXKYQDRA-----LNIINGILVFWTWFLFL 229
Db 282 QHLYFTAMLPMLRFSWTGQVQWFKENQNEYKYQRMNMFWEQATIVG---HWAMVYQYL 338
QY 230 ALLEFV-PIQHIOFWLNHLAENL 250
Db 339 FLLEPTWPLRVAVYFIISQMGGL 360

Search completed: January 1, 2004, 06:58:36
Job time : 49.1975 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:39:42 ; Search time 4853.01 Seconds
(without alignments)
16303.117 Million cell updates/sec

Title: US-09-857-524B-7
Perfect score: 1934
Sequence: 1 gcacgagcacacacagtaaaa.....aaaaaaaaaaaaaaaaaaaaa 1934

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: gb_htg:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	690	35.7	1594	6 AX007239	AX007239 Sequence
2	690	35.7	1610	8 BNAJ4160	AXJ224160 Brassica
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4	672.8	34.8	110149	8 AC005397	AC005397 Arabidops
5	643.4	33.3	1856	8 AF005096	AF005096 Ricinus c
6	642.8	33.2	1591	8 HACTB5RN	X87143 Helianthus
7	642.8	33.2	1606	6 AX007273	AX007273 Sequence
8	642.6	33.2	1491	8 BT003379	BT003379 Arabidops
9	642.6	33.2	1652	8 AY087345	AY087345 Arabidops
10	642.6	33.2	1678	6 AX007241	AX007241 Sequence
11	642.6	33.2	1704	8 AF428420	AF428420 Arabidops
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13	642.6	33.2	1743	8 BT000442	BT000442 Arabidops
14	642.6	33.2	95993	8 ATP2A19	AL122962 Arabidops
15	639.2	33.1	1350	6 AX505863	AX505863 Sequence
16	622.6	32.2	1478	8 AY055117	AY055117 Echium ge
17	618.4	32.0	1684	6 AR076814	AR076814 Sequence
18	618.4	32.0	1684	6 AR084177	AR084177 Sequence
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21	618.4	32.0	1685	6 AR020904	AR020904 Sequence
22	618.4	32.0	1685	6 AR200408	AR200408 Sequence
23	618.4	32.0	1685	6 I38430	I38430 Sequence 4
24	618.4	32.0	1685	6 AF007561	AF007561 Borago of
25	616.8	31.9	1687	8 BOUT9010	U79010 Borago offi
26	616.2	31.9	1450	8 AY055118	AY055118 Echium pi
27	604.4	31.3	1341	8 AF406816	AF406816 Aquilegia
28	603.6	31.2	1633	8 AF001394	AF001394 Arabidops
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30	567.6	29.3	1385	8 AY234126	AY234126 Primula v
31	559	28.9	1681	8 AY234124	AY234124 Primula f
32	555	28.7	1702	6 AR200409	AR200409 Sequence
33	524.4	27.1	1410	8 AY234125	AY234125 Primula f
34	502	26.0	1788	8 AF031194	AF031194 Trifolium
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36	399.4	20.7	1618	8 AY234127	AY234127 Primula v
37	191	9.9	535	6 AX058838	AX058838 Sequence
38	153	7.9	291	6 AR246607	AR246607 Sequence
39	138.8	7.2	1572	8 AB090360	AB090360 Nucor cir
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43	112	5.8	266	6 AR247897	AR247897 Sequence
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45	77.4	4.0	2040	6 AX058830	AX058830 Sequence

ALIGNMENTS

RESULT 1
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LOCUS AX007239
DEFINITION Sequence 1 from Patent WO0000593.
ACCESSION AX007239
VERSION AX007239.1 GI:9995105
KEYWORDS
SOURCE
ORGANISM
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS
TITLE
1 Zaehring, U., Heinz, B., Schmidt, H. and Sperling, P.
Sphingolipid-desaturase

JOURNAL

Patent: WO 0000593-A 1 06-JAN-2000;
ZAEHRINGER ULRICH (DE); HEINZ ERNST (DE); SCHMIDT HERMANN (DE);
SPERLING PETRA (DE); GVS GES FUER ERWERB UND VERMER (DE)

FEATURES	Location/Qualifiers
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	Query Match	35.7%;	Score 690;	DB 6;	Length 1594;
	Best Local Similarity	69.7%;	Pred. No. 1,55-140;		
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DB	61	AGACAAAGAGAGAGATTCATTAACAAGCGATGATCTGAAAAACACACCAACCCGGAGATT	120		
QY	378	TATGAGTCTCAATTCAGAGTAAAGGTGTCATATGTCATGATTTGGTCAAGAGACCCCTG	437		
DB	121	TATGAGTCTCAATTCAGAGCAAAAGCTTACGAGCTTCCACCTGGGTCAAAATCCATCCG	180		
QY	438	GTGGTGAATGTTCCATCTCAAAACCTGTGAGCCAGAGTGCATGATCATTTACATAGCAT	497		
DB	181	GAGCGAAGACGCATCTTAACCTCGCCGGTCAGAGAGTCAACGACGCGTTACGCTT	240		
QY	498	ACCATCTGGCAGACATGTCACACCTTGAATAATCTTCACTGGTACCACTCAGTG	557		
DB	241	ACCATCCCGAAGCCGATCGGCCACCTCGAATAACCTCACAAAGGGTATCCACGTAAG	300		
QY	558	ACTTCAAGGTCTTGAAGTGTCCAAAGCTACAGAAAGCTTGACATGATTTCAAAAT	617		
DB	301	ACCAACACGTGTCCGACGTGTGGGTGACTACCGTCTTTAGCCCGAGATTTCCAAAC	360		
QY	618	TGGGCTTTTGAACACCAAGGGAGATGACATTCATATGACCCCTTGACATCTGTGCTGTA	677		
DB	361	GCGGACTTTCGATTAATAAAAGGTACACGATCTTTTACACGCTACAGTGCCTGCTGCA	420		
QY	678	TGTTCTCATTTGTACTCATAGTGTTCGAGAGTGACATAGTGTGAGGCTCATTTGAGTT	737		
DB	421	TGCTCGGCGGCTGTGTATACGTGTGTGTGATGACAGCATATAGGCCCACTTAATAT	480		
QY	738	CAGGCAATGCTTAAAGGTTGCTTGGATGCAAAAGTCTTATGTGGCCATGATTTGACC	797		
DB	481	CCGCGCTTGTCTGGGCTCTTCTTGGAATACAGAGGCTTACGTGGGACATGACTGTGTC	540		
QY	798	ACTATGTGTATTATGACAAACCAATGTTTCAACAGGTGACACATCTCTTCTGGAACT	857		
DB	541	ATTACAAAGTACGTCACAAAGAACCGTGTATTAACCTGTCCAGCTTTGTCTGTAACT	600		
QY	858	GCTTGACCGGAGTAAAGCATGCTTGTGTGGAAGTGACTCACAAATGTCACCAATTTGGT	917		
DB	601	GCAATACCGGATATCATTCGCTGTGTGGAATGACCAATACGCTTACCATATCTCTT	660		
QY	918	GCAACAGCTTTGACCATGACCTGTATCTGACAGCATGCCGCTCTTTCAGATTTGTCGC	977		
DB	661	GTATATGCTTTGACCAAGATCTGTATCTCCAGCATATCCGTCTTTAGCGGCTCACA	720		
QY	978	GGTTCCTCAATTCATTAACCTCTCATTTCTATGGAGAGAGTGGAGTTTGAATTTCAATG	1031		

Db		721	AGTCTTTAAGTCGATGAGCTCAGCTTTCTATGGAGGAAGTTGAGCTTGATCCACTAG	780
Qy		1038	CTAGGCTTTGATCTGTACACGACTTTACTTTTACCGGTAATGTGTGCCAGGG	1097
Dc		781	CTGATCTCTTGATCAGATACCAACACTGTGTCTTTATCCAAATCATGTGTGTGGGGGAA	840
Qy		1098	TCAACTTGATCTGCAGACAACTCTGCTAATGTGTTTCGAGGGCAAAAGTCAGGATGTAG	1157
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AUTHORS		Sperling, P., Zahringer, U. and Heinz, E.		
TITLE		A sphingolipid desaturase from higher plants. Identification of a new cytochrome b5 fusion protein		
JOURNAL		J. Biol. Chem. 273 (44), 28590-28596 (1998)		
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AUTHORS		Sperling, P.		
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JOURNAL		Submitted (13-FEB-1998) Sperling P., Physiologie, Institut fuer Allgemeine Botanik der Universitaet Hamburg, Ohnhorststrasse 18, D-22609 Hamburg, GERMANY		

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 1 (bases 1 to 1869)

AUTHORS Libisch, B., Michaelson, L. V., Lewis, M. J., Shewry, P. R. and Napier, J. A.
 TITLE Chimeras of Delta6-fatty acid and Delta8-sphingolipid desaturases
 JOURNAL Biochem. Biophys. Res. Commun. 279 (3), 779-785 (2000)
 MEDLINE 21092516
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 Sperleng, P., Libisch, B., Zahringer, U., Napier, J. A. and Heinz, E.
 AUTHORS Functional identification of a delta8-sphingolipid desaturase from
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 JOURNAL Arch. Biochem. Biophys. 388 (2), 293-298 (2001)
 MEDLINE 21260464
 PUBMED 11368168
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 Libisch, B., Sperleng, P., Heinz, E., Sayanova, O. and Napier, J. A.
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Town,C.D. and Kaul,S.	
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DEFINITION	Ricinus communis desaturase/cytochrome b5 protein mRNA, complete cds.			Qy	626	TTTGCACCAAGAGGAGTGTCACTTATCATCACCCTTGACATCTGTTGCTGATATGTTCTC	685
ACCESSION	AF005096			Db	451	TTTGAAGAAAGAGGAGCATTCGCTTATTAATCTTGTCTATGATATGCTACTTGGCT	510
VERSION	AF005096.1	GI:4101625		Qy	686	ATTGATCTATGATGTTCTGAGTGTCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG	745
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ORGANISM	Ricinus communis (castor bean)			Db	571	TTAATGGGTTTATGATGATACAAAGTGGGTGATATGATATGATATGATATGATATGAT	630
REFERENCE				Qy	806	TTTATGACACCAACATGCTTCAACAAAGTGTGACAGATCTCTCTGGAACTGCTTGACC	865
AUTHORS	Sayanova, O., Smith, M.A., Lapinskas, P., Stebart, A.K., Dobson, G., Christie, W.W., Shewry, P.R. and Napier, J.A.			Db	631	GTTATGATAGAGCGTCGATTCATTCGTTGGGAGATCTTATCTGGAAATTTCTTGCA	690
TITLE	Expression of a borage desaturase cDNA containing an N-terminal cytochrome b5 domain results in the accumulation of high levels of delta6-desaturated fatty acids in transgenic tobacco			Qy	866	GGGATTAAGCATTTGCTGTGGAAGTGTACTCAATGTCTACCAATTCGTCGACACG	925
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 94 (8), 4211-4216 (1997)			Db	691	GGATTCAGATTTGCTGTGGAAGTGTACTCAATGTCTACCAATTCGTCGACACG	925
MEDLINE	97268723			Qy	926	CTTGACATGACCTGATCTGACAGCATGCGGCTTTGCACTTTCGCGGCTTCTC	985
PUBMED	9108131			Db	751	CTTGATTTTGATTCAGATCTGACAGCATGACCTTCTTTCGCGTATCTTCAAAATTTTC	810
AUTHORS	Napier, J.A. and Shewry, P.R.			Qy	986	AATTCATACCTTCATTTCTATGAGGAGAAAGTTGAGTTGATTCATTCATGCTAGATT	1045
TITLE	Direct Submission			Db	811	AGTTCAATTCATCTTATTTTATGAAAGAAATGATATTTGATTTGTCTGCAAGATTC	870
JOURNAL	Submitted (22-MAY-1997) Cell Biology, IACR-Long Ashton Research Station, Long Ashton, Bristol BS18 9AF, UK			Qy	1046	TTGATCTGTACAGACATCTTATCTTTTACCCGGTATGTTGTTGTCAGAGGCTTGA	1105
FEATURES				Db	871	TTGTTAGTTATCAGATTTGACGTTTATCCGTGATGTTGTTGCTAGATTTAATTTG	930
source				Qy	1106	TATCTGACACATTTCTGATATGTTTGTGAGCGCAAAAGTGCAGATAGAGCTTGAC	1165
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	SKFESITSYFVERKMFDCARFLVSLVDFYPMCFARINLPAOSISLLSKRR			Qy	1586	CTACAGCTAGGAGACTTAAACAACCTGCGCTTAAGATTTGTGTGGAAGCTGTTAAT	1645
	VANRGEILGVLFVMTWYPRVLSCLPMGEBRVMPVAFSVTRIOHVQCLNHPSSV			Db	1411	TTGCAAGCTAGGAGACTTAAACAACCTGCGCTTAAGATTTGTGTGGAAGCTGTTAAT	1645
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ORIGIN							
Query Match	33.3%	Score 643.4	DB 8	Length 1856			
Best Local Similarity	68.2%	Pred. No. 2.4e-130					
Matches 909	Conservative 0	Mismatches 421	Indels 3	Gaps 1			

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RESULT 7

AX007273 1606 bp DNA linear PAT 06-SEP-2000
 LOCUS Sequence 35 from Patent WO000593.
 DEFINITION AX007273
 ACCESSION AX007273.1 GI:9995126
 VERSION
 KEYWORDS

SOURCE

ORGANISM Helianthus annuus (common sunflower)
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
 Heliantheae; Helianthus.

REFERENCE

1 Zaehring, U., Heinz, E., Schmidt, H. and Sperling, P.
 Sphingolipid-desaturase
 Patent: WO 0000593-A 35 06-JAN-2000;
 ZAEHRINGER ULRICH (DE); HEINZ ERNST (DE); SCHMIDT HERMANN (DE);
 SPERLING PETRA (DE); GVS GES FUER ERWERB UND VERMER (DE)

JOURNAL

FEATURES

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CDS

BASE COUNT 412 a 338 c 370 g 486 t
 ORIGIN

Query Match 33.2%; Score 642.8; DB 6; Length 1606;
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 Matches 929; Conservative 0; Mismatches 477; Indels 0; Gaps 0;

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RESULT 9	
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DEFINITION	Arabidopsis thaliana clone 34427 mRNA, complete sequence.
ACCESSION	AY087345
VERSION	AY087345.1 GI:21406069
KEYWORDS	FLI CDNA.
SOURCE	Arabidopsis thaliana (chale cress)
ORGANISM	Arabidopsis thaliana
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Equisetophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE	1 (bases 1 to 1652)
AUTHORS	Haas, B.J., Volkovskiy, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.

TITLE	Full-length messenger RNA sequences greatly improve genome annotation
JOURNAL	Genome Biol. 3 (6), RESEARCH0029 (2002)
MEDLINE	22088475
PUBMED	12093376
REFERENCE	2 (bases 1 to 1652)
AUTHORS	Broyer,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.
TITLE	Full-length cDNA from Arabidopsis thaliana unpublished
JOURNAL	3 (bases 1 to 1652)
REFERENCE	Broyer,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.
AUTHORS	Feldmann,K.
TITLE	Direct Submission Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
JOURNAL	This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Laet ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the 5' length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.
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ORIGIN	
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Best Local Similarity	66.0%; Pred. No. 3.6e-130;
Matches 930;	Conservative 0; Mismatches 479; Indels 0; Gaps 0
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Oy	370 GGGAGATTATGATGATCTCAATTTCAAGGTAAAGTGTACATGTCTCAGATTGGTGCAAGA 429
Dd	269 TGAGAGATCTATGATTCGGATTCCAAGGCAAGGTGTCAAACGTCCTCCATTGGATTAAAC 328
Oy	430 GCACCCTGGTGTGATGTTCCAAATCTCAAACTTGTCTGGCCAGAGATGTCACTGATGCATT 489
Dd	329 TCATCCCCGGAGCCACACGGTGAATTCCTCGTTGGTCAAGACGTACCGATGCTTT 388
Oy	490 CATAGCATTAACATCTGGCACAGATGGTGCACACCTTGAAAAAATCTTCATCGGTGTACCA 549
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RESULT 10
AX007241
LOCUS 1678 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 3 from Patent WO000593.
ACCESSION AX007241
VERSION AX007241.1 GI:9995107
KEYWORDS
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.
REFERENCE
Zehring, U., Heinz, B., Schmidt, H. and Sperling, P.
Sphingolipid-desaturase
Patent: WO 000593-A 3 06-JAN-2000;
ZAEHRINGER ULRICH (DE); HEINZ ERNST (DE); SCHMIDT HERMANN (DE);
SPEERLING PETRA (DE); GVS GES FUER EXMERB UND VERNER (DE)
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 Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J.,
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 JOURNAL
 Arabidopsis cDNA clones
 Submitted (05-OCT-2001) Salk Institute Genomic Analysis Laboratory
 (SIGNAL). Plant Biology Laboratory, The Salk Institute for
 Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
 USA
 COMMENT
 RIKEN Genomic Sciences Center (GSC) members carried out the
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 Hayashizaki,Y. and Shinozaki,K.
 The Salk, Stanford, PGSC (SSP) Consortium members carried out the
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 Davis,R.W., Theologis,A. and Ecker,J.R.
 Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
 this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
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Mayer, K.F.X., Quetier, F. and Salanoubat, M.
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 95993)
TITLE EU Arabidopsis sequencing project.
JOURNAL Direct Submission
AUTHORS Submitted (31-JAN-2000) MIPS, at the Max-Planck-Institut fuer
TITLE Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
JOURNAL lemcke@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de
COORDINATOR Marcel Salanoubat and Francis Quetier, Groupe
d'Interet Public, Centre National de Sequencage - GENOSCOPE, 2 rue
Gaston Cremieux, BP191, 91006 Evry Cedex, France;
http://www.genoscope.cns.fr
COMMENT Information on performance of analysis and a more detailed
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exon	/gene="F2A19.20"	/number=8	complement (23904)	.23969)
intron	/gene="F2A19.20"	/number=9	complement (23970)	.24071)
exon	/gene="F2A19.20"	/number=9	complement (24072)	.24227)
intron	/gene="F2A19.20"	/number=10	complement (24228)	.24326)
exon	/gene="F2A19.20"	/number=10	complement (24327)	.24383)
intron	/gene="F2A19.20"	/number=11	complement (24384)	.24684)
exon	/gene="F2A19.20"	/number=11	complement (24685)	.24729)
intron	/gene="F2A19.20"	/number=12	complement (24730)	.24813)
exon	/gene="F2A19.20"	/number=12	complement (24814)	.24909)
intron	/gene="F2A19.20"	/number=13	complement (24910)	.24999)
exon	/gene="F2A19.20"	/number=13	complement (25000)	.25075)
intron	/gene="F2A19.20"	/number=14	complement (25076)	.25141)

Query Match 33.2%; Score 642.6; DB 8; Length 95993;
 Best Local Similarity 66.0%; Pred. No. 4.5e-130;

Matches	930; Conservative	0; Mismatches	479; Indels	0; Gaps	0;
Qy	310	GGTTGTTGAGAGAGAGAGATACCTGAGAGAGGAGGTCACAACAAGA	369		
Db	80396	GGCGGAGAGACGAGAGAGAGATACCTGAGAGAGAGATCTTAAAAACACACAAATC	80455		
Qy	370	GGGAGATTTATGATCTCAATTCAAGGTAGGTGTACATGTCTCAGATTGGGTCAAGA	429		
Db	80456	TGGAGATCTATGATTCGCGATTCAGGCAAGGTCTACAGTCCGATTTGAATTAAC	80515		
Qy	430	GCACCTGTGTGTGATTTCCAACTCTAAACCTTGTGCGCAGATGTCACTATGATTT	489		
Db	80516	TCATCCCGAGGCGACACGAGTATTCATCTCTGTGTGTCMAAGACCTCACCGATGCTT	80575		
Qy	490	CATGACATACCATCTGCGACAGCATGTGACACTTGAAATTTCTTCACTGCTACCA	549		
Db	80576	CATGCAATTCATCCCGAACCGTTTGACACATCTGACCATCTTTCACCGGTTACCA	80635		
Qy	550	CCTCAGTACTTCAAGGTCTCTGAGTGTCCAAAGACTACAGAAAGCTTGATCTGATT	609		
Db	80636	CATCAGAGATTTCCAAATCTCCGAACTCACGCGATTACGCTGTATGCTGCGAGTT	80695		
Qy	610	CTCAAAATGGGTCTTTTGAACCAAAAGGCGATGCTCATGACACCTTGATCTGT	669		
Db	80696	TCGTAAATCGGTCTCTTCGAAACAAAGGTACAGTACTCTTACACTTACGCTTCGT	80755		
Qy	670	TGCTGTATGTTCTCTATGACTCTATGAGTGTCTGAGGTCATGTTGTGGGCTCA	729		
Db	80756	CGCCGCATGTTCTCGAGTCTCTACGGTGTGTTGCTTGTACCTTCGCTTCGCTCA	80815		
Qy	730	TTTGGTTTCAAGGCAATGCTTAAAGGTGCTTGTGATCAAAAGTCTTATGTGGCCATGA	789		
Db	80816	CCAAATGCGCGCGCGCTTCGCTCTCTGTGATCAGAGCGCTTACATAGCTCACA	80875		
Qy	790	TTCTGSCCATGTGTGTATGACACCAATGTTTCAACAAGTTGACAGATCTCTC	849		
Db	80876	TTCTGTATATTAATCTTATGATGTCGAAATCTTATACAGATTCCTCAGCTTCTC	80935		
Qy	850	TGGAACTGCTTGAACCGGGAATAGCATGCTGTGTGAGAGGCTACAAATGCTCACCA	909		
Db	80936	CGTAACTGTCTACCGGAATCTCAATGCGGTGAGAAATGAGCTCAATAGCTCATCA	80995		
Qy	910	CATTGCGTGCACAGCCTTGACATGACCTGATCTGACAGACATGCGGCTTTTGCAGT	969		
Db	80996	TCTAGCTTGTAAAGCCTTCGATTTACATCCAGATCTAACACATCCCTGCTTCGCGGT	81055		
Qy	970	TTGCTGCGGCTTCTTCAATTCATACCTCTCATTTCTATGAGAGAAATGAGTTGA	1029		
Db	81056	CTCCACCAAAATCTTCTCTCATATGACCTGAGATTCAGATGCGAAACTCAGGTTGA	81115		
Qy	1030	TTTCAATGCTAAGTTCTTGAATCTGCTACCGACATTTTAAACCGGTAATGTGCT	1089		
Db	81116	TCCAGTGGCAGATCTTATGACCTTACCACTTATCTTATATTCAGATTAATGCTT	81175		
Qy	1090	TGCCAGGCTCACTTGTATCTGACAGCAATCTGCTAATGTTTTCGAGGCCAAAAGTGA	1149		
Db	81176	TGGAAGATCAATCTCTTCAATCAACGTTCTCTGCTCTTCCAAAGCTGAGATACC	81235		
Qy	1150	GGATGAGCCTTGAACATTAATGAGGATCTTGTGTTTGAACCTTGCTTCCCTTTTAACT	1209		
Db	81236	AGATCGTGTCTTAACTTTCGCGGAAATCTTATGCTTTCGAGCTGTGCTCCACTTTAGT	81295		
Qy	1210	GTTCTGCTGCGAAATTTGGCTGAGAGGTTATGTTGTGTTGCTAGCTTTGCTGTTG	1269		
Db	81296	CTCATGTCTTACCAATGCGCTGAGAAATCTTCTTGTCTTCAACAGCTTACCGGTAC	81355		
Qy	1270	TTCCATCAGACATTCAGTCTGTTGAATCACTTTGCTCAATGTATATGTGCGGCC	1329		
Db	81356	GGCGCTTCAACACATTCATTTACGCTTAACTTTGCTGCTGATGTCTACGTTGCTC	81415		
Qy	1330	ACCGAGTGGGAATACGTTGTTGAAGACAGACAGTGTGATGATATCTTGTGC	1389		
Db	81416	ACCCACGGTATGACATGTTTGAAGAACGCGCGGAAACATCATATCTCTTGTAG	81475		

Qy	1390	CTCTTCGATGATGGTGTGTTTTCGGTGGCTGCAGTTTCAAGCTTGAGCAATCATTTGTTCC	1449
Db	81476	ATCATATACATGATGGTGTCTTGGTGATTAAGTTTCAGCTTGACATCATTTGTTCC	81535
Qy	1450	AAGCTACCTCCGGCCAAATTGAGGAAGATTTTGCCCTTGGTATGACCTTTGCAGAA	1509
Db	81536	TGCGTTACCTGTGTGCAATCTCCGAAAGTTTCTCCGGTGTTCAGAACCTTTGCAGAA	81595
Qy	1510	GCATTAATTTGCGCTATAGAGCTGTTCATTTTGGAGAGCCAAATCAGTGCACATTAGAC	1569
Db	81596	GCAATATCTCCGATATGAGATATGTGTGTGTTGAACAAATGTGTTGCCATTTACAC	81655
Qy	1570	CCTCAGGACTGCTGCCCTCAAGAGCTAAGGACCTTAACAAACCTGCCCTACAGATTGTT	1629
Db	81656	TTTGAAAGCAGCAGCACTTATCAAGCTAAGACGTGGCTTAATCCGGTGTTTAAGACTTGGT	81715
Qy	1630	GTGGGAAGCTGTATAATCCCATGGCTGAGGCATTTGGAGTTTAAAGTTTAAAGATTTCG	1689
Db	81716	TTGGGAAGCTTGTAAATCTCATGGCTAAAGATTTTAATCAAAACAAATATGCTTTGT	81775
Qy	1690	TCAAGGCTTTTGTGTTTGTGTTTCCCT	1718
Db	81776	TTGGGTTAAATTTGATGTGTGTTTAT	81804

RESULT 15	
AX505863	
LOCUS	1350 bp DNA
DEFINITION	Sequence 558 from Patent WO0216655.
ACCESSION	AX505863
VERSION	AX505863.1 GI:23387100

SOURCE	ORGANISM
Arabidopsis thaliana (thale cress)	Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Spermatophyta, Magnoliophyta, eudicotyledons: core eudicots: rosids, eustosids II, Brassicales; Brassicaceae, Arabidopsis.	

REFERENCE
AUTHORS
TITLE
JOURNAL
1 Harper, J.F., Krepps, J., Wang, X. and Zhu, T.
Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
Patent: WO 0216655-A 558 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)

FEATURES	location/Qualifiers
source	1..1350
	/organism="Arabidopsis thaliana"
	/mol_type="genomic DNA"
	/db_xref="taxon:3702"
BASE COUNT	325 a 359 c 274 g 392 t
ORIGIN	

Query Match	33.1%	Score 639.2	DB 6	Length 1350
Best Local Similarity	67.1%	Pred. No. 2e-129		
Matches 505; Conservative	0	Mismatches 443	Indels 0	Gaps 0

OY	310	GGTTGTTGAGAGAGAGAGAGTACTAACCTTCAGAGAGCTGAAGGTCACACAAGGA	369
Db	3	GGCGGAGAGACGGGAGMAAAAGTACATTTCGACGAAGAGCTTTAAAAACACACAACAATC	62
OY	370	GGGAGATTATGATGATCTCAATTCAGAGTAAGGTCACATGCTCGATTGGGTCAAGGA	429
Db	63	TGGAGATCTATGATATCGCATTTCAGGCAAGGCTCTACAAAGTCTCCGATTGGATTAAAC	122
OY	430	GCACCTGGTGTGATGTTTCAATCTCAAACTTGTGCGCAGAGATGCACTGATCATTT	489
Db	123	TCATCCCGGAGCGACACGGTATTTCTCAATCTCGTTGGTCAGAAAGTCACGATGCTTT	182
OY	490	CATAGCATTCATCTCTGCGACACAGATGTCACACTTGAATAATTTTCACTGCGTACCA	549
Db	183	CATGCGATTTCAATCCCGGAACCGCTTGGACCATCTTCGACACATCTCTTCAACCGGTATACA	242

QY	550	CCTCAGTGTACCTAAGAGCTGTGAGTGTCCAAAGACATACAGAAAGCTTGATCTGAGTT	609
Db	243	CATCAGAAATTTCCAAAGTCTCCGAAGTCTACGCGATTACCGTGTAGGGCTGCCAGTT	302
QY	610	CTCAAAATTTGGAGTCTTTTGTGACACCAAGGGGCAATGTCACTTCATGSCACCTTGACATCTGT	669
Db	303	TCGTAAATCTGGTCTCTTCGAAACCAAGGTACAGTTACTCTTACACTTAAAGCTTGTGT	362
QY	670	TGCTGTATGTTTCTCATGTGTACTCTATAGTGTCTGAGGTGCATCTAGTGTGTGGGCTCA	729
Db	363	CGCGGCACATGTTCTCGGAGTTCTCTACGGTGTGTTTGAGCTGTATCCGCTTGTGCTCA	422
QY	720	TTTGGGTTCAGGACATGCTCTTAGAGGTTCCTTTGATGCAAGTGTATTGTGGGCACTGA	789
Db	423	CCAAATCGCCCGCGGCTTCTCGGCTCTCTGTGATTCAGAGCGCTTACATAGGTCAAGA	482
QY	790	TTCTGGCCACTATGTGGTTATGACAAACCAATGGTTTCAACAAGGTGACAGATCTCTGC	849
Db	483	TTCTGTGTATTACGTTATCATGTGAAACAAATCTTATACAGATTGCTCAGCTTCTCTC	542
QY	850	TGGGAATGCTTGAACCGGGAATPAAGCATTTGCTTGTGTAAGTGAATCAAAATGCTCACCA	909
Db	543	CGGTAACTGTCTACCGGAATCTCAATGGGTGGGAAATGAGATCACAATGCTCACCA	602
QY	910	CATTGCGTGAACAGCCTTGAACATGACCCGTGATCTGACAGACATGCCGCTTTTGCAGT	969
Db	603	TCATGCTGTAAACGCTTCGATTAAGATCCAGATCTACACACATCCCTGCTTCGCCGT	662
QY	970	TTCTGCGGGTCTTCAATTCATTAACCTCTCATTTCTATGAGGAAAGTTGAGTTTGA	1022
Db	663	CTCACCAAAATTTCTTCTCTAATTGACCTCGAGATTCTACGATCGGAAACTCAGCTTTGA	722
QY	1030	TTTCAATGCTAGTCTTGTCTTGAATCTGCTACACAGACATTTACTTTTACCGGTAATGTGT	1083
Db	723	TCAGTGGCGAGATTTCTTAGTACAGTATCAACAATTACTTATTATCCAGTTATGTGTT	782
QY	1090	TGCCAGGTCACATTGTATCTGCAGACAAATTTGCTATTTGTTTGCAGCGAAAGTGCA	1145
Db	783	TGGAAGATCAATCTCTTCAATTAACGTTTCTCTGTCTTCTTCCAAACGTGAAGTAC	842
QY	1150	GGATPAGCCTTGAACATPAAATGGGAGTCTGTGTGTTTGTGACTTGGTCCCTCTTTTATG	1205
Db	843	AGATGTGTCTTAAACCTTCGCGGAATCTTAGTCTTCTGAGCTGGTGTCCACCTTTAGT	902
QY	1210	GTTCTTGCCTGCAAAATTTGGCCTGAGAGGGTATAGTTGTGTCTAGCTTGTGCTTGG	1265
Db	903	CTCATGTCTACCAACTGGCCTGAGAGATTTCTTGTGTCTTACACAACTTACCGCTAC	962
QY	1270	TTCCATCCAGACATTCAGTTCTGTTTGAATCACTTGTCTGCAAAATGTATATGTCCGCC	1328
Db	963	GCGCGTTCAACACATTCATTAATCAAGCTTAAACATTTGCTGCTGTATGTCTACGTTGGTCC	1022
QY	1330	ACCGAGTGGGAATGACTGTGTGTTGAGAGACAGACAAATGTATCATTTGATATCTCTTGTGC	1388
Db	1023	ACCCACCGGTGCGACCTGGTTCGAGAGCAAGCGCGCGGAAACAATCGATATCTCTTGTAG	1082
QY	1390	CTCTTTCAGTATGTTGTTTTTTCGAGGCTTGCAGATTTCAAGCTTATGATCTTGTCTCC	1449
Db	1083	ATCATATCATGATTTGGTCTTGTGGTATTAACATTTCAAGCTTGAACATCTATTTGTTGCC	1142
QY	1450	AAGGCTACCTGGGTCCCAATTTGAGAGAAATTTGCCCTTGTGTATGTACCTTTGCAAGAA	1509
Db	1143	TCGCTTACCTGTTGCCATCTCCGGAAGTTTCTCCGGTGGTTCAAGAGCTTTTCAAGAA	1202
QY	1510	GCATTAATTTGGCTTATAGAGCTTGTCAATTTTGGAGGCCAATCAGTGTGACAAATTAAGAC	1568
Db	1203	GCATTAATCTTCGGATATGAGAGTATGTGTGTGTGAAAGCAAAATGTGTGACATTAAACAC	1262
QY	1570	CCTCAGGACGTGCTCCCTACAAAGCTTAGAGATTAAACAACCTGCGCCTTAAGAAATTTGTT	1629
Db	1263	TTTGAAGACAGACGCTTATCAAGCTTAGAGAGCTGTATATCCGGTGTTAAGAACTTGGT	1322
QY	1630	GTGGGAAGCTGTATATACCATGTGCTCA	1657

QY 1630 GTGGAGCTGTTAATACCCATGGCTGA 1657

Fri Jan 2 09:49:10 2004

us-09-857-524b-7.rge

Page 20

Db 1323 TTGGGAGCCTTGAATACTCATGGCTAA 1350

Search completed: December 31, 2003, 21:04:31
Job time : 4857.01 secs

XX WP1: 2000-412236/35.
DR P-PSDB: AAY71554.
XX
XX Polynucleotide encoding delta-6 desaturase enzyme useful for producing
PT transgenic plants and for producing antibodies specific to which is
PT useful for screening cDNA expression libraries -
XX
XX Claim 2, Page 46; 57pp; English.
XX
XX The present sequence is a cDNA encoding sphingolipid desaturase
CC from clone *set.ph0017.b4*:f15 isolated from soybean seedling cDNA
CC library, *set*. The present sequence is useful for producing
CC transgenic plants having altered levels of sphingolipid desaturase which
CC in turn would alter the fatty acid composition. The enzyme is useful
CC for producing polyclonal or monoclonal antibodies. The polynucleotide
CC is also useful as primer or probe for screening cDNA libraries to
CC isolate desired full-length cDNA clones.
XX
XX Sequence 1934 BP; 505 A; 367 C; 448 G; 614 T; 0 other;
XQ

Qy	721	GTGGGCTAATTGGGTTAGGCAAGCTCTTCTTGGGGTTGGCTTGGATGCAAGAGCTATGT	780
Db	721	GTGGGCTAATTGGGTTAGGCAAGCTCTTGGGGTTGGCTTGGATGCAAGAGCTATGT	780
Qy	781	GGGCGATGATCTGGCCACTATGTGTATGCAACCAATGTTTCAACMAAGTTGCACA	840
Db	781	GGGCGATGATCTGGCCACTATGTGTATGCAACCAATGTTTCAACMAAGTTGCACA	840
Qy	841	GATCCTCTCTGGGAACTGCTTGACCCGGAGTAAGCAATTGCTGTGTGGAAAGTGCATCACAA	900
Db	841	GATCCTCTCTGGGAACTGCTTGACCCGGAGTAAGCAATTGCTGTGTGGAAAGTGCATCACAA	900
Qy	901	TGCTCACAACAATGGTGSCAACAGCCTTGACCATATGACCTGATCTGACGACACATGCGGT	960
Db	901	TGCTCACAACAATGGTGSCAACAGCCTTGACCATATGACCTGATCTGACGACACATGCGGT	960
Qy	961	CTTTCGAGTTTCGTGCGGGTCTTCAATTCCATACTCTCAATTCTATGAGAGGAAGTT	1021
Db	961	CTTTCGAGTTTCGTGCGGGTCTTCAATTCCATACTCTCAATTCTATGAGAGGAAGTT	1021

Query Match	100.0%	Score 1934;	DB 21;	Length 1934;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1934; Conservative	0;	Mismatches	0;	Gaps 0;

Db 1021 GGAGTTTGAATTCATTGCTAGTCTCTGCTACGACACTTACTTTTACCCGGT 108

[illegible]

Db	1061	AATGCTGTGGCCAGGGTCAACTTGTATCTGCAGCAAAATTCGTCTATTGTTTTCCAGGGG	114
Qy	1141	AAAAGTCAGGATAGAGCCTTGAACATATAGGGGATCCCTGTGTTTTGGACTTGGTTCC	120
Db	1141	AAAAGTCAGGATAGAGCCTTGAACATATAGGGGATCCCTGTGTTTTGGACTTGGTTCC	120
Qy	1201	TCTTTTAAGTCTTCCCTGCCAAATTTGGCTGAGAGGGTATGTTTGTCTGCTAGCTT	126
Db	1201	TCTTTTAAGTCTTCCCTGCCAAATTTGGCTGAGAGGGTATGTTTGTCTGCTAGCTT	126
Qy	1261	TGCTGTTTGTTCACATCCAGCAATTCAGTTCGTGTTTGAATCACTTGTGCGCAAAATGATA	132
Db	1261	TGCTGTTTGTTCACATCCAGCAATTCAGTTCGTGTTTGAATCACTTGTGCGCAAAATGATA	132
Qy	1321	TGTCGGGCGCACCGAGTGGGAAATGACTGTTTGGAGAAGCAGACAGTGTACATTGGATAT	138
Db	1321	TGTCGGGCGCACCGAGTGGGAAATGACTGTTTGGAGAAGCAGACAGTGTACATTGGATAT	138
Qy	1361	CTCTTGTGCTCTTCGATGAGTATGGTTTTTGGTGCGTTCGACTTTCAGCTTGAGCATCA	144
Db	1361	CTCTTGTGCTCTTCGATGAGTATGGTTTTTGGTGCGTTCGACTTTCAGCTTGAGCATCA	144
Qy	1441	TTTGTGTTCCAAAGCTACCTCGGTGCCAATTAGAGAAATTTGGCTTTGGTTAGTACCT	150
Db	1441	TTTGTGTTCCAAAGCTACCTCGGTGCCAATTAGAGAAATTTGGCTTTGGTTAGTACCT	150
Qy	1501	TTGCAAGAGCAATATTTGGCTTATAGAGCTTGTCAATTTTGGAGGCGCAATCAGTGGAC	156
Db	1501	TTGCAAGAGCAATATTTGGCTTATAGAGCTTGTCAATTTTGGAGGCGCAATCAGTGGAC	156
Qy	1561	AATTAGAACCTCAGAGACTGTGCTGCCCTACAAAGCTAAGGCACTTAACAAACCTCGCCCTAA	162
Db	1561	AATTAGAACCTCAGAGACTGTGCTGCCCTACAAAGCTAAGGCACTTAACAAACCTCGCCCTAA	162
Qy	1621	GAAATTTGTTGGGAAGCTGTTAATAACCATGGCTGAGGCAATTTGGAGTTTTAGAGTTT	168
Db	1621	GAAATTTGTTGGGAAGCTGTTAATAACCATGGCTGAGGCAATTTGGAGTTTTAGAGTTT	168
Qy	1661	AGGATTTTGTCAAGGCTTTTTTTTTTTTGTCTTCCTTAAAGAAAGAAAAAATTCCTCA	174
Db	1661	AGGATTTTGTCAAGGCTTTTTTTTTTTTGTCTTCCTTAAAGAAAGAAAAAATTCCTCA	174
Qy	1741	TTGTATTTTGTACCCCGCACTTTCAGATTGGGCTTGAATTTAATCTTTTGTGTAGG	180
Db	1741	TTGTATTTTGTACCCCGCACTTTCAGATTGGGCTTGAATTTAATCTTTTGTGTAGG	180

Db	1801	TGTGGTGTACAAATGATGGTGTATGCAGATGTTATCGATGCTTGCATCAAT	1867
Qy	1861	ACAAATTCATATCATGTATGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1920
Db	1861	ACAAATTCATATCATGTATGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1920
Qy	1921	AAAAAAAAAAAAAAAAA 1934	
Db	1921	AAAAAAAAAAAAAAAAA 1934	
RESULT 2			
AAZ44832	ID AAZ44832 standard; DNA; 1594 BP.		
AAZ44832;			
27-APR-2000	(first entry)		
B. napus sld1 DNA.			
Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;			
transgenic plant; crop plant; delta-8-unsaturated long-chain base;			
tolerance; resistance; soil salinity; ion stress; toxicity; drought;			
cold; frost; phytopathogenic microorganism; flowering time; cosmetic;			
pharmaceutical; food; chemical raw material; de.			
Brassica napus.			
Key	Location/Qualifiers		
CDS	51..1400		
FT	/*tag= a		
FT	/product= "sld1"		
DE19828850-AL.			
30-DEC-1999.			
27-JUN-1998;	98DE-1028850.		
27-JUN-1998;	98DE-1028850.		
(GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.			
Heinz E, Zaehring U, Schmidt H, Sperling P;			
WPI; 2000-127549/12.			
P-PSDB; AAF51333.			
New sphingolipid desaturase that selectively introduces double bond			
into sphingolipids and capnoids -			
Claim 11; Fig 1; 62pp; German.			
This invention describes a novel sphingolipid desaturase that selectively			
introduces a double bond into the sphingobase of the ceramide residue of			
sphingolipids and capnoids. A DNA sequence encoding the sphingolipid			
desaturase, or a vector containing the DNA sequence, can be used to			
produce transgenic plants, especially crop plants, with an increased or			
decreased delta-8-unsaturated long-chain base content or an altered			
delta-8-unsaturated long-chain base cis/trans ratio, especially to			
compensate for a delta-8-unsaturated long-chain base deficiency, to			
exclude production of delta-8-unsaturated bases, to increase tolerance			
or resistance to soil salinity, ion stress or toxicity, drought, wet			
conditions, cold or frost and/or phytopathogenic microorganisms, or to			
alter size growth and flowering time. Cells, transgenic organisms or			
plants containing the DNA sequence can be used to produce sphingolipids			
and capnoids with unsaturated sphingobases. The sphingolipids or capnoids			
can be used in cosmetic, pharmaceuticals and foods and as chemical raw			
materials. This sequence encodes the Brassica napus sphingolipid			
desaturase sld1 protein described in the method of the invention.			

Seq	Sequence	594 BP	382 A	369 C	375 G	468 T	0 other
Query Match	35.7%	Score	690	DB	21	Length	1594
Best Local Similarity	69.7%	Pred. No.	1,16	125			
Matches	933	Conservative	0	Mismatches	405	Indels	0
						Gaps	0
QY	AGAGGAGGAAGAGTACATTAACCTCCAGAGGCGTGAAGGGCTCAACAACAAGAGGAGATT	377					
DB	AGACAAAGAAAGATTCAATTCACAGCAATGATCTGAAAAAACAACACCAGAGATT	120					
QY	TATGATCTCAATTCAGAGTAAGGTGTACATGTCAGATTGGGTCAAGAGCAACCTG	437					
DB	TATGATCTCAATTCAGAGCAAAATCTACAGACGTCTCCACTGGGTCAAAATCCATCCG	180					
QY	GTGTGATGTTCCAAATCTTCAAACCTTGCGCCAGATGTCATGATGATTCATACAT	497					
DB	GAGCGAAGCAGCATCTTAAACCTCCCGGTCAAGACGTCAACGACGCGTTATCGCTT	240					
QY	ACCATCTGGCAGACATGTGTCAACCTTGAAAAATTTTCACTGGCTTACCACTCACTG	557					
DB	ACCATCCCGGAACCGCATGGCGCACTTCGAAACCTTCACAAAGCGCTACACAGTGAAG	300					
QY	ACTTCAAGAGTCTCGAGAGTGTCCAAAGACTACAGAAAGCTTGATCTGAGTTCTCAAAAT	617					
DB	ACCAACACAGTGTCCGAGGTGTGCGGTACACGTCTGTTAGCCGAGTTTTCAAAC	360					
QY	TGGGTCTTTTTCAGACCAAGAGGAGATGCACTTCATGCAACCTTGATCTGTGCTGTTA	677					
DB	GGGAGCTTTCGATTAATAAAGGTACAGTACCTTTTACAGCTCACAGTACGCTGCTGCA	420					
QY	TGTTCTCATTTTACTCTATGAGTGTCTGAGAGTGCATAGTGTGTGGCTCATTTGGGTT	737					
DB	TGCTCGCGCGGTGTATACGGTGTGTGTGATGACAGAGATATGGGCCCATTAATAT	480					
QY	CAGGATGCTCTTGAAGGTTGCTTTGATGACAAATGCTTATGAGGCGCATATTCTGGCC	797					
DB	CCGCGCTTCTGCTGGGCTTCTCTGATATACAGACGCTTATGATGGACATATCTGTGTC	540					
QY	ACTATGTGTATATGACAAACCAATGATTTTCAACAAGTTTGACACAGATCTCTGSGGAAT	857					
DB	ATTACAAAGTACGTCAACGAAGCCGTATATACTGTACAGCTCTGTCTGGTAATCT	600					
QY	GCTTGACCGGGATATAGCAATGCTTTGTGGAAATGGAATCACAATGCTTCAACAATTGGCT	917					
DB	GCAATCACCGGATATCATCGCGTGTGGAAATGAGACATTAACGCTCACCATATCTCTT	660					
QY	GCAACACGCTTGACATGACCCGTATGTGACGACATGCGGCTTTTGACGTTTCTGTCG	977					
DB	GTAATATCTTGACACAGATCTGATGTCCAGCAATCCGTCTTAAAGCGTCTTCAACA	720					
QY	GATTCCTCAATTCATTAACCTCTATTTCTATATGGAAGAAATGAGATTTGATTTCAATG	1037					
DB	AGTTCTTTAAGTGCATACGTACAGTTCATATGGAAGAAATTTACGTTTGCATCACTAG	780					
QY	CTAGGTTCTTGATCTGTACACAGCACTTTTATCCCGGTATATGTGTGTCACAGG	1097					
DB	CTGATCTTGATGATGACCTACCAACATCTGTCTTTATTCATATGATGTGTGGAGAA	840					
QY	TCAACTGTATCTGACAGCAATTTGCTATGTGTTTGAGAGCGAAAAATGACAGATAGAG	1157					
DB	TCAATCTCTTATTCACAAAGTTTATCTTTTGCTATATCTGAAACGTTAAGTCTTATGAG	900					
QY	CCTTGAACATTAATGGGATCCCTGTGTGTTTGGACTTGGATCCCTTTTATGATGCTTGGC	1217					
DB	CTTTGAACATTAATGCGGATCTTGTGTTTCTGTGAGAGTGTGTTCTCTTTTATGATATCTTC	960					
QY	TGCCAAATGGCTGAGAGGATTATGTTTGTGCTGTAGCTTGTGCTGTTGTTTCATCC	1277					
DB	TACCAAACTGGCAAGAGAGATCATCTTTGCTTTTAAAGATGGCGTCAACGCGATTC	1020					
QY	AGCAGATTCAGTTCTGTTTGAATATCTTTGTGCAAAATGATATGTGTGGGCTACCGAGTG	1337					
DB	AGCAGCTTCAAGTTCTGTTTAAACATTTTGTGGGAGATGTTTAAACCGGCTCCGCTAATG	1080					

QY 1338 GGATGATCTGGTTGAGAGCAGACAGTGTATCTGATATCTTGGCTCTTGA 1397
DB 1081 GGAACGATTTGGTTTGGAGAGCAACAGCTGTAGCTTGAATATCTGTAGTGTATTA 1140
QY 1398 TGAATGGTTTTCGTTGGCTTGGACATTTGACCTTGAACATCATTTGTTTCAAGGCTAC 1457
DB 1141 TGAATGGTTTTCGTTGGCTTGGACATTTGACCTTGAACATCATTTGTTTCCCTAGGCTAC 1200
QY 1458 CTGGTGGCAATTTGAGAGCAAGATTTGCTTGTGTAGTACCTTTGCAAGAGCATTAAT 1517
DB 1201 CGCCTTGCATCTAGAGGAGATTTTCCTGTGTAGAGACCTTTGTAAGAGCATATATC 1260
QY 1518 TGCCTTATAGAGGCTGTGATTTTGGAGAGGCAATCACTAGTGAACATTTGCAAGGCTAC 1577
DB 1261 TACCGTATAGAGGCTGTGATTTTGGAGAGGCAATCACTAGTGAACATTTGCAAGGCTAC 1320
QY 1578 CTGGTGGCAATTTGAGAGCAAGATTTGCTTGTGTAGTACCTTTGCAAGAGCATTAAT 1637
DB 1321 AAGCGGCGGTTCAAGCTAGAGATGACTAATCTGTGTGTGAGATTTGCTATGGAGAG 1380
QY 1638 CTGTTAATACCATGCT 1655
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AC AAC42244;
XX
DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 34823.
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KM Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
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OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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Db 118 GCGGATCAACGAGAGAGATCGTTACAGGAGAGATTGAAAAACCAACCAACC 177

Qy 370 GGGAGATTATGATCTCAATTCAAGGTAAGGTATACATSTCTCAGATTGGTCAAGCA 429
Db 178 TGGAGATTATGATTTGATTCAGATTCAAGTAAAGTTTACGACGTTCCGATTGGTTAATC 237

Qy 430 GCACCTGTGTGTGATGATTCATTCAAACTTGTGCGCAGAGATGCTACTGATGCA 489
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Qy 490 CATGACATACCATCTCCGACACAGATGTCACACTTGAAATTTCTTCACTGGCTACCA 549
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Qy 550 CCTCAGTACTTCAAGGCTCTGAGTGTCCAAAGACTACAGAAAGCTTGATCTGAGTT 609
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Qy 730 TTGCGTTCAAGCATGCTTTAGGGCTTTTGGATGAAAGTCTTATGCGGCATGA 789
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Qy 970 TTCTGCGGTTCTTCAATTCATACCTCTCATTTCTATGAGAGAGTTGAGTTGA 1029
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Qy 1090 TGCAGGCTCACTGATGATGACAGACATTTGCTATTTTTCGAGGAGAAAGTGA 1149
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Qy 1150 GATAGAGCTTGAACATTAATGAGGATCTGTGTTTGAAGTGTCTCTTTAGT 1209
Db 958 AGATCGGCTTGAACATCCCGGAATTTAGTTTCTGACATGTTCCCTCTTACT 1017


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Qy      1136  AGCGGAAAAGTGACGAGATGAGCCTTGAACTAAATGGGGATCCTGTGTTTGGACTTG 1195
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Qy      1436  CATCATTTGTTTCCAGGCTACCTCGGTCATTTGAGGAAGATTTGGCCTTGCTAGT 1495
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Qy      1616  CCTAAGATTTGTTGGGGAAGCTGTTAATCCATGCTGAGGCATTTGGAGTTTAG 1675
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DT      17-OCT-2000 (first entry)
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KW      Hybridisation assay; genetic mapping; gene expression control;
KW      protein identification; signal transduction pathway;
KW      metabolic pathway; promoter; termination sequence; ss.
XX
OS      Arabidopsis thaliana.
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PD      06-SEP-2000.
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Db      1349  TCGGTTACCTCGGTCGAATTTGAGAGATTTGCTTGTGTTAGTACCTTTGCAAGAA
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Qy      1630  GTGGAGCTGTTTATATCCATGCTGAGGATTTGAGATTTTGAAGTTTGAAGATTTG
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KW      tolerance; resistance; soil salinity; ion stress; toxicity; drought;
KW      cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
KW      pharmaceutical; food; chemical raw material; ds.
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PR      27-JUN-1998; 98DE-1028850.
XX
(GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
XX
PI      Heinz E, Zaehring U, Schmidt H, Sperling P;
XX
DR      WPI; 2000-127549/12.
XX
PT      P-PSDB; AAY51334.
XX
PS      New sphingolipid desaturase that selectively introduces double bond
PS      into sphingolipids and capnoids -
XX
XX      Claim 11; Fig 3; 62pp; German.
XX
CC      This invention describes a novel sphingolipid desaturase that selectively
CC      introduces a double bond into the sphingobase of the ceramide residue of
CC      sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
CC      desaturase, or a vector containing the DNA sequence, can be used to
CC      produce transgenic plants, especially crop plants, with an increased or
CC      decreased delta-8-unsaturated long-chain base content or an altered
CC      delta-8-unsaturated long-chain base cis/trans ratio, especially to
CC      compensate for a delta-8-unsaturated long-chain base deficiency, to
CC      exclude production of delta-8-unsaturated bases, to increase tolerance
CC      or resistance to soil salinity, ion stress or toxicity, drought, wet
CC      conditions, cold or frost and/or phytopathogenic microorganisms, or to
CC      alter size growth and flowering time. Cells, transgenic organisms or
CC      plants containing the DNA sequence can be used to produce sphingolipids
CC      and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
CC      can be used in cosmetics, pharmaceuticals and foods and as chemical raw
CC      materials. This sequence encodes the Arabidopsis thaliana sphingolipid
CC      desaturase sld1 protein described in the method of the invention.
XX
SQ      Sequence 1678 BP; 416 A; 408 C; 339 G; 515 T; 0 other;
Query Match      33.2%; Score 642.6; DB 21; Length 1678;
Best Local Similarity 66.0%; Pred. No. 2e-116;
Matches 930; Conservative 0; Mismatches 479; Indels 0; Gaps 0;
Qy      310  GGTGTTGAGAGAGAGAGATCAATTAACCTGAGAGAGCTGAGGCTCACAACAAGA 369
Db      174  GCGGAGAGAGAGAGAGAGATCAATTAACCTGAGAGAGAGCTTAAACCAACAACAATC 233

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Qy 370 GGGAGATTATGATCTCAATTCAAGGTAAGGTGACAAATGCTCAGATTGGGTCAAGGA 429
Db 234 TGGAGATCTATGATATCGGATTCAGGCAAGGTCTACACGCTCCGATGGAATTAAC 293
Qy 430 GCACCTGTGTGTGATGTTCCAACTCAACCTTGCTGGCCAGGATGTCACTGATGCAAT 489
Db 294 TCATCCGGAGGCGACAGGTGATTCGATCTGGTGTCAAGACGTCAACGATGCTTT 353
Qy 490 CATACATACATCTCTGGACACAGATGTCAACCTTAAATAATTTCTACCTGGCTACCA 549
Db 354 CATGCAATTCATCCGGACACGCTTGGCACCATCTCCACCATCTTCCACCGGTACCA 413
Qy 550 CCTGATGACTTCAAGTCTCTGAGGTGTCACAAAGACTACAGAAAGCTTGACATGAGTT 609
Db 414 CATGAGATTTCCAGTCTCCGAGTCTCAAGCTCAAGCATTACCGTATGCTGCCGATTT 473
Qy 610 CTCAAAATTTGGGCTCTTTTGAACACCAAGGCGATGCTTCAAGCCTTGACATCTGT 669
Db 474 TCGTAATCTGGTCTCTTGAACCAAGGTCAAGTCTCTACACTCTTAAGCTTGTGT 533
Qy 670 TGCTGTATGTTCTCTCATTTGATCTATGTTGTCTGAGGTGACTAGTGTGGGCTCA 729
Db 534 CGCGCCATGTTCCCTCGAGTCTCTACGGTGTGTTGGCTTGACCTCGCTTCTGCTCA 593
Qy 730 TTTGGGTTCAAGGCAATGCTCTTAGGGTGTCTTGAATGAAAGTGTATATGTTGGGCTCA 789
Db 594 CCAATTCGCGCGCGCTTCTGGTCTCTCGATCTCGAATCAAGCGGCTTATATAGGCTACGA 653
Qy 790 TTCTGGCCACTATGTTGTTATGACAAACCAAGTTTCAACAGTTGACAGATCTCTC 849
Db 654 TTCTGGTATTAAGTTATCATGTGACAAATCTTATTAACAGATTCGCTCAGCTTCTCTC 713
Qy 850 TGGGACTGCTTACCGGGAATAGCATGTTGTTGGAAGTGAATCAATGCTCAACA 909
Db 714 CGGTAACTGTCTCAACCGGAATCTCAATCGGTGGAATGAGTCAATGCTCATCA 773
Qy 910 CATGCGGCAACAGGCTTGAACCATGACCTGATCTGAGACACATGCGGCTTTTGACGT 969
Db 774 TCTAGCTTGAACAGCTCTGATTAAGCATCAATCAACATCCCTGCTTCTGCGGT 833
Qy 970 TTGCTCGGGTCTTCAATTCATTAACCTCTCATTTCTATGGAAGAAATGGAATTTGA 1029
Db 834 CTCACCAAAATCTTCTCTCTATTAACCTCGAGATTTCAAGATGGAATCACTGTTGA 893
Qy 1030 TTTCAATGCTAGGTTCTGATCTGCTACAGACATTTACTTTTACCCTGATGTGT 1089
Db 894 TCCAGTCCGAGATCTTAGTCACTATCAACATTTACTTATTCAGATATGTGCT 953
Qy 1090 TGGCAGGCTCACTGTATCTGACAGACAACTCTGCTATTTTGGAGCGCAAGTCA 1149
Db 954 TGGAAATCAATCTTCAATTCATTAACAGTTTCTCTGCTCTTCAACCGGAATACC 1013
Qy 1150 GGATAGAGCTTGAACATTAATGGGATCTTGTGTTTGAAGTTGCTTCTTCTTGTAGT 1209
Db 1014 AGATGTGCTTAAACTTCGCGGAATCTTAGTCTTGGATTTGGTCCACTGTAGT 1073
Qy 1210 GTCTTGCTGCCAAATGGCTGAGAGGTTATGTTGTGCTTGCTAGCTTGTGTTTG 1269
Db 1074 CTCATGTCTACCAAACTGGCCGAGAGATTTCTTCTGCTTCAACAGCTTCAACGCTAC 1133
Qy 1270 TTTCATCCAGACATTTCACTTCTGTTGAATACCTTGTGGAATGATATGTGGGCC 1329
Db 1134 GCGGCTTCAACATTTCAATTAACCTTAACTTGTGCTGATGCTTGAAGTTGCTC 1193
Qy 1330 ACCGATGGGAATGACTGGTTGAGAGACAGCAAGTGTATCATTTGATCTTCTTGTGC 1389
Db 1134 ACCCACCGTACGACTGTTTGAAGAGCAAGCGCGGGAACATTCATCTTGTAG 1253
Qy 1390 CTCTTCATGATGATGTTTGTGTTGCTTGGAGTTTCAAGTTTCAAGCATTTGTGCTC 1449
Db 1254 ATCATATCATGATGTTGTTCTTGTGATTAACATTTCAAGCTTGTGATCATTTGTGCC 1313

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Qy 1450 AAGCTACCTCGGTGCCAATTTGAGAGATTTGCGCTTTGGTTAGTACCTTTGCAAGA 1509
Db 1114 TCGCTTACTCTGTTGCCATCTCCGAAAGTTTCTCCGTTGGTTCAAGGCTTTGCAAGAA 1373
Qy 1510 GCATTAATTTGCTTATAGAGCTTGTCAATTTGGAGGCCAATAGTGAACATTTAGAC 1569
Db 1374 GCATTAATCTTCCGATGAGATATGCTGTTTGAAGCAAAATGTTGACATTTAACAC 1433
Qy 1570 CCTGAGAGCTGCGCTTACAGCTAGGACTTAACAAACCTGCCCCCTAAGAAATTTGT 1629
Db 1434 TTTAAGACAGCACTTATATCAAGTTAAGACAGCTGCTAATCCGTTAGAACTTGT 1493
Qy 1630 GTGGAAGCTGTATATCCATGCTGAGGCAATTTGAGTTTGAAGTTTGAAGATTTTG 1669
Db 1494 TTGGGAAGCTTTGAATCTATGCTAAATGATTTTAAATCAAAACAAATATGCTTTGT 1553
Qy 1690 TCAAGTCTTTTCTTTTCTTTTCTTCT 1718
Db 1554 TTGGTTAAATTTGATGTTGTTTAT 1582

```

RESULT 8

AB212753
ID AB212753 standard; DNA, 1350 BP.

XX AB212753;

XX 21-JAN-2003 (first entry)

DE Arabidopsis thaliana stress regulated gene SEQ ID NO 558.

XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

OS Arabidopsis thaliana.

PN W020021655-A2.

XX 28-FEB-2002.

XX 24-AUG-2001; 2001WO-US26685.

XX 24-AUG-2000; 2000US-227866P.

PR 26-JAN-2001; 2001US-264647P.

PR 22-JUN-2001; 2001US-300111P.

XX (SCRI) SCRIPPS RES INST.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Harper JF, Krepe J, Wang X, Zhu T;

PI WPI, 2002-304127/34.

DR WPI, 2002-304127/34.

PT Identifying a stress condition to which a plant cell has been exposed

PT and producing plants with increased tolerance to these abiotic stresses

XX Claim 6; SEQ ID NO 558; 577bp + Sequence listing; English.

XX The invention relates to identifying a stress condition to which a plant

XX cell has been exposed, comprising:

XX (a) contacting nucleic acid representative of expressed polynucleotides

XX in the plant cell with an array or probes representative of the plant

XX cell genome; and

XX (b) detecting a profile of expressed polynucleotides in the plant cell

XX characteristic of a stress response. The method is useful in the

XX production of transgenic plants, cells and seeds and in producing plants

XX with increased tolerance to abiotic stresses. The present sequence is that

XX of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used

XX in methods of the invention.

XX Note: The sequence data for this patent is not represented in the printed

XX specification but is based on sequence information supplied to Derwent by

XX the European Patent Office.

XX

CC seed-specific manner in transgenic plants, when placed under control
 of the sunflower albumin gene 5' regulatory region (AAV34397).

XX Sequence 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 other;

Query Match 32.0%; Score 618.4; DB 19; Length 1684;
 Best Local Similarity 66.5%; Pred. No. 1,1e-111;

Matches 886; Conservative 0; Mismatches 446; Indels 0; Gaps 0;

QY 326 AAGAAATCATTAACCTTCAGAGAGCTGAAGGCTCAACAACAGAGGAGATTATGATC 385
 DB 58 AAGAAATCATTAACCTTCAGAGAGCTCAAGAACCCGATTAACCCGAGATCTATGATC 117
 QY 386 TCAATTCAGAGTAAAGGTATCAATGCTCAGATTGGGTCAGAGAGACCCGTTGGTAT 445
 DB 118 TCGATTCAAGGGAAGGCTATGATGTTTGGATTGGGGAAGAACCATCAGTGGAGCC 177
 QY 446 GTTCCATCTCAAACTTGTGCGCAGAGATGCTAGTATGATTCATATACATACCT 505
 DB 178 TTCCCTTGAAGAGCTTGTGTGTCAGAGGTAATGATGATTTGTTGCAATTCATCT 237
 QY 506 GGCACAGATGTCACACCTTGAAAAATTCTTCACTGCTACACCTCAGTACTTCAAG 565
 DB 238 GCCTCTACATGGAAGAACTTGATTAAGTATTTCACTGGGTAATTTATCTTAAAGATTACTCT 297
 QY 566 GTCTCTGAGTGTCCAAAGACTACAGAAAGCTGATCTGATCAAAATTGGGCTT 625
 DB 298 GTTCTGAGGTTCTTAAAGATTATAGAAAGCTTGTGTTGAGTTCCTTAAAGGAGTTG 357
 QY 626 TTTGACACCAAGGAGCATGCTCATTCATGCAACCTTGATCTGTGCTTATGTTCTC 685
 DB 358 TATGACAAAAAGCTCATATATATGTTGCAACTTGTGCTTATAGCAATGCTTGTGCT 417
 QY 686 ATTGACTCTATGCTGTTCTGAGTGACATGATGTTGGGCTCATTTGGGTTCAAGCATG 745
 DB 418 ATGAGTGTATAGGGGTTTGTGTTGTAGAGGTTGTTGTAACATTTGTTCTGGGTTG 477
 QY 746 CTCTTAAAGGTTGCTTGAATGCAAGTCTTATGAGGCGCATGATTTGGGCGACATG 805
 DB 478 TTGATGGGTTTCTTGAATTCAGATGAGTGGATGGAACATGATGCGGCGATTATAG 537
 QY 806 GTTATGACAAACCAATGTTTCAACAGGTTGACACAGATCTCTCTGGGAACTGCTTGAAC 865
 DB 538 GTAGTGTCTGATTCAGGCTTAATAGTTTATGGGTAATTTTGGCGAAATGTTCTTCA 597
 QY 866 GGGATTAAGATTGCTTGGTGAAGTGACTCAATGCTCACCACATTTGCGTCAACAC 925
 DB 598 GGAATTAAGATTGCTTGGTGAAGTGAAATGAAACCAATATGACATCATTTGCCGTATAGC 657
 QY 926 CTGACCAATGACCTGATCTGACAGCAATGCCGCTTGTGCACTTGGCGGCTTCTTC 985
 DB 658 CTGAAATTAAGACCTGATTTTAAATATATACATTCCTGTGTTGTGCTTCAAGTTTCT 717
 QY 986 AATTCATTAACCTCTCATATTTCTATGGAGGAGAGTTGAGTTGATTTGATTTGCTAGTTC 1045
 DB 718 GGTTCACCTCCTCATTTCTATGAGAAAGAGTTGACTTTGACTTTTATCAAGATTTC 777
 QY 1046 TTGATCTGACAGCACTTAACTTTTAAACCGGTAATGTTGTTGCCAGGCTCAACTTG 1105
 DB 778 TTTGTAAGTTATCAATGACATTTTAACTTATATGTTGCTGCTAGGCTCAATATG 837
 QY 1106 TATCTGACAGCAATTTCTGATTTGTTTTCGAGGCGAAAAAGTCAAGATAGACCTTGAAC 1165
 DB 838 TATGTAACAATCTCTATATATGTTTGAACAAAGAAAGTGTCTTATGACACTCAGGA 897
 QY 1166 ATAATGGGATCTTGTGTTTGAAGTTGGTTCCTCTTATGATGCTGCTGCAAT 1225
 DB 898 CTCTTGGATGCTTATGTTCTGATTTGGTATCCCGTGTCTTGTGTTGCTTAT 957
 QY 1226 TGGCTGAGAGGGTATGTTTGTGCTTGTGCTTGTGCTTGTGTTTGTTCATCCAGACAT 1285
 DB 958 TGGGTTGAAGAAATATATGTTTGTATGCAAGTTATACGTGACGTGAATGCAACAAGT 1017

QY 1286 CAGTCTGTTGAATCACTTGTGCAATGATATGTCGGCCACCGAGTGGATGAC 1345
 DB 1018 CAGTCTCTTGAACCACTTCTCTCAAGTATATGTTGGAAGCACTTAAAGGATATAT 1077
 QY 1346 TGGTTGAGAGACAGACAGTGTATCATTTGATATCTTGTGCTTGTGATGATTGG 1405
 DB 1078 TGGTTGAGAAACAAACGATGAGACACTTGACATTTCTGTCTCTCTTGATGATTTGG 1137
 QY 1406 TTTTGGGTGGCTTGCAGTTTTCAGCTTGACATATTTGTTTCCAGGCTACCTGGTGC 1465
 DB 1138 TTTATGATGATGCAATTTCAATTCGAATTTAGCATCATTTTGTCCAGATGCTTAGATGC 1197
 QY 1466 CAATTGAGAAATTTGCGCTTGTGTTAGTACCTTTGCAAGAACATTAATTTGCTTAT 1525
 DB 1198 AACCTTGAAGAAATCTGCGCTAGTATGATGATGATGCAAGAAACATTAATTTGCTTAC 1257
 QY 1526 AGGAGCTTTCATTTTGGAGGCGCAATCAGTGCATTTAGGACCTTCAGACTGCTGCC 1585
 DB 1258 AATTATGATCTTCTCTCAAGGCGCAATGAATGACACTCAGAACATTGAGGACACAGCA 1317
 QY 1586 CTACAGCTAGGAGCTTAAACAAACCTGCGCTTAAAGAAATTTGTTGGGAACTGTTAAT 1645
 DB 1318 TTGAGGCTAGGAGTATTAACCAAGCGCTCCGAAAGATTTGTTAGGAGAGCTTCTTAC 1377
 QY 1646 ACCCATGAGCTGA 1657
 DB 1378 ACTCATGTTTA 1389

RESULT 10
 AAX24917
 ID AAX24917 standard; cDNA; 1684 BP.
 XX
 AC AAX24917;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Borage delta-6 desaturase cDNA.
 XX
 KM Delta-6 desaturase; borage; oleosin; Acs21, promoter;
 KM transgenic plant; seed; lipid; fatty acid; oilseed; vegetable oil;
 KM gamma-linolenic acid; octadecatrienoic acid; de.
 OS Borage officinalis.
 XX
 FH Key Location/Qualifiers
 FT 43..1389
 FT /*tag= a
 XX
 PN MO9845461-A1.
 PD 15-OCT-1998.
 XX
 PF 09-APR-1998; 98WO-US07179.
 PR 09-APR-1997; 97US-0831575.
 XX
 PA (RHON) RHON-POULENC AGROCHIMIE.
 XX
 PI Li Z, Thomas TL;
 XX
 DR WPI: 1999-180333/15.
 DR P-F8DB; AAM98130.
 XX
 PT Nucleic acid containing oleosin 5'-regulatory region - useful for
 PT modulating fatty acid synthesis and lipid metabolism in plants,
 PT particularly to increase content of gamma-linolenic acid
 PS Example 2; Page 59-61; 101pp; English.
 CC The present sequence encodes borage delta-6 desaturase (see
 CC AAM98130), an enzyme that catalyses the conversion of linoleic acid
 CC to gamma-linolenic acid (GLA). Delta-6 desaturase cDNA was

CC isolated from a borage membrane-bound polysomal cDNA library
 CC using a partial clone, obtained from an EST database search, as
 CC probe. The borage delta-6 desaturase nucleic acid can be
 CC operably linked to the seed-specific 5' regulatory region (see
 CC AM24916) of the Arabidopsis thaliana oleosin AtS21 gene in claimed
 CC expression cassettes of the invention. Transgenic plants, e.g.
 CC sunflower, soybean, maize, tobacco, cotton, peanut, oilseed
 CC rape or Arabidopsis are obtained that show increased levels of
 CC GLA or octadecatrienoic acid. The levels of desirable fatty
 CC acids in oilseed crops can be manipulated to provide seed
 CC oils of use in human health and industrial applications.

XX Sequence 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 other;

Query Match 32.0%; Score 618.4; DB 20; Length 1684;

Best Local Similarity 66.5%; Pred. No. 1.1e-111;

Matches 886; Conservative 0; Mismatches 446; Indels 0; Gaps 0;

QY 326 AAGAGTACATATACCTCAGAGAGCTGAAGGCTCAACAAGAGAGAGATTATGATC 385
 DB 58 AAGAAATACATTACTCAGATGAATCAAGAACACGATMAACCGAGATCTATGATC 117
 QY 386 TCAATTCAGGTAGGTGTACATCTCTCAATTTGGTCAAGAGACCTGTGTGAT 445
 DB 118 TCGATTCAAGGGAAGCCTATGATGTTCGATTTGGTGAAGACATCCAGTGGCAGC 177
 QY 446 GTTCCAACTCAACCTGTGCGCAGATGTCACTGTATGATATGATACATCTCT 505
 DB 178 TTTCCTTGAAAGCTTGTGTGTCTCAAGAGTACATGATGATTTGTTCATCTCT 237
 QY 506 GGACACAGCATGTACACCTTGAAAATTTCTTCACTGCTACACCTCAGTACTTCAAG 565
 DB 238 GCTCTACATGGAAGATCTTGATTAAGTTTTCATGCTGATATATCTTAAAGATTACTCT 297
 QY 566 GTCTGTAGGTGTCAAGACTACAGAAAGCTTGATCTGAGTTCTAAAATTTGGTCTT 625
 DB 298 GTTCTGTAGGTGTCTAAAGATTAATAGAAAGCTGTGTGATTTCTAAATTTGGTCTT 357
 QY 626 TTGACACCAAGGCGATGTCACTTACATGCAACCTTGATCTGTCTGTATGTTCTC 685
 DB 358 TATGACAAAAGGCTATATATATTTGCAACTTTGCTTAAAGCAATCTGTGCT 417
 QY 686 ATTGACTCTATGCTGTCTGAGTGCACTAGTGTGTGGGCTCATTTGGTTCAGGCATG 745
 DB 418 ATGAGTGTATGGGCTTTTGTGTGAGGCTGTTTGTGATCATTTTTCGCGGT 477
 QY 746 CTCTTAGGGTGTCTTGGATGCAAGTCTTATGTGGCCATGATTTGGCCACTATGTG 805
 DB 478 TTGATGGGGTTCCTTGGATTCAGAGTGTGTGATGACATGATGCTGGCATTATATG 537
 QY 806 GTTATGACAAACCAATGTGTTCAACAAGTGTGACAGATCTCTCTGGGAAGCTGTGACC 865
 DB 538 GTAGTGTGATTCAGGCTTAATTAAGTTATGGGTATTTTGGTCMAATTTGCTTTCA 597
 QY 866 GGATTAACCATTTGCTGTGGAAGTGAATGCAATGCTCAACATGCGGGAACAGC 925
 DB 598 GGAATAGTATTTGGTGTGGAATGGAACATTAATGACATCAATGCTGTATATGAC 657
 QY 926 CTGACCAATGACCTGATCTGACGACATGCGGCTTTTGGAGTTTCGTGCGGTTCTTC 985
 DB 658 CTTGAATATGACCTGATTTCAATATATACATTCCTTGTGTGTCTTCCAGTTTCTT 717
 QY 986 AATTCATTAACCTGCTCATTTTCTATGGAGAAAGTTGAGTTGATTTCAATGCTAGGTTG 1045
 DB 718 GATTACACCTCCTCATTTCTATGAGAAAGTTGACTTTTGACTCTTTATCAAGATTC 777
 QY 1046 TTGATCTGCTACGACCATTTACTTTTACCCGGTAATGTGTGTCAGAGGCTCAACTG 1105
 DB 778 TTGTAGTATTCACATTTGACATTTTAACTTATATGTGTGCTGAGCTCAATATG 837
 QY 1106 TATCTGACAGACATTTCTGCTATGTTTTCAGAGCCAAAGTGCAGATAGACCTTGAAC 1165
 DB 838 TATGACATCTCTCATATGTGTGACCAAGAAATGTGTCTCTATCGAGCTCAGGA 897

QY 1166 ATAAGGGAGATCTTGTGTTTGGACTTGGTCCCTCTTTAGTGTCTTGCCGCAAT 1225
 DB 898 CTCTGGAGAGCTTATGTTTCTCATTTGGTACCCGTTGCTGTTCTTGTGGCTTAT 957
 QY 1226 TGCGCTGAGAGGTTATGTTTGTGCTTGTAGCTTGTCTGTGTTTTCATCAGACAT 1285
 DB 958 TGGGGTGAAGAAATTAATGTTTATGCAAGTTTATCAGTACGTGAATGCAACAAGTT 1017
 QY 1286 CAGTTCTGTTGATTCATCTTGTGCAAAATGATATGTCGGGCCACCGAGTGGGAATGAC 1345
 DB 1018 CAGTTCTCTGGAACCACTTCTTCAAGTGTATATGTTGAAAGCCTAAGGGAATAT 1077
 QY 1346 TGGTTTGAAGACAGACAAGGTGATCATTTGATATCTTGTGCTCTTGATGATTTG 1405
 DB 1078 TGGTTTGAAGAAACAAGGATGAGACACTTGCATTTCTTGTCTCTTGATGATTTG 1137
 QY 1406 TTTTTCGCTGCTTGCAGTTTCACTTGAAGCATTTGTTTCCAAAGCTACCTCGGTG 1465
 DB 1138 TTTGATGTTGATGCAATTCGAATTCGAATTTGAGCATATTTGTTCCAAAGATCCTAGATGC 1197
 QY 1466 CAATTGAGAAATTTGCGCTTGTGTTAGTGAACCTTGGCAAGACATATTTGCTTAT 1525
 DB 1198 AACCTTAGAAATCTGCGCTTACGTATGATGATGCAAGAAACATATTTGCTTAC 1257
 QY 1526 AGAGCTTGTGATTTTGGAGGCGCAATCAATGACATTTGAGACCTCAGACTGCTGCC 1585
 DB 1258 AATTATGATCTTCTTCCAAAGCCAAATGAATGACCTCAGAACTTGAAGACAGCA 1317
 QY 1586 CTACAGCTAGGAGCTTAACAAACCTGCGCTTAAGATTTGTTGGGAAGCTTTAT 1645
 DB 1318 TTGAGGCTAGGGAATATACCAACCGCTCCGGAAGATTTGTATGGGAAGCTTTCAC 1377
 QY 1646 ACCCATGCTGA 1657
 DB 1378 ACTCATGTTAA 1389

RESULT 11
 ID AAT30395 standard; DNA, 1685 BP.
 AC AAT30395;
 DT 15-SEP-1996 (first entry)
 XX Borage delta-6-desaturase gene.
 DE Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;
 KW polyunsaturated fatty acid; octadecatrienoic acid;
 KM chilling resistance; oilseed; ss; db.
 XX Borage officinalis.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 44..1390
 FT /*tag= a
 XX
 PN M09621022-A2.
 XX
 PD 11-JUL-1996.
 XX
 XX 28-DEC-1995; 95WO-IB01167.
 PF 30-DEC-1994; 94US-0366779.
 PR
 XX
 PA (RHON) RHONE POULENC AGROCHIMIE.
 XX Freybsineb GL, Nuccio M, Nunberg AN, Reddy AS, Thomas TL;
 FI WPI; 1996-333997/33.
 XX P-PSDB; AAR98455.
 DR
 XX

PR 10-OCT-1991; 91US-0774475.
 PR 08-JAN-1992; 92US-0817919.
 PR 14-SEP-1994; 94US-0307382.
 PR 28-JAN-1997; 97US-0789936.
 XX
 PA (RHON) RHONE-POULENC AGROCHIMIE.
 XX
 PI Thomas TL;
 XX
 DR WPI: 2002-380944/41.
 DR P-PSDB; AAU79830.
 XX
 PT Novel nucleic acid encoding evening primrose delta6-desaturase which
 PT converts linoleic acid to gamma linolenic acid useful for producing
 PT gamma linolenic acid in transgenic plant or bacteria
 XX
 PS Example 9; Column 29-32; 53pp; English.
 XX
 CC The invention describes an isolated nucleic acid encoding an evening
 CC primrose Delta6-desaturase. The nucleic acid and a vector expressing the
 CC nucleic acid are useful for producing a plant such as sunflower, soybean,
 CC maize, tobacco, peanut, carrot or oil seed rape plant, with increased
 CC gamma linolenic acid (GLA) content, and also for inducing or increasing
 CC production of GLA in a bacteria or plant deficient, lacking in or
 CC producing low levels of GLA. The nucleic acid is also useful for inducing
 CC chilling tolerance in plants. This sequence encodes the borage delta6
 CC desaturase involved in the production of gamma linolenic acid.
 XX
 SQ Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 other;
 Query Match 32.0%; Score 618.4; DB 24; Length 1685;
 Best Local Similarity 66.5%; Pred. No. 1.1e-111;
 Matches 886; Conservative 0; Mismatches 446; Indels 0; Gaps 0;

QY 926 CTGACCATGACCCCTGATCTGCAGACATGCCGCTCTTGCAAGTTGCTGCGGTTCTTC 985
 |||||
 Db 659 CTGGAATATGACCCCTGATTTACATATATACATCTCTGTGTGCTTCCAACTTTT 718
 |||||
 QY 986 AATTCATAACCTCTCATTTCTATGGAGAGAGTTGAGTTGATTCATTGCTAGGTTG 1045
 |||||
 Db 719 GGTCACTCACCTCTCATTTCTATGAGAAAGTTGACTTTTACTCTTATCAAGATTC 778
 |||||
 QY 1046 TTGATCTGCATACAGCATTTACTTTTACCCGCTATATGTGTGTGCGCAGGCTCACTTG 1105
 |||||
 Db 779 TTGTGAGTTATCAACATGAGATTTTACCTATATGTGTGTGCTGAGGCTCAATATG 838
 |||||
 QY 1106 TATCTGAGACAAATTCGATATTGTTTTCAGCGGAAAGTGACGATAGACCTTGAC 1165
 |||||
 Db 839 TATGTACATCTCTCATATATGTTTTCACAGAGAAATGTCTTATCGAGCTCAGGA 898
 |||||
 QY 1166 ATATGGGATCTTGTGTGTGTGACTGTGCTTCCCTTTTATGTGTGCTGCTCCAAAT 1225
 |||||
 Db 899 CTTTGGAGATGCTAGTGTCTCGATTGTGACCCGTTGCTGTGTTCTTGTTCCTTAT 958
 |||||
 QY 1226 TGCGCTGAGAGGTTATGTTTGTGCTTGTGCTGCTTGTGCTTGTGCTTGTGCTTGTG 1285
 |||||
 Db 959 TGGGCTGAAAGATTTATGTTTGTATTCAGAAATTCAGTGAATGCAATGCAATGTT 1018
 |||||
 QY 1286 CAGTCTGTTGATCATCTTGTGCAATGTATATGTGCGGCCACCGAGTGGGATGAC 1345
 |||||
 Db 1019 CAGTCTCTTGAACCACTTCTCTTCAAGTGTATATGTGAAAGCTTAAAGGAAATAT 1078
 |||||
 QY 1346 TGCTTTGAGAGAGACAGACAGATGTATCTCTTGTGCTTGTGCTTGTGATGAG 1405
 |||||
 Db 1079 TGCTTTGAGAGAGAGAGATGAGATGAGACCTTGAATTTCTTGTGCTTGTGATGAG 1138
 |||||
 QY 1406 TTTTTCGTGCTTGTGCACTTGTGAGATCATTTTGTTCAGAGCTTACCTGCTG 1465
 |||||
 Db 1139 TTTTCATGTGTGATGCAATTCGAAATGAGCATCATTTGTTCCCAAGATGCTTGAATGC 1198
 |||||
 QY 1466 CAATGAGAGAAATTTGCTTGTGTATGACCTTGTGCAAGAAAGCAATATTTGCTTAT 1525
 |||||
 Db 1199 AACTTATGAGAAATCTGCTCTTACGTATGAGATGACAGAAACATATTTGCTTAC 1258
 |||||
 QY 1526 AGAGCTTGTATTTTGGAGGCCAATCACTGACAAATTTAGAGACCTTCAGAGCTGCTGC 1585
 |||||
 Db 1259 AATTATGACATCTTCTTCCAGAGCCAAATGAAATGACATCTGAGACATTTGAGGAAACAGCA 1318
 |||||
 QY 1586 CTACAGCTTAGGACCTTAAACAAACCTGCTTAAAGATTTTGTGGAAGCTGTTAT 1645
 |||||
 Db 1319 TTGACGCTAGGATATATACCAAGCCGCTCCGAAAGATTTGATGGAAGCTCTTAC 1378
 |||||
 QY 1646 ACCATGCTGA 1657
 |||||
 Db 1379 ACTCATGTTAA 1390
 |||||

RESULT 13
 ABX15366
 ID ABX15366 standard; cDNA; 1685 BP.
 XX
 AC ABX15366;
 XX
 DT 17-Apr-2003 (first entry)
 XX
 DE Borage delta-6-desaturase #1 cDNA.
 XX
 XX Delta-6-desaturase; gene; ss; delta-12-desaturase; sunflower; soybean;
 KM maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
 KM octadecatrienoic acid; alpha-linolenic acid; delta-15-desaturase;
 XX borage.
 XX Borage officinalis.
 OS
 XX Key Location/Qualifiers
 FH
 FT CDS 44..1390

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FT      /tag= a
FT      /product= "Borage delta-6-desaturase #1"
FT      /transl_except= (pos:1151..1153, aa:Ser)
XX      US2002108147-A1.
XX      08-AUG-2002.
XX      21-DEC-2001; 2001US-0029756.
XX      13-OCT-1992; 92US-0953952.
XX      19-SEP-1997; 97US-0934254.
XX      10-OCT-1991; 91US-0774475.
XX      08-JAN-1992; 92US-0817919.
XX      14-SEP-1994; 94US-0307382.
XX      28-JAN-1997; 97US-0789336.
XX      (THOM/) THOMAS T L.
XX      Thomas TL;
XX      WPI; 2003-066659/06.
XX      P-PSDB; ABG73095.
XX      Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
XX      for producing plant with increased gamma linolenic acid content, and
XX      for inducing octadecatrienoic acid production in plant
XX      Example 9; Fig 5A; 55pp; English.
XX      The invention relates to a nucleic acid encoding an evening primrose
XX      delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
XX      nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
XX      for producing a plant (such as sunflower, soybean, maize, tobacco,
XX      peanut, carrot or oil seed rape plant) with increased gamma-linolenic
XX      acid (GLA) content by transforming a plant cell with the nucleic acid or
XX      vector and regenerating a plant with increased GLA content from the plant
XX      cell, for inducing or increasing production of GLA in an organism lacking
XX      in or producing low levels of GLA and for inducing production of
XX      octadecatrienoic acid in at least one of a plant deficient or lacking
XX      in or producing low levels of octadecatrienoic acid, a bacterium which
XX      produces alpha-linolenic acid or a bacterium which exhibits a
XX      delta-15-desaturase activity on a GLA substrate. This sequence represents
XX      cDNA encoding a borage delta-6-desaturase polypeptide.
XX      Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 other;
SQ      Query Match      32.0%; Score 618.4; DB 25; Length 1685;
      Best Local Similarity 66.5%; Pred. No. 1.1e-111;
      Matches 886; Conservative 0; Mismatches 446; Indels 0; Gaps 0;
      QY      326 AAGAAATCATTAATCTTCAAGAGAGCTGAAGGCTCAACAAGAGAGGAGATTATGATC 385
      DB      59 AAGAAATCATTAATCTTCAAGAGAGCTGAAGGCTCAACAAGAGAGGAGATTATGATC 118
      QY      386 TCAATTAAGGTAAGGTATCAATCTTCAAGAGAGGCTGAAGGCTCAACAAGAGAGGAGATTATGATC 445
      DB      119 TCGATTCAAGGGAAGGCTTATGATGATTTTCGATTTGGGTAAGAGACATTCAGTGGCAGC 178
      QY      446 GTTCCAAATCTCAAACTTGTGCGCAGAGATGCTAGTGAATTCATTAAGATTCATCT 505
      DB      179 TTTCCCTGAAGAGCTTGTGCTGTCAGAGATGATGATGATTTGTTGATTCATCT 238
      QY      506 GGCACAGATGCTACACCTTGAATAATTTTCACTGCTACACCTCAAGTGAATTCAG 565
      DB      239 GCCTTACATGAGAAATCTTATGATGATTTTCACTGGGATTTATCTTAAGATTAATCT 298
      QY      566 GTCTGTAGGTCTCAAGAGACTAGAGAACTTGAATTCATGATTTCTCAAAATTTGGGTCT 625
      DB      299 GTTCTGTAGGTCTCAAGAGACTAGAGAACTTGAATTTCTCAAAATTTGGGTCT 358
      QY      626 TTTGACACCAAGGAGATGCTACCTTCAAGACCTTGAATGCTGTTATGTTCTTC 685

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DB      359 TATGACAAAAAGGCTCATATTAATGTTTGAACCTTTGCTTTATAGCAATGCTGTTGCT 418
QY      686 ATTGTACTATGAGTGTCTGAGGTGACATGATGTGAGGCTCATTTGGTTCAGGACATG 745
DB      419 ATGAGTGTATAGGGGTTTGTGTTGTTGAGAGGTTTGTGTTGATCTTTGTTGTTGTTG 478
QY      746 CTCTTAAGGTTGCTTTTGAATGCAAAAGTCTTAATGAGGCAATGTTGCGCACTATG 805
DB      479 TTGATGGGGTTTCTTTGATTCAGAGTGTGATGATGATGATGATGATGATGATGATG 538
QY      806 GTTATGACAAACCAATGTTTCAACAGATTGACAGATCTCTCTGGGAATGCTTGACC 865
DB      539 GTATGCTGATTAACAGCTTAATTAATGATTAATGATTAATGATTAATGATTAATGAT 598
QY      866 GGATTAAGCAATGCTTGTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 925
DB      599 GGAATTAAGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 658
QY      926 CTGACCATGACCTGATCTGACAGACATGCGGCTCTTGCAGTTTGTGCGGTTCTTC 985
DB      659 CTGATATGACCTGATTTACATATATACATCTCTGTTGTTGTTGTTGTTGTTGTTGTTG 718
QY      986 AATTCCATTAACCTCTCAATTTCTATGAGAGAGAGTTGAGTTGATTCATTTCTAGTTTC 1045
DB      719 GATTCACTCACTCTCAATTTCTATGAGAGAGAGTTGAGTTGATTCATTTCTAGTTTC 778
QY      1046 TTGATCTGCTACCGACCTTACTTTTACCGGTTATGTTGTTGTTGTTGTTGTTGTTGTT 1105
DB      779 TTGTAAGTTATCAACATTTGACATTTTACCTTAATTAATGTTGTTGTTGTTGTTGTTGTT 838
QY      1106 TATCTGACAGCAATTTCTGCTATTTGTTTTCGAGCGAAAGTGAAGTGAAGTGAAGTGAAG 1165
DB      839 TATGTACATATCTCATTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 898
QY      1166 AATAAGGGATCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1225
DB      899 CTCTGGGATGCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 958
QY      1226 TGCGCTGAGAGGTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1285
DB      959 TGGGGTGAAGAAATTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1018
QY      1286 CAGTTCTGTTGTAATCACTTTGCTGCAATGATATATGTTGTTGTTGTTGTTGTTGTTGTTG 1345
DB      1019 CAGTTCTGTTGTAATCACTTTGCTGCAATGATATATGTTGTTGTTGTTGTTGTTGTTGTTG 1078
QY      1346 TGTGTTGAGAGAGACAGACAGTGTATCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1405
DB      1079 TGTGTTGAGAGAGACAGACAGTGTATCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1138
QY      1406 TTTTTCGTTGCTGAGTTTCACTTGAAGATGATTTGTTGTTGTTGTTGTTGTTGTTGTTG 1465
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QY      1466 CAATTGAGAGATTTTGGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1525
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QY      1526 AGAGCTTGTGATTTTGGAGGCAATCAATGATGATGATGATGATGATGATGATGATGATG 1585
DB      1259 AATTATGATCTTTCTCAAGAGCAATGATGATGATGATGATGATGATGATGATGATGATG 1318
QY      1586 CTACAGTATAGGACTTAAACCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1645
DB      1319 TTGAGAGGTAGAGATTAACCAAGCCCTCCGAGAAATTTGTTGTTGTTGTTGTTGTTG 1378
QY      1646 ACCATGAGCTGA 1657
DB      1379 ACTCATGTTAA 1390

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RESULT 14
ABK49503

ID	ABK49503 standard; DNA; 1702 BP.
XX	
AC	ABK49503;
XX	
DT	15-JUL-2002 (first entry)
XX	
DE	DNA encoding Evening primrose delta6-desaturase.
XX	
KM	delta6-desaturase; sunflower; soybean; maize; tobacco;
KW	peanut; carrot; oil seed rape; gamma linolenic acid; GLA;
KM	chilling tolerance; gene; de; evening primrose.
XX	
OS	Oenothera biennis.
XX	
EH	Key
FT	Location/Qualifiers
FT	CDS
XX	48..1406
XX	/tag= a
XX	/product= "delta6-desaturase"
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PN	US6355861-B1.
XX	
PD	12-MAR-2002.
XX	
PF	19-SEP-1997; 97US-0934254.
XX	
PR	13-OCT-1992; 92US-0959952.
PR	10-OCT-1991; 91US-0774475.
PR	08-JAN-1992; 92US-0817919.
PR	14-SEP-1994; 94US-0307382.
PR	28-JAN-1997; 97US-0789936.
XX	
PA	(RHON) RHONE-POULENC AGROCHIMIE.
XX	
PI	Thomas TL;
XX	
DR	WPI; 2002-380944/41.
XX	
DR	P-PSDB; AAU79851.
XX	
PT	Novel nucleic acid encoding evening primrose delta6-desaturase which
PT	converts linolenic acid to gamma linolenic acid useful for producing
PT	gamma linolenic acid in transgenic plant or bacteria
XX	
PS	Claim 2; Column 41-46; 53pp; English.
XX	
CC	The invention describes an isolated nucleic acid encoding an evening
CC	primrose Delta6-desaturase. The nucleic acid and a vector expressing the
CC	nucleic acid are useful for producing a plant such as sunflower, soybean,
CC	maize, tobacco, peanut, carrot or oil seed rape plant, with increased
CC	gamma linolenic acid (GLA) content, and also for inducing or increasing
CC	production of GLA in a bacteria or plant deficient, lacking in or
CC	producing low levels of GLA. The nucleic acid is also useful for inducing
CC	chilling tolerance in plants. This sequence encodes the evening primrose
CC	delta6 desaturase involved in the production of gamma linolenic acid.
XX	
SO	Sequence 1702 BP; 358 A; 471 C; 446 G; 427 T; 0 other;
Query Match	28.7%; Score 555; DB 24; Length 1702;
Best Local Similarity	64.8%; Pred. No. 2.8e-99;
Matches 889; Conservative	0; Mismatches 470; Indels 12; Gaps 4
Oy	321 AGGAGAAAGATCAATCACTTAAGGATGCTCAATGCTCAATTTGGGTCAAGGACCACTTGAG 440
Db	58 AAGCTTAAAGATATATCAACGGGGGAGCACTTCGGCCGACAAAGATCCGGCGATCTCT 117
Oy	381 GGATCTCAATTCAGATTAAGGATGCTCAATGCTCAATTTGGGTCAAGGACCACTTGAG 440
Db	118 GGATCTCAATTCAGGCGCAAGGATGCTCAATGCTCTTCGGTGGCGGAGCACTTCGAG 177
Oy	441 GTGATGTTCAATTCACAACTTGCTGGCGCAGATGTCACTGATTCATTATAGCATACC 500
Db	178 GCGAAGTCCCGCTCTCAAGTGTGGCGGCGGCAAGATCAACGACCTTCATGAGTACC 237
Oy	501 ATCTCGGACAGCATGTCACACTTTGAAAATTTCTTCACTGG---CTAACCTTCAGTG 557

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Qy	558	ACTT	CA	AGG	CTC	TAG	GGT	GTG	CCA	AA	GACT	AC	GAA	AGCT	TC	GAT	CT	GAT	CT	CA	AAAT	617	
Db	238	ACTT	CGA	AGT	GTG	CGA	AGAT	CTC	CA	AGAT	CTAC	CGG	AGG	CTTT	TTGA	AC	GAT	AGT	CG	CGT	357		
Qy	618	TGG	GTCTTT	TTGA	CA	CAA	AGG	CGAT	GTCA	TTCA	TGA	CA	CCCTT	GCAT	CTG	TGCT	TTA				677		
Db	358	CCG	GAT	CTT	CGA	GA	AGAA	GGG	CCAC	CA	ATCAT	GTGA	CGTT	CGT	CGG	CGTT	GG	GTCA			417		
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Db	418	TGAT	GG	CGG	CAAT	CGT	CTTA	CGG	CGT	GG	CGT	CGA	GT	CGG	AT	CTCA	CA	GTCT			477		
Qy	738	CAG	GAT	CTCT	CTTA	AGG	TTG	CTTT	GGAT	GCA	AA	GTCTTA	TG	GGG	CCAT	GTAT	CT	GGCC			797		
Db	478	GGG	GG	CACT	CGT	GGG	CTT	GTG	GTG	AT	CCA	AG	CGG	CGAT	AT	TGG	GG	CCAT	GA	CT	CGGC	537	
Qy	798	ACT	AT	GTG	GTAT	TGA	CA	AA	CCAA	TG	TTT	CA	CA	AG	TTG	CA	CAG	AT	CCT	CT	CT	857	
Db	538	ATT	AC	AGT	AT	GTG	CA	AA	CCG	TG	AT	CA	CA	GA	AT	CA	CG	CA	AT	CT	CA	597	
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Db	598	TCTT	AA	CGG	AA	TCA	GCAT	CGG	TGT	GTG	AA	GTGA	CC	CA	CA	CG	CC	CA	CA	CT	CGCT	657	
Qy	918	GCA	AC	AGCTT	GAC	CAT	ACC	CTG	ATCT	GTG	CA	GAC	AT	CCG	GTCTT	TC	GAT	TTG	GT	GT	CGC	977	
Db	658	GCA	AC	AGCT	GTGA	CTAC	GA	CCCC	CA	CTCC	CA	GAC	AT	CCG	GTAT	TC	CG	CT	CA	CC	717		
Qy	978	GATT	CT	CAAT	TCAT	CTCA	CTT	CTCAT	TTT	CTAT	TG	GA	GA	AGT	TGA	TTT	CA	TTG			1037		
Db	718	GACT	CTT	CA	AT	CTCA	CTAC	CTG	GTCTT	CTAT	TG	GG	CG	AGT	CCT	GA	AA	TT	CG	CA	AGT	777	
Qy	1038	CTA	GGT	TT	TGAT	CTG	CTA	CCA	GAC	CTT	ACT	TTT	TAC	CGG	TAT	TGT	GT	TG	CA	AGG	1097		
Db	778	CAC	GGT	CTT	AGT	CAG	CTA	CGA	CA	CTG	GA	CC	TAC	CGG	TCAT	TGAT	CTT	CGG	CC	AG	837		
Qy	1098	TCA	AT	CTG	AT	CTG	CAG	CA	AA	TT	CTG	CA	TTT	TG	GA	GG	CA	AA	AT	GTG	CA	1157	
Db	838	TCMA	CTT	TAT	CA	TCA	GA	CC	CTTTT	TAT	TGCT	CTC	TA	CA	GA	GG	CG	CA	CT	CT	CA	CGG	897
Qy	1158	CCT	GA	CA	TAA	TGG	GGAT	CC	TGT	GTG	TTG	GA	CA	CTT	TGG	CT	CC	CTT	TAT	GTG	CT	1217	
Db	898	CTT	AA	CTT	AAT	TGG	GTAT	TCG	CG	GT	TTT	CT	GA	AG	TG	TTT	CCG	CT	CT	CGAT	CT	957	
Qy	1218	TG	CA	AA	TTG	GC	CTG	AG	GG	TTAT	GT	TG	CTG	CTA	GC	TTG	CT	GT	CT	TTT	CA	1277	
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Qy	1278	AG	CA	AT	CT	CAG	TTG	TTG	TA	TCA	CTT	TG	CG	AA	AT	TA	TG	TG	CGG	CG	CA	1337	
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DB 1318 GGATGCGGCGGCTTACGGCGGCTGACCTTAATTCGCCGCCCTTACGAACCTGGGT 1377
 QY 1629 TGTGGAGCTGTTATATACCATGCTGAGCATTGTGAGTTTAAAGTT 1679
 DB 1378 ATGGGAGCTTATACACCATGATGTTGTTGTTGTTGTTGTTGTT 1428

RESULT 15
 ABX15367
 ID ABX15367 standard; cDNA; 1702 BP.
 XX ABX15367;
 AC
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Evening primrose delta-6-desaturase #1 cDNA.
 XX
 KM Delta-6-desaturase; gene; ss; delta-12-desaturase; sunflower; soybean;
 KM maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
 KM octadecatrienoic acid; alpha-linolenic acid; delta-15-desaturase;
 KM evening primrose.
 OS Oenothera biennis.
 XX
 XX
 XX Key Location/Qualifiers
 FT CDS 48..1406
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 FT /product= "Evening primrose delta-6-desaturase #1"
 XX
 XX US2002108147-A1.
 XX
 PD 08-AUG-2002.
 XX
 PF 21-DEC-2001; 2001US-0029756.
 XX
 XX 13-OCT-1992; 92US-0959952.
 PR 19-SEP-1997; 97US-0934254.
 PR 10-OCT-1991; 91US-0774475.
 PR 08-JAN-1992; 92US-0817919.
 PR 14-SEP-1994; 94US-0307382.
 PR 28-JAN-1997; 97US-0789936.
 XX
 XX
 PA (THOM/) THOMAS T L.
 FI Thomas TL;
 XX
 DR WPI; 2003-066659/06.
 DR P-PSDB; ABG73416.
 XX
 PT Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
 PT for producing plant with increased gamma linolenic acid content, and
 PT for inducing octadecatrienoic acid production in plant
 PS
 PS Claim 2; Fig 10; 55pp; English.
 XX
 CC The invention relates to a nucleic acid encoding an evening primrose
 CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
 CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
 CC for producing a plant (such as sunflower, soybean, maize, tobacco,
 CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
 CC acid (GLA) content by transforming a plant cell with the nucleic acid or
 CC vector and regenerating a plant with increased GLA content from the plant
 CC cell, for inducing or increasing production of GLA in an organism lacking
 CC in or producing low levels of GLA and for inducing production of
 CC octadecatrienoic acid in at least one of a plant deficient or lacking
 CC in or producing low levels of octadecatrienoic acid, a bacterium which
 CC produces alpha-linolenic acid or a bacterium which exhibits a
 CC delta-15-desaturase activity on a GLA substrate. This sequence represents
 CC cDNA encoding an evening primrose delta-6-desaturase polypeptide.
 XX
 XX Sequence 1702 BP; 358 A; 471 C; 446 G; 427 T; 0 other;
 Query Match 28.7%; Score 555; DB 25; Length 1702;

Best Local Similarity 64.8%; Pred. No. 2.8e-99;
 Matches: 889; Conservative 0; Mismatches 470; Indels 12; Gaps 4;
 QY 321 AGAAGAAAGTATACATACCTCAGAGAGCTGAAGGTCAACAAGAGAGAGATTAT 380
 DB 58 AAGCTAAGAAATATATACAGCGGAGGAGCTCCGCGCAACAACATCCGGCATCT 117
 QY 381 GGATCTCAATTTAAGGTATGATGATACATGTCTCAGATGAGGTCAAGAGACACCTGGT 440
 DB 118 GATCTTCATCCAGGAGAGGTCTACGACGTCTCGGTGGCGGAGACACCCGGCG 177
 QY 441 GTGATGTTCCAAATCTCAAACTTGTGCGGAGAGATGCTACTGATGATTCATATACCAT 500
 DB 178 GCGAGGTCCGCTCTCAGTCTGGCGGCGAGAGCGTCAACGACGCTTATTCGTATCC 237
 QY 501 ATCTGGCAAGCATGTGTACACCTTGATAAAATTTCTTCACTGG---CTACACCTCATG 557
 DB 238 ACCCGGACAGCGGTGGCGGATCTGATTCGCTTACCGGCTACTACTACTCAAG 297
 QY 558 ACTTCAAGTCTCTGAGGTGCTCAAGACTACAGAAAGCTTGATCTGAGTCTCAAAAT 617
 DB 298 ACTTCAAGTCTGAGATCTCCAGAGATCTCCAGAGCTACCGGAGCTTTGAAGAGATGCGG 357
 QY 618 TGGGTCTTTTGAACCAAGAGGAGATGCACTTCAATGACACCTTGATCTGTGCTGTA 677
 DB 358 CCGGATCTTCAGAGAAAGAGGACCAACATCATGTGACGTTGCTGCGGTTGCGGTCA 417
 QY 678 TGTTCCTCATTTGACTCTATGATGATGATGATGATGATGATGATGATGATGATGAT 737
 DB 418 TGATGGCGGCAATGCTCTACGCGGTGCTGCGGTGCTGCGGTGCTGCGGTGCTGCT 477
 QY 738 CAGGCATGCTCTTAGGGTGTGCTTGTGATGCAAGTGTGATGATGATGATGATGATGAT 797
 DB 478 GCGGCGACTGCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 537
 QY 798 ACTATGTGTTATGACCAACATGTTTCAACAAGTTGACAGATCTCTTGGAACT 857
 DB 538 ATTACAGAGTATGATCCAAACCGGTGATACAAAGATCAGCAATCATAGCAGGACA 597
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 DB 718 GATTCCTCAATTCATACCTCTCATTTCTATGAGGAGAAATGAGATTGATTTCAATG 777
 QY 1038 CTAGTCTTGAATGCTGATCAGACATTTTATCCCGGTATGATGATGATGATGATGAT 1097
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 QY 1278 AGCATTCAGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1337
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Db      1078 GCGACAACTGGTTCGAGAGCAGAGAAAGGAGCATGATATACGTGCCACCGTGA 1137
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Db      1138 TGGACTGGTTCCTTGGTGGGCTGCAAGTTCAGTTGAGACACACTTGTCCCTAGGCTGC 1197
QY      1458 CTCGGTCCCAATTGAGGAAAGATTTGCGCTTTGTTAGTGACCTTTGCAAGAGCATTAAT 1517
Db      1198 CGCGTGGGCAAGCTTAGGAAAGATTCGCCCTTGGCTCGGGACTTGTATAGAAAGCAGGGA 1257
QY      1518 TGCCTTATAGAGAGCTTGTCATTTG---GAGGCCATTCAGTGAACAATTAGAACCTCA 1574
Db      1258 TGCCTATAGAGAGCTTGCGGTTTGGGACGACGCTTAATGTCAGGACAAATTCGACGCTGA 1317
QY      1575 GGAATGCTGCCCTTCAAGCTAGGAGCTTAA---CAAACCTGCCCCCTAAGAA---TTGT 1628
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QY      1629 TGTGGGAAGCTGTTAATACCCATGCTGAGGCATTTGAGAGTTT 1679
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Search completed: December 31, 2003, 16:16:45
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:48:07 ; Search time 2947.44 Seconds
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Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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27: em_gse_vrt1:*
28: gb_gse1:*
29: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	479.8	24.8	1764	11	AY103762

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8	443.4	22.9	892	14	CB291093
9	432.4	22.4	868	14	CB291094
10	395	20.3	817	14	CB893839
11	391.8	20.3	588	12	BM143768
12	389.4	20.1	571	12	BI787611
13	389.4	20.1	575	14	CA938317
14	388.2	20.1	741	13	BU028011
15	387.6	20.0	676	13	BQ402431
16	387	20.0	742	13	BU025031
17	385	19.9	673	13	BF003445
18	384.2	19.9	736	13	BU025987
19	383.6	19.8	721	14	CB972537
20	381.4	19.7	403	9	AI988466
21	381.4	19.7	722	13	BU024653
22	377	19.5	725	13	BU025380
23	373.8	19.3	737	13	BU025297
24	372.8	19.3	585	13	BU811579
25	372.6	19.3	702	13	BU025281
26	372.2	19.2	585	14	CB829088
27	361.8	18.7	717	13	BU028018
28	360.4	18.6	957	10	BF268631
29	359.2	18.6	826	14	CB972811
30	358.8	18.6	607	14	CD037696
31	355	18.4	823	28	BH687867
32	354.6	18.3	715	28	BH927841
33	352.4	18.2	692	13	BU025175
34	350.8	18.1	674	14	CB002504
35	350	18.1	744	13	BO281359
36	349.8	18.1	673	14	CB002410
37	349.8	18.1	696	14	BQ153475
38	347.6	18.0	765	13	BU024179
39	346.2	17.9	505	10	BG726179
40	345.6	17.9	471	14	CB829321
41	345.4	17.9	664	13	BU023904
42	345.4	17.9	666	13	BU024529
43	344	17.8	819	28	BH236433
44	343.2	17.7	652	14	CD005403
45	338.4	17.5	748	13	BQ976973

ALIGNMENTS

RESULT 1
LOCUS BE658198/c
DEFINITION GM700005A20G6 Gm-r1070 Glycine max cDNA clone Gm-r1070-1836 3',
mRNA sequence.
ACCESSION BE658198
VERSION BE658198.1 GI:9984146
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE 1 (bases 1 to 776)
Vodkin, J., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Corryell, V., Erpelting, J., Rapp, C., Shoop, E., Pardin, J., Liu, B., and Lewin, H. A Functional Genomics Program for Soybean (NSF 9872565)
Other ESTs: AI748200 corresponding to Gm-cl011-238 (5').
Contact: Vodkin, J.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)
Lewin, H. A., Director, Keck Center for Comparative and Functional Genomics
University of Illinois
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-6147


```

/clone lib="Gm-cl011"
/notes="Vector: Bluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; This cDNA library was constructed from mRNA isolated
from immature cotyledons (100-200mg) of greenhouse grown
plants. The cDNA library was prepared using the life
Technologies superscript cDNA library construction kit.
Complementary DNA was synthesized from mRNA using a poly
(dT) sequence with a Not I restriction site. Sal I
linkers adapters were ligated to the blunt-ended cDNA
fragments followed by NotI digestion. The cDNA fragments
were directionally cloned into the NotI-Sal I restriction
site of the pSPORT 1 vector. The ligated cDNA fragments
were transformed into E. coli Electromax DH10B host cells.
This library was constructed by Dr. Lila Vodkin and Dr.
Anu Khanna."
BASE COUNT      119 a      126 c      143 g      187 t      4 others
ORIGIN
Query Match      29.5%; Score 571.4; DB 9; Length 579;
Best Local Similarity 99.1%; Pred. No. 5.3e-45;
Matches 572; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY      826  CACCAAGGTTGCACAGATCTCTCTGGGAAGTGGTGAACCGGATTAAGATTGCTGGTG 885
DB      3    CACCAAGGTTGCACAGATCTCTCTGGGAAGTGGTGAACCGGATTAAGATTGCTGGTG 62
QY      886  GAATGGAAGTCAATGATGTCACACATGTCGTGCAACAGCCTTGACCATGACCTGATCT 945
DB      63    GAATGGAAGTCAATGATGTCACACATGTCGTGCAACAGCCTTGACCATGACCTGATCT 122
QY      946  GCAGCAGATGCCGCTCTTTCAGTTTCGTCGGGTTCTTCAATTCATACCTCTGATTT 1005
DB      123  GCAGCAGATGCCGCTCTTTCAGTTTCGTCGGGTTCTTCAATTCATACCTCTGATTT 182
QY      1006  CTATGGAGAGAGTTGAGATTGATTCATTCGTTAGGTTCTTGATCTGTACAGCACTT 1065
DB      183  CTATGGAGAGAGTTGAGATTGATTCATTCGTTAGGTTCTTGATCTGTACAGCACTT 242
QY      1066  TACTTTTACCGGTATGATGATGTCGACGGGTCACTGTATCTGACAGCACTTCTGCT 1125
DB      243  TACTTTTACCGGTATGATGATGTCGACGGGTCACTGTATCTGACAGCACTTCTGCT 302
QY      1126  ATTGTTTTCGAGCGCAAAAGTGCAGATAGAGCCTTGAAATATGAGGATCTTGTT 1185
DB      303  ATTGTTTTCGAGCGCAAAAGTGCAGATAGAGCCTTGAAATATGAGGATCTTGTT 362
QY      1186  TTGAGCTTGGTCCCTCTTTTATGTCCTGCTGCCAATTTGCTGAGAGGTTATGTT 1245
DB      363  TTGAGCTTGGTCCCTCTTTTATGTCCTGCTGCCAATTTGCTGAGAGGTTATGTT 422
QY      1246  TGTGCTTTCAGTCTGCTGTTTGTTCATCCAGCAGATTCAGTTCTGTTGAATCACTT 1305
DB      423  TGTGCTTTCAGTCTGCTGTTTGTTCATCCAGCAGATTCAGTTCTGTTGAATCACTT 482
QY      1306  TGTGCAAAATGATATGTCGGGCGCACGAGATGGAATGACTGTTTGAGAGAGCAAG 1365
DB      483  TGTGCAAAATGATATGTCGGGCGCACGAGATGGAATGACTGTTTGAGAGAGCAAG 542
QY      1366  TGTGATCATGATATCTCTTGTGCTCTTGATGAT 1402
DB      543  TGTGATCATGATATCTCTTGTGCTCTTGATGAT 579
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BE347857      592 bp      mRNA      linear      EST 04-DEC-2001
LOCUS      gp06107.y1 Gm-cl041 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION      Gm-cl041-2102 5' similar to TR:082348 082348 PUTATIVE CYTOCHROME
B5. i. mRNA sequence.
ACCESSION      BE347857
VERSION      BE347857.1 GI:9259710
KEYWORDS      EST.
SOURCE      Glycine max (soybean)

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ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabiales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 592)
REFERENCE
AUTHORS
Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Corryell,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Steptoe,M., Rheising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schuk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., Mccam
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished
TITLE
JOURNAL
COMMENT
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Trace considered overall poor quality This clone is available
through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway
Huntsville, AL 35801 For further information call: (800)-533-4363
or contact via email: ccu@resgen.com
Insert Length: 149 Std Error: 0.00
High quality sequence stop: 1.
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1..592
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/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl041-2102"
/issue_type="Senescing leaves, mature plant, greenhouse
grown"
/lab_host="DH10B"
/clone_lib="Gm-cl041"
/notes="Vector: pTR73Pac (Pharmacia); Site 1: EcoRI;
Site 2: HindIII; This library was constructed from mRNA
isolated from senescing leaf tissue of mature greenhouse
grown plants of the cultivar Williams. Complementary DNA
was synthesized from mRNA using a 3' anchored poly(dT)
primer. EcoRI adapters were ligated to the blunt-ended
cDNA fragments followed by digestion with EcoRI and
HindIII. The cDNA fragments were directionally cloned
into the EcoRI-HindIII restriction site of the pTR73-Pac
vector. The ligated cDNA fragments were transformed into
DH10B host cells. This library was constructed by Dr.
Randy Shoemaker."
BASE COUNT      132 a      124 c      139 g      197 t
ORIGIN
Query Match      25.2%; Score 487.6; DB 10; Length 592;
Best Local Similarity 89.2%; Pred. No. 3.7e-37;
Matches 526; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY      822  GTTTCACCAAGTTGACAGATCTCTCTGGGAAGTGGTGAACCGGATTAAGATTGCTT 881
DB      3    GTTTCACCAAGTTGACAGATCTCTCTGGGAAGTGGTGAACCGGATTAAGATTGCTT 62
QY      882  GGTGGAAGGAGCTACATATGCTACACATATGCGGCAACAGCCTTGACCATGAGCCCTG 941
DB      63    GGTGGAAGGAGCTACATATGCTACACATATGCGGCAACAGCCTTGACCATGAGCCCTG 122
QY      942  ATCTGACAGCATATGCGGCTCTTTCAGTTTCGTCGGGTTCTTCAATTCATTAACCTCTC 1001
DB      123  ATCTGACAGCATATGCGGCTCTTTCAGTTTCGTCGGGTTCTTCAATTCATTAACCTCTC 182
QY      1002  ATTTCTATGAGAGGAAGTTGAGTTGATTCATTCGTTAGTTCTGATCTGTACAGC 1061
DB      183  ATTTCTATGAGAGGAAGTTGAGTTGATTCATTCGTTAGTTCTGATCTGTACAGC 242
QY      1062  ACTTACTTTTACCGGTATATGTCGTCACAGGTCAACTTGATCTGCAGACAATTC 1121

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Db 243 ACTTACTTTTACCCGTATGATGAGTTCAGGGGTCACTGTATCTCAGACAAATTC 302
 QY 1122 TGTATTTGTTTGGAGCGGAAAGTGAAGATAGAGCTTGAACATTAATGGGATCTTG 1181
 Db 303 TGTATTTGTTTGGAGCGGAAAGTGAAGATAGAGCTTGAACATTAATGGGATCTTG 362
 QY 1182 TGTATTTGTTTGGAGCTTCCCTCTTTTGTGATGCTTGCCTGCAAAATGGGCTGAGAGGTTA 1241
 Db 363 AGTTTGGATCTTGTCTCTCTTTGAGTCTTTCCTGCTCAAAATGGGCTGAGAGGTTA 422
 QY 1242 TGTATTTGTTTGGAGCTTCTTGTGTTTGTTCATTCAGACATTCAGTTCTGTTTGAATC 1301
 Db 423 TGTCTGAGCTTGTAGCTAGCTAGATGCTTCATTCATTCATTCATTCATTCATTCATTC 482
 QY 1302 ACTTGTGCAATATGATATGATGAGGCGGACCGAGTGGGAATGACTGTTTGAAGAGCA 1361
 Db 483 GCTATGATGAGATGATATGATGAGGCGGACCGAGTGGGAATGACTGTTTGAAGAGCA 542
 QY 1362 CAAGTGTATCATGATATGATGAGGCGGACCGAGTGGGAATGACTGTTTGAAGAGCA 1411
 Db 543 TCAGTGTATCATGATATGATGAGGCGGACCGAGTGGGAATGACTGTTTGAAGAGCA 592
 RESULT 4
 LOCUS AY103762 1764 bp mRNA linear HTC 16-OCT-2002
 DEFINITION Zea mays P0087385 mRNA sequence.
 ACCESSION AY103762
 VERSION AY103762.1 GI:21206840
 KEYWORDS HTC.
 SOURCE Zea mays
 ORGANISM Zea mays
 BUKARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 1764)
 Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M., and Tingey, S.V.
 Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes
 Unpublished (2002)
 2 (bases 1 to 1764)
 Coe, S.H.
 Direct Submission
 Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
 Misouri, Columbia, MO 65211, USA
 If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
 location/Qualifiers
 1. 1764
 /organism="Zea mays"
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 /clone_11b="Maize Mapping Project/Dupont Consensus Library"
 /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
 BASE COUNT 310 a 602 c 456 g 396 t
 ORIGIN
 Query Match 24.8%; Score 479.8; DB 11; Length 1764;
 Best Local Similarity 60.9%; Pred. No. 9.2e-37;

Matches 816; Conservative 0; Mismatches 517; Indels 6; Gaps 2;
 QY 335 ATAACTCAGAGAGGTGAAGGTCACAAAGAGAGAGATTTATGATCTCAATTCAA 394
 Db 155 ATCTCTCCAGAGAGGTCCTCCGCTTCCAGCTTCCGCGAGAGACTCTGATCTTCATCTCC 214
 QY 395 GGTAAAGTGTACATGTCATGATTTGGGTCAAGAGACACCTGGTGTGATGTTCCAAATC 454
 Db 215 GCGAGCTGTAGAGAGTCAGCGCTTGTCTCCCAACACCGCGGCGGACCTCCGCTT 274
 QY 455 TCAAACTCTGCTGCGAGAGATGCTAGTATGATATGATATGATATGATATGATATGAT 514
 Db 275 CTCACCTCTGCGGAGAGAGACCGACCGCTTGCCTGACCGACCGCTTGCCTGAG 334
 QY 515 TGTGACACCTTGAATAATTTCTTCACTGCTACCACTGATGATGATGATGATGATGAT 574
 Db 335 CGCCGCTCTCCGCGCTTCT 391
 QY 575 GTGTCCAAAGACTACAGAAAGCTTGATCTGATGATGATGATGATGATGATGATGATGAT 634
 Db 392 GCTTCCGCGAGTACCGCGCTCTCTGCGAGTATCTCTGCGGCGCTCTCTGAGAG 451
 QY 635 AAGGCGATGTACCTTCATGACACCTTGCATCTGTTGCTGTATGTTCTCATTTGATCTC 694
 Db 452 GTGCGCCCAACCCCAAGGTCCAGCTCTGCTGATGCGCTCTCTCTCTCTCTCTCTCTCT 511
 QY 695 TATGATGTTCTAGAGGTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 754
 Db 512 TACCTGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 571
 QY 755 TTGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 814
 Db 572 TTGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 631
 QY 815 ACCAATGTTTCAACAAGTTTGAACAGATCTCTCTGGAATCTCTTGAACCGGATTAAG 874
 Db 632 CATCCGCTCTGACCGCTCTGACCGCTCTGACCGCTCTGACCGCTCTGACCGCTCTGAC 691
 QY 875 ATGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 934
 Db 692 ATGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 751
 QY 935 GACCTGATCTGACGACATGCGGCTTGTGAGTTTGTGCGGCTTCTTCAATTCATTA 994
 Db 752 GACCTGATCTGACGACATGCGGCTTGTGAGTTTGTGCGGCTTCTTCAATTCATTA 811
 QY 995 ACCTGCTATTTTATGAGAGAGAGTTGATGATGATGATGATGATGATGATGATGATGAT 1054
 Db 812 TGTGCTTACTTCTAACCAAGGACCTGCGGCTTGAAGCGGCTTGAAGCGGCTTGAAGCG 871
 QY 1055 TACGACACTTAACTTTTAAACCGGTAATGATGATGATGATGATGATGATGATGATGAT 1114
 Db 872 TACGACACTTAACTTTTAAACCGGTAATGATGATGATGATGATGATGATGATGATGAT 931
 QY 1115 ACAATCTGCTATGTTTTCAGAGCGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1174
 Db 932 TCGCGCTCTGCTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 991
 QY 1175 ATCTTGTGTTTGAAGTGTGCTTCTCTTGTAGTGTGCTTGTGCTTGTGCTTGTGCTTGT 1234
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 QY 1235 AGGCTATGTTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1294
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 Db 1112 CTGAACCACTTCTGCTGCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1171
 QY 1355 AAGCAGACAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1414
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QY 1415 GGCTTCAGTTGAGCTTGAGCATCTTTGTTCCAGGCTACCTGGTCCCAATTGAG 1474
 DB 1232 GGCTTCAGTTGAGCTTGAGCATCTTTGTTCCAGGCTACCTGGTCCCAATTGAG 1291
 QY 1475 AAGATTTGCGCTTTGGTTAGTGAACCTTTGCAAGAGCATTAATTTGCTTAATGAGGCTTG 1534
 DB 1292 AAGGTTGACACCGGCGCGCTTGGACAGAGCATGAGGCTCACTTAATTTGACAGCC 1351
 QY 1535 TCATTTTGGAGGCGCATCTGAGCAATTAAGACCTTCAGAGCTGCTGCCCTACAGCT 1594
 DB 1352 ACATTTGCGGCTTCAATGCTTCAATGAGAGCACTTCAGGCTGCTGATTCAGAGGCC 1411
 QY 1595 AGGAGCTTAACA---ACCTGCGCCCTAAGAAATTTGTTGGAGAGCTTTAATACCAT 1651
 DB 1412 AGGAGCCCTTCAAGTGTGTGCTCCGAAAGATTTGATGGAGGCTGTGAAACCCAT 1471
 QY 1652 GGCTGAGGCAATTTGAGCTT 1670
 DB 1472 GGATTAATGGATGAAGAT 1490

RESULT 5
 BI311411 772 bp mRNA linear EST 20-JUN-2001
 LOCUS EST5131161 GESD Medicago truncatula cDNA clone pGESD10F10 5' end,
 DEFINITION mRNA sequence.

ACCESSION BI311411
 VERSION BI311411.1 GI:14985738
 KEYWORDS EST.
 SOURCE Medicago truncatula (barrel medic)
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eustosids I; fabales; Fabaceae; Papilionoideae; Trifoliales;
 Medicago.

REFERENCE 1 (bases 1 to 772)
 AUTHORS Grusak M.A., Samac D.A., Town C.D., Van Aken S., Utterback T., Cho
 J. and Fraser C.M.
 ESTs from developing reproductive tissues of Medicago truncatula
 Unpublished
 CONTACT: Michael A. Grusak
 USDA/ARS Children's Nutrition Research Center
 Baylor College of Medicine
 1100 Bates Street, Houston, TX 77030-2600, USA
 Tel: 713-798-7074
 Fax: 713-798-7078
 Email: mgrusak@bcm.tmc.edu
 B398266

TITLE JOURNAL
 COMMENT TIGR sequence name: MTPAT29TK
 More information is available at: www.medicago.org
 Seq primer: Skmod (CTA gaa cta gtc gat cc).
 Location/Qualifiers

FEATURES
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 1..772
 /organism="Medicago truncatula"
 /mol_type="mRNA"
 /culti_var="A17"
 /db_xref="taxon:3880"
 /clone="pGESD10F10"
 /issue_type="Immature seeds"
 /dev_stage="Immature seeds, 11 to 19 days after
 pollination"
 /clone_id="GESD"
 /note="Vector: Bluescript SK-; Site 1: EcoRI, Site 2:
 XhoI; Immature seeds, collected from pods ranging in age
 from 11 to 19 days after pollination, were harvested from
 greenhouse-grown plants. Seeds were removed and
 separated from pod walls and were immediately frozen in
 liquid nitrogen. Seeds throughout the age range were
 pooled for mRNA extraction. cDNA was prepared from polyA+
 enriched RNA. The cDNA was directionally ligated into
 the Unizap XR vector from Stratagene and packaged using
 Gigapack III Gold packaging extracts. Plasmids containing

cDNA inserts were excised from the recombinant lambda-Zap
 phage using Ex-assisit helper phage and propagated in
 XOLR cells.

BASE COUNT 172 a 158 c 161 g 281 t
 ORIGIN

Query Match 24.7%; Score 478.4; DB 12; Length 772;
 Best Local Similarity 77.8%; Pred. No. 2,2e-36;
 Matches 591; Conservative 0; Mismatches 166; Indels 3; Gaps 1;

QY 902 GCTACCAATTCGCTGCAACAGCTTGAACCATGACCTGATGCAAGCAGCCGCTC 961
 DB 6 GCTCATCATATGCTTGCATATAGTCTGATTAATGATCTGATTTGAGAGATATCCCTGTT 65
 QY 962 TTTCAGATTTCGTCGGGCTTTTCAATTCATACCTTCATTTTATGAGAGAGCTTG 1021
 DB 66 TTTCGCTGCTCAATGCGGATTCCTTGGTGAATTAATCTTAATTCATATGATACAGTTA 125
 QY 1022 GAGTTGATTTTCATTCCTGATCTGATCTGCTACAGACATTTACTTTTACCGGTA 1081
 DB 126 AAGTTGATGCTTTGTCAGAGTTTCTTATCAGTTACAGATATCACTTTTACCTGTC 185
 QY 1082 ATGTGTGTCAGAGGCTCAATTTGATTCGACAGACATTCGCTATTTGCTG---AGG 1138
 DB 186 TTGTGTTTGAAGAGGCTTAATCTTCACTTCAAAATTTTGTGCTTGTTCGCAATCA 245
 QY 1139 CGAAAGTCAGAGTATGAGCTTGAACATTAATGAGGATCTTGTGTTTGGATTTGCTT 1198
 DB 246 CGAAATGCTCGATGAGCTTTTACAAATCAGATGAGTATGAGTGTGTCGACATTTGCTT 305
 QY 1199 CCTCTTTATGTCCTTGCCTGCAAAATGAGGCTTGAAGGCTTATTTGTTGCTTGTAGC 1258
 DB 306 CCTCTCTATGTCACACCTTCCCAATTTGAGGAGGAGCTATGTTGTTCTTCTTGT 365
 QY 1259 TTGCTGTTTTCATTCAGACATTCAGTCTGTTTGAATCATCTTGTGCAAAATGTA 1318
 DB 366 TTGTTGTTTTCATTCAGACATTCAGTCTGTTTGAATCATCTTGTGCAAAATGTA 425
 QY 1319 TATGTCGGGCGACCGAGTGGATGATCTGTTTGAAGAGCAAGTGTATATTTGAT 1378
 DB 426 TATCTGCTGTCACCGAGCGGAATGATGTTTCAAAACMAACACATGAGATTTGAT 485
 QY 1379 ATCTTTGAGCCCTTCAGATGATGATTTGTTTGGTGGCTGCTGAGTTTACGTTAGCAT 1438
 DB 486 ATCACTTTGTCAGATGATGATTTGTTTGGTGGCTGCTGAGTTTACGTTAGCAT 545
 QY 1439 CATTTGTTTCAAGGCTTACCTGCTGCAATTTGAGAGAGATTTGCTTGTAGTGAC 1498
 DB 546 CATTTGTTTCAAGGCTTACCTGCTGCAATTTGAGAGAGATTTGCTTGTAGTGAT 605
 QY 1499 CTTTGCAGAGATTAATTTGCTTATGAGAGCTTGTCAATTTTGGAGGCCAATCACTG 1558
 DB 606 CTATGCAAGAGATTAATTTGCTTATGAGAGCTTGTCAATTTTGGAGGCCAATCTTTG 665
 QY 1559 ACAATTAGGACCTTCAGAGCTGCTGCTTCAACAGTTAGGAGACTTAACAACCTGCGCT 1618
 DB 666 ACTCTCAAGACTTTTGAAGCTGCTGCTTCAATGAGAGAGATTTTCAACACTGCTTCA 725
 QY 1619 AAGAAATTTGTTGGAGAGCTGTTAATACCATGCTGAG 1658
 DB 726 CAGAACTTGTGTGGAGAGCTTTTATATCTCAATGCTGAG 765

RESULT 6
 BG647198 783 bp mRNA linear EST 24-APR-2001
 LOCUS EST508817 HOGA Medicago truncatula cDNA clone pHOGA-15P24 5' end,
 DEFINITION mRNA sequence.
 ACCESSION BG647198
 VERSION BG647198.1 GI:13782310
 KEYWORDS EST.
 SOURCE Medicago truncatula (barrel medic)
 ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosoids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

1 (bases 1 to 783)

Hahn, M.G., Ojansen-Reubs, T., Samac, D., Town, C.D., Van Aken, S., Utebach, T., Cho, J., and Fraser, C.M.
ESTs from roots of Medicago truncatula treated with oligogalacturonides of DP 6-20

Unpublished
Contact: Michael G. Hahn
Complex Carbohydrate Research Center
University of Georgia
220 Riverbend Road, Athens, GA 30602-4712, USA
Tel: 706-542-4457
Fax: 706-542-4412
Email: hahn@ccrc.uga.edu
G30804e TIGR sequence name: MTMBV96TK More information is available at: www.medicago.org
Seq primer: Skmod (CTA gaa cta gtc gat cc).
Location/Qualifiers

FEATURES
Source
1..783
/organism="Medicago truncatula"
/mol_type="mRNA"
/cultiivar="A17"
/db_xref="taxon:3880"
/clone="phOGA-15P24"
/tissue_type="3 day old seedling roots"
/dev_stage="24 hours after treatment in the dark at 26 C with 0.5 mg/ml oligogalacturonides (DP 6-20) in the presence of 100 ug/ml Gentamicin"
/lab_host="XLOLR"
/clone_11b="HOGA"
/note="Vector: pBluescript SK-. Site 1: EcoRI, Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOLR cells."

BASE COUNT 173 a 142 c 169 g 299 t

ORIGIN

Query Match 24.4%; Score 471.2; DB 10; Length 783;
Best Local Similarity 76.8%; Pred. No. 1e-35;
Matches 602; Conservative 0; Mismatches 178; Indels 4; Gaps 2;

QY 696 ATGGTCTTCTGAGGTGCACTAGTGTGGCTCATTTGGGTTGAGGATCTTTAGGAT 755
DB 1 ATGGTGTGTGTGTGACAAAGTGTGGCTCATTTAGGTTCTGATGTTGTGGTT 60
QY 756 TGGCTTGGATGCAAGTCTTATGTGGCCATGATTTGGCCACTATGTGTTATGACA 815
DB 61 TGGTATGAGTGAAGAACTTATATGTGTCATGATTTGTCATTTATGAGGTTATGCGA 120
QY 816 CCAATGTTTCAACAAGTTCACAGATCTCTCTGGAGCTGTTTACCGGATATGCA 875
DB 121 GTGGAAGTATTAACAATTTAGCAACAATTTTGTGTATTTGATACGTGATTAAGA 180
QY 876 TTGCTTGGTGAAGTGAAGTCAACATCTCACACATTTGGGTGCAACAGCTTGACCAT 935
DB 181 TTGCTTGGTGAAGTGAAGTCAACATCTCATATATTTGCTTGAATAGCTTGATTA 240
QY 936 ACCCTGATCTGACAGACATCCGGTCTTTTSCAGATTTGTCGGGTTCTTCAATTCATA 995
DB 241 ATCTGATTTGACAGATATCCCTGTTTTCGTCGTCTCATCGCATTTCTTGTGATTA 300
QY 996 CCTCTCATTTCTATGGAGAGAGTGAAGTTGATTTTCAATGCTAGTCTTATCTGCT 1055
DB 301 AATCTTATTTCTATGATGACAGTAAAGTTGATGCTTTGTCAAGGTTTCTTATACGTT 360
QY 1056 ACAGACCTTACTTTTACCCGGTATGTTGTGTCAGAGGTCATTTGATCTGACGA 1115
||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

DB 361 ACCAGATATACACTTTTACCTCTGTTGTTTTCGAAGGCTTAACCTTACCTTCAAA 420
QY 1116 CAATTCCTCATTTGTTTGG---AGCGAAAGTGAGATGAGCTTGAACATATATG 1172
DB 421 CATTTTGTCTGTTTGGTTCATCAGCAAGATGTTCTTATAGCTTTCACATCATGG 480
QY 1173 GGATCCCTGTTGTTTGGACTGGTTCCTCTTTTATGTTCTTGGCCCAATTTGGCTG 1232
DB 481 GTATCGGTGTTCTGAGCTGTTGTTCTCTGTTATGTCAGGCTCCCAAGTTGGCCAG 540
QY 1233 AGAGGTTATGTTTGTCTTGTAGCTTGTCTGTTTGTTCATCAGACATTCAGTTCT 1292
DB 541 AAAGGCTCATGTTTGTCTTGTCTTGTGTTTGTGTTTGTTCATCACAATCTTCAATTC 600
QY 1293 GTTGAATCATCTTGTGCAAAATGTTATGTGGGCGACCGAGTGGGAATGATGCTGTTG 1352
DB 601 GTTGAACCATTTGCTGTGCAAAAGTGTATCTGCTCACCGAGCGGAATGATGTTCT 660
QY 1353 AGAAGCAGACAAGTGTATGATGATATCTTGTGCTCTTGTGATGATGATGTTTTCG 1412
DB 661 AGAACAACACGCTGGAACATTTGATATCATCTGTTTCAACATGATGATGATGTTCTTG 720
QY 1413 GTGGCTTGACGTTTACGTTTACATCATTTGTTTCCAAAGGCTTACCTCGTCCAAATGA 1472
DB 721 GTGGTTGACAGTTTACGTTTGAACATCATTTGTTTCCAA-GCTTCTAGGGCTCAATGA 779
QY 1473 GGAA 1476
DB 780 GGAA 783

RESULT 7
CA935212 449 bp mRNA linear EST 30-DEC-2002
LOCUS saus0d04.y1 Gm-c1071 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1071-4376 5' similar to TR:082348 O82348 PUTATIVE CYTOCHROME B5. /, mRNA sequence.
CA935212
ACCESSION CA935212.1 GI:27423692
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
1 (bases 1 to 449)
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available through: Reggen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@reggen.com web site: www.reggen.com
Seq primer: -40RP from Gibco.
Location/Qualifiers
1..449
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1071-4376"

/tissue type="immature pods (~2cm long) of greenhouse
 grown plants"
 /lab host="DH10b"
 /clone_lib="Gm-cl071"
 /note="Vector: pSPOT1; Site_1: NotI; Site_2: SalI; The
 cDNA library was constructed from mRNA isolated from
 immature pods (approximately 2cm long) of greenhouse grown
 plants. The library was prepared using the Life
 Technologies Superscript cDNA library construction kit.
 Complementary DNA was synthesized from mRNA using a
 poly(dT) sequence with a NotI restriction site. SalI
 linkers adapters were ligated to the blunt-ended cDNA
 fragments followed by NotI digestion. The cDNA fragments
 were directionally cloned into the NotI-SalI restriction
 site of the pSPOT1 vector. The ligated cDNA fragments
 were transformed into E.coli Electromax DH10b host cells.
 This library was constructed in the laboratory of Dr. Lila
 Vodkin by Anu Khanna at the University of Illinois at
 Urbana-Champaign. email: l-vodkin@uiuc.edu"

BASE COUNT	86 a	86 c	115 g	162 f
ORIGIN				

Query Match	23.2%	Score 449;	DB 14;	Length 449;
Best Local Similarity	100.0%	Pred. No. 1.9e-33;		
Matches 449;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1015	GAACITGGAGTTTATATTCATTTGGCTAGGTTCTTGAATCTGTAACGAGACTTAACTTTTA	1074
Db	1	GAACITGGAGTTTATATTCATTTGGCTAGGTTCTTGAATCTGTAACGAGACTTAACTTTTA	60
QY	1075	CCCCGTAATGTGTGTGGCCAGGGTCACTTGTAATCTGACAGACAATTTGCTAATGTGTTTC	1133
Db	61	CCCCGTAATGTGTGTGGCCAGGGTCACTTGTAATCTGACAGACAATTTGCTAATGTGTTTC	120
QY	1135	GAGCGCAAAATGCGAGGATAGAGCCCTTAACAATAATGGGGATCCCTGTGTTTGGACCTGC	1193
Db	121	GAGCGCAAAATGCGAGGATAGAGCCCTTAACAATAATGGGGATCCCTGTGTTTGGACCTGC	180
QY	1195	GTTCCCTCTTAAATGTGTCTTGCCTGCAAAATGGCTGAGAGGGTTAATGTTTGTGCTTGC	1254
Db	181	GTTCCCTCTTAAATGTGTCTTGCCTGCAAAATGGCTGAGAGGGTTAATGTTTGTGCTTGC	240
QY	1255	TAGCTTTGCTGTTTGTTCATTCACGACAATTCAGTTCGTGTTGAATCACTTGTCTGCAAA	1314
Db	241	TAGCTTTGCTGTTTGTTCATTCACGACAATTCAGTTCGTGTTGAATCACTTGTCTGCAAA	300
QY	1315	TGTATATGTGGGGCCACCGAGTGGGAATGACTGTTTGAAGAAGCAGACAAGTGTACATT	1374
Db	301	TGTATATGTGGGGCCACCGAGTGGGAATGACTGTTTGAAGAAGCAGACAAGTGTACATT	360
QY	1375	GGATATCTCTTGTCCTCTTCATGATGATGTGTTTTCGATGGCTTGCAGTTTCACTTGA	1434
Db	361	GGATATCTCTTGTCCTCTTCATGATGATGTGTTTTCGATGGCTTGCAGTTTCACTTGA	420
QY	1435	GCATCATTTGTTTCCAAAGCTACCTCGGT	1463
Db	421	GCATCATTTGTTTCCAAAGCTACCTCGGT	449

LOCUS	DEFINITION	ACCESION	VERSION	KEYWORDS	SOURCE	ORGANISM
CB21093/c						
CB291093	892 bp mRNA					
U98CS01.02bd10.b1	Washington Naval orange cold acclimated flavedo & albedo cDNA library Citrus sinensis cDNA clone U98CS01_02bd10, mRNA sequence.	CB291093				
CB291093.1	GI:28616550					
	EST.					
	Citrus sinensis					
	Citrus sinensis					
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid II; Sapindales; Rutaceae; Citrus.					

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 892)	Close,T.J., Collura,K., Fenton,R.D., Feuebachner,O., Kim,H.R., Koldra,D., Wanamaker,S., Wing,R. and Yu,Y.	Development of EST Resources and New Genetic Markers for California Citrus	Unpublished	Contact: Timothy Close Department of Botany & Plant Sciences, University of California Riverside, CA, 92521-0124 Tel.: 9097873318 Fax: 9097874437 Email: timothy.close@ucr.edu Seq primer: T7.
		Location/Qualifiers		
		1. .892		

BASE COUNT	306 a	194 c	167 g	225 t
ORIGIN				

Query Match	22.9%	Score 443.4;	DB 14;	Length 892;
Best Local Similarity	79.4%;	Pred. No. 3.8e-33;		
Matches 525; Conservative	0;	Mismatches 136;	Indels 0;	Gaps 0;

Qy	AGGAAGTGGAGTTGATTCATTCGTAGGCTTGACCTGACAGCACTTACTACTT	1072
Qy	1013	
Db	AGAAATTTAGATTTCGATTCCTGCTGCTAGATTCCTTGAGATTACAGACATTTGACATTT	832
Db	891	
Qy	TACCCGGTATGTGTGTGTCAGGGTCAACTGTATCTGCAGACAATTCCTGATGTTT	1133
Qy	1073	
Db	831	
Db	TACCCCTGTATGTGTGTGTCAGAGTAAATTTATATTACAGACACTTTGTATATGTTT	772
Qy	TCGAGGGCAAAAGTCAGATAGAGCCTTGACATTAATGGGATCCTGTGTTTGGACT	1192
Qy	1133	
Db	771	
Db	TCAAAGGTAAAGGTCCAGATAGAGCCTTGACATCAATGGGTACTCTGTCTTTTGGACT	712
Qy	TGCTTCCTCTTTTAGTGTGTGCTGCTGCACAAATTGGCCTGAGAGGTTATGTTGTGCTT	1252
Qy	1193	

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Db      711 TGGTCCCACTTCAAGTTTATCTACCAAGCGCTTAAAGGGTGATGTTTGATG 652
Qy      1253 GCTAGCTTCTGTTTCTTTCATCCAGCAATTCAGTTCTGTTGAATCCTTTGCGCA 1312
Db      651 GCAAGTTTCTGTCACGGCCATCCACATTCAGTTTGTAAACCACTTGTGCGCA 592
Qy      1313 AATGATATCTGGGGCCAGGAGTGAGTACGTTGTAAGAGCAGCAAGAGTGACA 1372
Db      591 AAGCTGATTTTGGTCCGCTTAAAGGAAATGACTGGTTTAGAAGCAAGAGTGAGCA 532
Qy      1373 TTGGATATCTCTTGTGCTCTTCAGTGAATGTTTTCGAGGCTTGCAGTTTACGCTT 1432
Db      531 TTGGATATCTCTGCTCATCTTGGATGATTTGGTTTCAATGATGGGTTGAGTTTACGCTA 472
Qy      1433 GAGCATCATTTGTTTCCAGGCTACCTCGGTGCCAATTGAGAAAGATTGGCTTTGGTT 1492
Db      471 GAGCATCATTTGTTTCCAGGCTTCCAGGTTGCCAAGTTGAGAAAGATTGGCTTTGGTTG 412
Qy      1493 AGTGACCTTGGCAAGACATTAATTTGCTTATAGAGCTTGTATTTTGGAGGGCCAT 1552
Db      411 AGGATTTTGGCAAGACATTAATTTGCTTATAGAGCTTGTATTTTGGAGGGCCAT 352
Qy      1553 CAGTGCACATTTAGACCTCTCAGGACTGCTGCCCTTACAGCTAGGAGCTTAAACCCCT 1612
Db      351 GTGTGACCATTTAGACCTCTGAGGGGTGCTGCTCTGCAAGCTCGGAGCTCAACAACTT 232
Qy      1613 GCCCTTAAGAAATTTGTTGGGAAAGCTGTTAATACCATGCTGAGGCAATTTGGAGTTT 1672
Db      291 GTCCCCAAGAAATTTGCTTGGGAAAGCTTAAATCATGCTGAGTGTGTTTCTTT 232
Qy      1673 T 1673
Db      231 T 231

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RESULT 9
LOCUS   CB291094/1 868 bp mRNA linear EST 28-FEB-2003
DEFINITION
UCRCS01_02bd10.g1 Washington Navel orange cold acclimated Flavedo &
albedo cDNA library Citrus sinensis cDNA clone UCRCS01_02bd10, mRNA
sequence.
ACCESSION
CB291094
VERSION
CB291094.1 GI:28616551
KEYWORDS
EST.
SOURCE
Citrus sinensis
ORGANISM
Citrus sinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eustosida II; Sapindales; Rutaceae; Citrus.
1 (bases 1 to 868)
Close,T.J., Collura,K., Fenton,R.D., Feuerbacher,O., Kim,H.R.,
Kudrna,D., Wamamaker,S., Wing,R. and Yu,Y.
Development of EST Resources and New Genetic Markers for California
Citrus
JOURNAL
Unpublished
COMMENT
Contact: Timothy Close
Department of Botany & Plant Sciences, University of California
Riverside, CA, 92521-0124
Tel: 9097873318
Fax: 9097874437
Email: timothy.close@ucr.edu
Seq primer: T3.
Location/Qualifiers
source
1..868
/organism="Citrus sinensis"
/mol_type="mRNA"
/cultivar="Washington Navel"
/db_xref="taxon:2711"
/clone="UCRCS01_02bd10"
/tissue_type="Rind containing flavedo and albedo"
/dev_stage="Mature fruit"
/lab_host="B. coli TUC121"

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/clone lib="Washington Navel orange cold acclimated
flavedo & albedo cDNA library"
/notes="Vector: lambda Uni-ZAP XR, excised phagemid;
Site_1: EcorI; Site_2: XhoI; Plants were grown in the
field at University of California, Riverside Agricultural
Operations since 1983. The action was Washington Navel
orange and the rootstock Carizzo Citrange. Tissue from
mature fruit was harvested at mid-day in January 2002
during a cold spell, when pre-dawn temperatures were
approximately -2 to 2 degree C. Approximately 2 cm median
sections of the rind were excised in the field from
several fruits, then wrapped in aluminum foil and frozen
quickly in dry ice. Total RNA was extracted using a phenol
extraction procedure described in J. Japanese Soc. Hort.
Sci. (1996) 64:809-814. Poly(A) RNA was purified. A cDNA
library was made, and 1 million primary lambda cDNA clones
were in vivo excised to give a population of plasmidic
SK(-) phagemids. All steps to this point were performed in
the TJ Close lab at the University of California,
Riverside (Fenton). Phagemids were plated, plasmid DNA
purified, cDNA clones archived, and DNA sequences
determined bi-directionally using an ABI350 at the
Arizona Genomics Institute, University of Arizona (Collura
, Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files
were transmitted to UC Riverside (by Yu), then processed
at UC Riverside (by Wamamaker) using the Harvest pipeline
(http://harvest.ucr.edu) to remove vector and cloning
oligo sequences and various contaminants, and to trim to a
high quality region. Sequences that retained a pruned 17
region of at least 100 bases were deposited to GenBank."
BASE COUNT
296 a 190 c 161 g 221 t
ORIGIN

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Query Match 22.4%; Score 432.4; DB 14; Length 868;
Best Local Similarity 80.1%; Pred. No. 4.2e-32;
Matches 508; Conservative 0; Mismatches 126; Indels 0; Gaps 0;
Qy 1040 AGGTTTATCGTCACAGCACTTACTTTTACCGGTATGTTGTCAGAGGTC 1099
Db 868 AGATTCTCTGTGATTAACAGCAATTTGACATTTTACCTGTTATGTTGTCAGAGTA 809
Qy 1100 AACTTGTATCTGCAGCAATTCCTGCTATTTGTTTCAGGCGAAGAGTGCAGATAGAGCC 1159
Db 808 AATTATATTTACAGACACTTTTGTATTGTTTAAACGTAAGGTCCAGATAGAGCC 749
Qy 1160 TTGAACATATAGGGGATCCTTGTGTTTGAATGCTTCCCTTTTATGTTGCTTGC 1219
Db 748 TTGAACATATAGGGGATCCTTGTGTTTGAATGCTTCCCTTTTATGTTTATCTTA 689
Qy 1220 CCAATTTGCGCGAGAGGGTATGTTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 1279
Db 688 CCAATTTGCGCGAGAGGGTATGTTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 629
Qy 1280 CACATTCAGTTCTGTTGATCACTTGTGCAATATGATGTCGGGCGACCGAGTGGG 1339
Db 628 CACATTCAGTTCTGTTGATCACTTGTGCAATATGATGTCGGGCGACCGAGTGGG 569
Qy 1340 AATGACTGTTGAGAGCAGACAGTGTATCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 1399
Db 568 AATGACTGTTGAGAGCAGACAGTGTATCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 509
Qy 1400 GATTGTTTTTGGGTTGCTGAGTTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 1459
Db 508 GATTGTTTTTGGGTTGCTGAGTTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 449
Qy 1460 CGGTGCAATTTGAGAGATTTGCTTGTGTTAGTACCTTTGCAAGAGCATTAATTTG 1519
Db 448 AGGTGCAATTTGAGAGATTTGCTTGTGTTAGTACCTTTGCAAGAGCATTAATTTG 389
Qy 1520 CTTTATAGAGCTTGTATTTTGGAGGCGCAATCACTGAGCAATTTAGAACCTCAGAGCT 1579
Db 388 CTTTATAGAGCTTGTATTTTGGAGGCGCAATCACTGAGCAATTTAGAACCTCAGAGCT 329

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QY	1580	GCTGCGCCACGAGCTAGGAGCACTTAACCAACCTGCCCTAAGAAATTTGTGGGAACT	163
Db	328	GCTGCTCTGCAGACTCGGAGACTTACAAACCTGTGCCCAAGAAATTTCTTTGGAACT	269
QY	1640	GTTAATACCATGCGCTGAGGCAATTTGGAGTTT	1673
Db	268	CTTAACTACATGGCTGAGTTGTGTTTCTTTT	235
RESULT 10			
CB893839			
LOCUS			
DEFINITION	EST646631 HOGA Medicago truncatula cDNA clone HOGA-29M7, mRNA		
ACCESSION	CB893839		
VERSION	CB893839.1		
KEYWORDS	EST.		
SOURCE	Medicago truncatula (barrel medic)		
ORGANISM	Medicago truncatula		
REFERENCE	Eukaryote, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eucoside 1; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.		
AUTHORS	1 (bases 1 to 817)		
TITLE	Hahn, M.G., Ojane-Reuhs, T., Samac, D., Town, C.D., Van Aken, S., Uetreck, T., Cho, J. and Frazer, C.M.		
JOURNAL	ESTs from roots of Medicago truncatula treated with oligogalacturonides of DP 6-20		
COMMENT	Unpublished Contact: Michael G. Hahn Complex Carbohydrate Research Center University of Georgia 220 Riverbend Road, Athens, GA 30602-4712, USA Tel: 706-542-4457 Fax: 706-542-4412 Email: hahn@ccrc.uga.edu TIGR sequence name: MTRMDK76TK More information is available at: www.medicago.org Seq primer: SKmod (CTA GAA CTA GCG GAT CC).		
FEATURES			
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	1..817		
	/organism="Medicago truncatula"		
	/mol_type="RNA"		
	/cultivar="A17"		
	/db_xref="taxon:3880"		
	/clone="HOGA-29M7"		
	/tissue_type="3 day old seedling roots"		
	/dev_stage="24 hours after treatment in the dark at 26 C with 0.5 mg/ml oligogalacturonides (DP 6-20) in the presence of 100 ug/ml Gentamicin"		
	/lab_host="X10LR"		
	/clone_lib="HOGA"		
	/note="Vector: phuescript SK-; Site 1: EcoRI; Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stragene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOUR cells."		
BASE COUNT	217 a 110 c 183 g 307 t		
ORIGIN			
	20.4%; Score 395; DB 14; Length 817;		
	Best Local Similarity 72.9%; Pred. No. 1.4e-28;		
	Matches 520; Conservative 0; Mismatches 191; Indels 2; Gaps 1;		
QY	244	TATTGTACTCTCATGTGCTGATTCAGTGATTTGTGTGTTGGTTAACACAGC	303
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QY	304	AATGAGGTTTGTAGAGAGAAAGAAATACATTAACCTCAAGAGCTGAAGGTCACAA	363
Db	165	TATTACCATGAGGTGTGAAGAAGAAATACATTAACCTTGAAGAACTGAAGAAAACATGA	224

QY	364	CAAGGAGGAGGATTTATGAGATCTCAATTCAGAGGATGACATGCTCAGATTGGGT	423
Db	225	CAAGAAGGGGATTTATGATCTCAATTCACGGGTAAGGTTTCAATGTTTCAGATTGGGC	284
QY	424	CAAGGACACCCCTGGTGGTGAATGTTCCAAATCTCAACCTTGCTGGCCAGATGTCACTGA	483
Db	285	TAAAAAACATCTGGTGGAGAGGTTGTTTGTGTAATCTTGCTGTCAGATGTAACTGA	344
QY	484	TGCATTTATAGCATACCATCTCTGGCACAGCATGGTCAACCTTGAAAAATTTCTTCACTGG	543
Db	345	TGCAATTCATAGCAATATATCCTGGTTACAGATGAAACATCTTACACAGTTTTCACATGG	404
QY	544	CTACACCCCTAGTACTTCAGAGGCTCTGAGAGTCTCCAAAGACTACAGAAAGCTTCATGC	603
Db	405	CTATTACTCTGAGATTTTAAAGTATCTGAAGTTCTTAAAGATTTAAGAGACTTTGTTTC	464
QY	604	TGAGTTCTCAAAATTTGGGTCCTTTTGAACACCAAGGCGATGTCATCTTATGACCCCTTGC	663
Db	465	TGAGTTGTGCAAAATGGGTTTGTGTTGAAGAAAGAACATGTTCTTTATTCACATTAAC	524
QY	664	ATCTGTTGCTGTATATGTTCTCATTTGACTTAAAGTGTCTGAGGTGCATTAAGTGTGTG	723
Db	525	ATCTGTGCTATTAATGCTTGTCTATTTGTTTGAAGGTGTGTGTGTGTGTTAACAAGTGTGG	584
QY	724	GGCTCATTTGGGTTTACAGGACATGCTCTTACGGGTTCTTTGATGCAAGATGCTTAATGTGG	783
Db	585	GGCTCATTTAGGTTCTGTGATATGTTGTGGGTTTGTCTATGATGCAAGATCTTATATTGG	644
QY	784	CCATGATTTGGCCACTATGTGTGTTATGACCAACCAATGTTTCAACAAGTTGACAGAT	843
Db	645	TCATGATTTCTGTCATATATGAGGTTATGTGAGTCGAAGTTATTAACAAATTAGACAAAT	704
QY	844	CCCTCTCGGGAACTGCTTGAACCGGATTAACCATGCTGTGGTGAAGTGAATTCACAAATGC	903
Db	705	TCTTGTGGTAATGTATGACTGTGTAATGATTTGTTGGGAAATGACATCTTAATATGC	764
QY	904	TCACCAATTTGCGTGCACACAGCTTGCACATGACCTGATCTGCAGCATGC	956
Db	765	TCATCATATTGCTTGCATATGCTGTATGATTGATCTGATTTGACAGCATATCC	817
RESULT 11			
BM143768			
LOCUS			
DEFINITION	588 bp mRNA linear EST 29-NOV-2001		
	saaj4e09.y1.Gm.c1072 Glycine max cDNA clone SOYBEAN CLOVE ID:		
	Gm.c1072-2921.5' similar to TR:082348 082348 PUTATIVE CYTOCHROME		
	B5.1, mRNA sequence.		
ACCESSION	BM143768		
VERSION	BM143768.1 GI:17153835		
KEYWORDS	EST.		
SOURCE	Glycine max (soybean)		
ORGANISM	Glycine max		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids		
	; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;		
	Glycine.		
REFERENCE	1 (bases 1 to 588)		
AUTHORS	Shoemaker, R., Keim, P., Vodkin, L., Erpelidg, J., Corvelli, V., Khanna		
	'A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,		
	Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers		
	'Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk		
	'R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann		
	'R., Waterson, R. and Wilson, R.		
TITLE	Public Soybean EST Project		
JOURNAL	Unpublished		
COMMENT	Contact: Shoemaker R/Public Soybean EST Project		
	Public Soybean EST Project		
	Washington University School of Medicine		
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: est@watson.wustl.edu		

This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site: www.resgen.com

Seq primer: -40RP from Gibco
High quality sequence stop: 426.
Location/Qualifiers

FEATURES

source

1. 588
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1072-2921"
/issue_type="seedlings induced for symptoms of SDS (Sudden Death Syndrome) disease"
/dev_stage="2-3 weeks old"
/lab_host="DH10B"
/clone_1lb="Gm-c1072"
/note="Vector: Bluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from 2-3 week old seedlings that were induced for symptoms of SDS (Sudden Death Syndrome) disease by the translocation of culture filtrate of Fusarium solani f. sp. glycines (Plant Cell Report 18:375-380). Cultivar PI 567374 is partially resistant to the disease SDS. Plant tissue (expanded leaves, folded leaves, and new shoots) were collected at 1, 6, 24, and 48 hrs. after inoculation and their mRNA pooled equally for cDNA construction. The library was prepared using the Stratagene Bluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA insert is protected from XhoI digestion via methylation during first strand synthesis. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the Bluescript vector. The ligated cDNA fragments were transformed into E. coli Electromax DH10B host cells. Plants were inoculated by Shuxian Li (Glen Hartman lab, University of Illinois). Library was constructed by Steve Clough (Lila Vodkin lab, University of Illinois)."

BASE COUNT 124 a 120 c 138 g 205 t 1 others
ORIGIN

Query Match 20.3%; Score 391.8; DB 12; Length 588;
Best Local Similarity 79.1%; Pred. No. 3.5e-28;
Matches 465; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

677 ATGTCCTCATTTGATCTATGCTGAGGTCAGTATGCTGAGGCTCATTTGGGT 736
1 ATGTTTCATTTGTTTATGCTATAGGTCAGTATGCTGAGGCTCATTTGGGT 60
737 TCAGGATGCTCTTAAAGGCTTTGGAGTCAAAAGTCTTATGCTGAGGCTCATTTGGC 796
61 GCTGCCCTTTGTTGGGCTTTGGATGCAAGCACTTACGGGTCTGACTGCGC 120
797 CATATGCTGTTATGACACCAATGTTTCAACAAGTTCACAGATCTCTCTGGGAC 856
121 CACTATGAGGTTTATGCTTACCCCTGGCTACAACAAAATTTGGCAAAATCTTTGTGGCAAT 180
857 TCGTTGACCGGATGAGCATTTGCTGTGAGAGTGAATGATCAATGCTCACCATTTGGC 916
181 TGCATGACTGGATATCATTTGATGAGGAGTGAAGTCAATGCTCACCATTTGCA 240
917 TGCACAGCCTTGACCATGCTGATCTGACAGACATGCGGCTTTTGGAGTTTGGTCG 976
241 TGCATGAGTCTTATGCTATGATCTGATCTGATCTGATCTTGTGCGGTGGACA 300
977 CGGTTCTTCATTTCCATCTCTCATTTCTATGAGGAGGAGTTGAGTTGATTTCAAT 1036
301 CGGTTCTTCATTTCCATCTCTCTCATTTCTATGAGGAGGAGGAGTTGAGTTGATTTCA 360
1037 GCTAGGTTCTTATGCTGCTACGACACTTTTACCGGGAATGCTGTTGGCAGG 1096

|||||
Db 361 TCAGGTTTCTCATGATGCTACAGACACTTCACTTACCCAGTTTGTGCTTGGCAAG 420
Qy 1097 GTCACTTTGATCTGACACCAATTTCTGCTATTGTTTTCAGCGGAGAAAGTGCAGATAGA 1156
Db 421 GTCAATTTGATCTGACACCTTTGCTGTTGTTCTTCAAGGAGAAAGTGCAGATAGA 480
Qy 1157 GCCTTACATATATGAGGATCCCTGTTTGGACTTGGTCCCTTTTATGCTCTGC 1216
Db 481 GCCTTACATATATGAGGATCCCTGTTTGGACTTGGTCCCTTTTATGCTCTTCA 540
Qy 1217 CTGCAATTTGGCTGAGAGGTTATGTTGCTTGTAGCTTTGCT 1264
Db 541 CTACCAATTTGGGAGAGGATGTTGTTGTTGCCAGTTTCT 588

RESULT 12
B1787611 571 bp mRNA linear EST 30-NOV-2001
LOCUS sa147f09.y1 Gm-c1065 Glycine max cDNA CLONE GENOME SYSTEMS CLONE
DEFINITION ID: Gm-c1065-6425 5', similar to TR:082348 082348 PUTATIVE
CYTOCHROME B5.;, mRNA sequence.

ACCESSION B1787611 GI:15815336
VERSION B1787611
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM

REFERENCE

1 (bases 1 to 571)

AUTHORS Shoemaker,R., Kelm,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Smaller,T., Gibbons,M., Page,D., Harvey,N., Schuck,R., Ritzer,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE Public Soybean EST Project
JOURNAL Unpublished
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 367.
Location/Qualifiers

FEATURES

source

1. 571
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1065-6425"
/issue_type="germinating shoots"
/lab_host="DH10B"
/clone_1lb="Gm-c1065"
/note="Vector: Bluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from germinating shoots of the cultivar Williams. The seeds were allowed to germinate for 24 hours prior to being cold stressed for 2 days at 4C. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the Bluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library

was constructed in the laboratory of Dr. Randy Shoemaker."

Query Match 20.1%; Score 389.4; DB 12; Length 571;
Best Local Similarity 80.4%; Pred. No. 66-28;
Matches 456; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 1024 GTTGTATTCATGTCAGTCTTGTATCTGCTACCGACCTTACTTATTTTACCCGGTAAT 1083
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QY 1084 GTGTGTTCAGAGGCTCAACTGTATCTGACAGCAATTCCTATTTGTTTTCAGAGGAAA 1143
DB 61 GTGCTTTCAGAGGCTCAATTTGTAAGCTTCCAGACTTGTCTTGTCTTCTTGAAGAAA 120
QY 1144 AGTCAGATAGAGCTTGAACATTAATGGGATCTTGTGTTTGAAGTTGTTCCCTCT 1203
DB 121 GGTCCAGATAGAGCTTGAACATTAATGGGATCTTGTGTTTGAAGTTGTTCCCTCT 180
QY 1204 TTATGCTCTGCTGCTCAATTTGCTGAGAGGTTATGTTGCTGCTGCTTTCG 1263
DB 181 GTTGATCTCTTCACTACCAATTTGGGAGAGAGGTCATGTTGTGCTGCTGCTTTCG 240
QY 1264 TGTGTTTCATTCAGACCAATTCATGTTGTTTGAATTCCTTGCAGAAATGATATGT 1323
DB 241 TGTGTTTCATTCAGACCAATTCATGTTGTTTGAATTCCTTGCAGAAATGATATGT 300
QY 1324 CGGCGCACCGAGTGGAGATGCTGTTTGAAGAGACAGCAAGTGTATCATTTGATATCTC 1383
DB 301 GGGCCACCAACAAATGGCAATGATGCTGTTTGAAGAGAAACGTTGGCAATGAGCAATTTT 360
QY 1384 TTGTGCTCTTGCATGATGATTTGTTTTCGTTGCTTGCATTTGACCTTGCATCATTT 1443
DB 361 TTGTGCTCTTGCATGATGATTTGTTTTCGTTGCTTGCATTTGACCTTGCATCATTT 420
QY 1444 GTTTCAGAGCTACCTCGGTCATTTGAGAGATTTGSCCTTGTGATGATGATCTTG 1503
DB 421 GTTTCAGAGCTACCTCGGTCATTTGAGAGATTTGSCCTTGTGATGATGATCTTG 480
QY 1504 CAGAAGCATTAATTTCTTATAGAGCTTGTATTTTGGAGGCAATCAGTGACAAAT 1563
DB 481 CAGAAGCATTAATTTCTTATAGAGCTTGTATTTTGGAGGCAATCAGTGACAAAT 540
QY 1564 TAGGACCTTCAGAGCTGCTGCTTACA 1590
DB 541 TAGGACCTTCAGAGCTGCTGCTTACA 567

RESULT 13
CA938317 575 bp mRNA linear EST 30-DEC-2002
LOCUS sav30908.y1 Gm-cl048 Glycine max cDNA clone SOYBEAN CLONE ID:
DEFINITION Gm-cl048-7215 5' similar to TR:082348 082348 PUTATIVE CYTOCHROME
B5.1, mRNA sequence.
ACCESSION CA938317 GI:27426797
VERSION CA938317
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
euosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 575)
Shoemaker R., Keim P., Vodkin L., Erpelting J., Corvelli V., Khanna
A., Balle B., Matra M., Hillier L., Kucaba T., Martin J., Beck C.,
Wyllie T., Underwood K., Stepien M., Theising B., Allen M., Bowers
Y., Peterson B., Swaller T., Gibbons M., Page D., Harvey N., Schuck
R., Riter E., Kohn S., Shin T., Jackson Y., Cardenas M., McCann
R., Waterston R. and Wilson R.
Public Soybean EST Project

JOURNAL COMMENT

Unpublished
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estwaterston.wustl.edu
This clone is available through: ResGen, Invitrogen Corp, 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: cduerksen.com web site:
www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 422.

FEATURES

source

1..575

/organism="Glycine max"

/mol_type="mRNA"

/db_xref="taxon:3847"

/clone="SOYBEAN CLONE ID: Gm-cl048-7215"

/issue_type="whole seedlings of greenhouse grown plants"

/dev_stage="1 week old"

/lab_host="DH10B"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI. The Clark NIL was constructed and seeded was provided
by Dr. J. Specht, University of Nebraska (Shoemaker and
Specht, 1995). The cDNA library was constructed from mRNA
isolated from whole seedlings of 1 week old greenhouse
grown plants. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site and a 3' anchor. EcoRI adapters were
ligated to the blunt-ended cDNA fragments followed by XhoI
digestion. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction site of the pBluescript
vector. The ligated cDNA fragments were transformed into
DH10 host cells (GibcoBRL). The library was constructed
in cooperation with Dr. Paul Keim's laboratory at Northern
Arizona University."

BASE COUNT 129 a 127 c 131 g 188 t
ORIGIN
Query Match 20.1%; Score 389.4; DB 14; Length 575;
Best Local Similarity 79.8%; Pred. No. 66-28;
Matches 459; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
QY 1038 CTAGGTTCTGATCTGCTACAGCACTTACTTTTACCCGGTAATGTGTGTCAGAGG 1097
DB 1 CAAGTTTCTCATTCAGACTTACAGCACTTCACTTACCAAGTTTGTCTTTCAGAGG 60
QY 1098 TCAATCTGATTCGACAGCAATTCGTAATGTTTTCAGAGGCAAAAGTGCAGATAGAG 1157
DB 61 TCAATCTGATTCGACAGCACTTGTGCTGTTCTCTGAGAGAAAGTGCAGATAGAG 120
QY 1158 CCTGAAACATTAATGGGAGATCTGTTTTCAGACTGTTGCTCTTTCAGAGTCTTGGC 1217
DB 121 CCTTAAACATTAATGGGAGATCTGTTTTCAGACTGTTGCTCTTTCAGAGTCTTGGC 180
QY 1218 TGCAGAAATGGGCTGAGAGGTTATGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1277
DB 181 TACCAATATGGGAGAGAAAGGCTCATGTTGTGTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 1278 AGCAGCATGATGTTGTTGTAATCACTTTCGCAATGTATATGTGGGAGCCAGAGTG 1337
DB 241 AGCAGCATGATGTTGTTGTAATCACTTTCGCAAGATGTATATGTGGGAGCCAGAAAG 300
QY 1338 GGAATGACGTTTGAAGAGAGCAAGTGAATGATATCTTGTGCTGCTGCTGCTGCTG 1397
DB 301 GGAATGACGTTTGAAGAGAGCAAGTGAATGATATCTTGTGCTGCTGCTGCTGCTGCT 360
QY 1398 TGAATGATGTTTTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1457
DB 361 TGAATGATGTTTTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

Oy	1458	CTCGGTGCAATTAGAGGAATTTTCGCTTGGTAGACCTTGACAAGACATAATT	1517
Dd	421	CAAAGGCACATTGAGGAAAATCTCACCCTTTGGTATTGACTTTTGCAGAAGACAACTT	480
Oy	1518	TGCCTTAATAGAGCTTGCTGCTATTTTGGAGGCCAATCAGTGCACAAATTAGAACCCCTCAGCA	1577
Dd	481	TGCCTTACAGACGTTTGACTTTGTGTGAGGCCAATCTTTGGACCTTAAAGACCCCTCAGCA	540
Oy	1578	CTGCTGCCCTTCACAGCTTGGGACCTTAACAAACCCCT	1612
Dd	541	CTGCTGCTCTTCAGGCCACGAAATCTCAGTAACCCCT	575
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LOCUS	Bu028011	741 bp	mRNA linear EST 23-AUG-2002
DEFINITION	OH99G05.Y9.ab1 OH_EFGHJ sunflower RHA280 Helianthus annuus cDNA clone OH99G05, mRNA sequence.		
ACCESSION	Bu028011		
VERSION	Bu028011.1	GI:22463531	
KEYWORDS	EST		
SOURCE	Helianthus annuus (common sunflower)		
ORGANISM	Helianthus annuus Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae; Helianthus. 1 (bases 1 to 741) Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Riesberg,L., Lin,H., Van Damme,M., Lavelle,D., Chevalier,P., Ziegler,D., Ellison,P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K. Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/ Unpublished Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore lab University of California at Davis (UCD) Asmndson Hall, UCD, Davis, CA 95616, USA Tel.: 1-(530)-742-1742 Fax: 1-(530)-752-9659 Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu] belongs to contig OH_Ca_contig742, see http://cgpb.ucdavis.edu/ for details. Plate: OHG9 row: G column: 05.		
REFERENCE			
AUTHORS			
JOURNAL			
COMMENT			
FEATURES			
source			
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	/lab_host="E.coli"		
	/clone_id="QH_EFGHU sunflower RHA280"		
	/note="Vector: pBRCDNA5flab; The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpb.ucdavis.edu/ TAG_Lib=OH_EFGHU sunflower RHA280 TAG_SISU=roots environmental stress TAG_SEQ=AICTCGCGGG"		
BASE COUNT	181 a	157 g	223 t
ORIGIN			
Query Match	20.1%;	Score 388.2;	DB 13; Length 741;
Best Local Similarity	70.4%;	Pred. No. 6.5e-28;	
Matches 519; Conservative	0;	Mismatches 218;	Indels 0; Gaps 0;

OY		827	AACAAGGTGGACAGATTCCTCTCTGCGGAACTGCTGAACCGGGAATAGACTTGTGTGG	886
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OY		887	AAGTGAATCAACAATGCTCACCAATTCGCTGCAACAGCCTTGACATGACCCTGATCTG	946
Db		64	AAGTGAACGATTAATGACATCACTATTGCTTGGCAACAGCTCGATTATATGACCCGATCTT	123
OY		947	CAGACATGCCCGGCTTTGCAAGTTGCTGCGCGGTTCTTCATTCATTAACCTTCATTTTC	1006
Db		124	CAACATTTTACCGAATGTTAGCGGTATCTTCGAAACTTTTCAACTGTTGACCTCGGTTTTC	183
OY		1007	TATGGAGAAGAGTTGAGATTGATTTGATTTCAATTCGCTAGGTTCTTGATCTGACACACTTT	1066
Db		184	TATGGAGACAGATTGACTTTCGACCCGTTAGCCGATTTCTTCGAGACTACCAACATCAC	243
OY		1067	ACTTTTATCCCGGATATGTGTGTGGCCAGGGTCAACTGTATCTGACACAAATTCGTCTA	1126
Db		244	ACGTATTATCCCGATCATGTGTGGTGGCCGATGTCAACTTTACTTACCAACAATATTGCTA	303
OY		1127	TTGTTTTCGAGCGCAAAATGACAGATATAGACCTTGAAACATTAATGGGATTCCTGTGTT	1186
Db		304	CTACTTTCAAACGAAAGATCCCGACCGCGGTTTAAACATTAATGGAACCTTATCTTC	363
OY		1187	TGACATTGTTCCCTCTTTTAGTGTCTTGGCTGCAAAATTTGGCCTGAGAGGTTATGTTT	1246
Db		364	TGAGCGTGTGTTCCGTTACTCGTGTCTGTCTTACCAACTGGCCGAAACGGGTGCGGTTT	423
OY		1247	GTCGTCCTAGCTTTGCTGTGTTTGTTCATCCAGACATTCAGTTCTGTTGAATCATCTTT	1306
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OY		1307	GCTGCAATATATATATGTCGGGGCACCGAGTGGGAATATCGTGTGTAAGAAGACACAAGT	1366
Db		484	GCGCCCAATGATATACGTGGGCCAACCAAGGGAGCAATGTGTTGAGAAACAACAAAT	543
OY		1367	GGTACATTGGAATATCTTGTGTGCTCTTCGATGATGATTGTTTTCGGTGGCTTGACGTTT	1426
Db		544	GGGACCATGACANTGTGGTGTCTTCAATACATGATTTGTTTTCGGCGGTTTACAGTTT	603
OY		1427	CAGCTTAGCATCATTTGTTTCCAAGGCTACCTCGTCCCATATGAGAAAGTTTCGCTT	1486
Db		604	CAATCTCAGGACCACTGTGTTCTTCAAGGTTCGCGGGGTGTCACTTGAGGTCCATATCTCCC	663
OY		1487	TTGGTTTAGTACCTTTGSCAAGAAGCATATTTGGCTATATGAGAGCTTGCTCATTTTGGGAG	1546
Db		664	ATTGTTTAGGGAACCTTGCAAGAAACATTAATCTTATATAGTATTTCAATTTTACGAT	723
OY		1547	GCCCAATCAGTGACCAAT	1563
Db		724	GCTAATGTGATGACACT	740
RESULT 15				
BO402431				
LOCUS		676 bp	mRNA	linear EST 22-MAY-2002
DEFINITION		BA_E00049E09f Gossypium arboreum 7-10 dpa fiber library Gossypium		
ACCESSION		BQ402431		
VERSION		BQ402431.1	GI:21090118	
KEYWORDS		EST.		
SOURCE		Gossypium arboreum		
ORGANISM		Gossypium arboreum		
REFERENCE		Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS		Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; rosids		
TITLE		1 (bases 1 to 676)		
JOURNAL		Wing, R.A., Friesch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry		
		D., Wood, T.C., Leslie, A. and Wilkins, T.A.		
		An integrated analysis of the genetics, development, and evolution		
		of the cotton fiber		
		Unpublished		

COMMENT

Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu
Total High Quality bases = 565
Seq primer: TAATACACTACTACTAGGG
High quality sequence start: 5
High quality sequence stop: 641.
Location/Qualifiers

FEATURES

source

1..676
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/note="Vector: PBK-CMV; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 151 a 149 c 150 g 226 t
ORIGIN

Query Match 20.0%; Score 387.6; DB 13; Length 676;

Best Local Similarity 76.6%; Pred. No. 7.9e-28;

Matches 513; Conservative 0; Mismatches 154; Indels 3; Gaps 3;

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QY 629 GACACCAAGGGGATGTCATTCATGACCCCTGACATCTGTGCTGTATGTTCCATTT 688
DB 2 GAACACGAAAGGAGATGGCTTTTGTTCATTAGCATCTGACCTGTCATGTTGCCATT 61
QY 689 GTACTATAGTGTCTGAGGTGCACATGATGTGTGGGCTCATTTGGGTTCCAGCATGCTC 748
DB 62 GTTCTTTAGCGTGTCTTGAGATGCGATAGCGTGTGGGCTCATCTGGGTGCGCCATGCTG 121
QY 749 TTAGGTTGCTTTGATGCAAAAGTGTATGTGGCCATATTTGCGCCATATGTGTT 808
DB 122 TTGGGATGTGTGATACAAAGTATACATGTCGTATGATTTCTGGACATTACAGGTA 181
QY 809 ATGACACCAATGGTTTCAACAAGTTGACAGATCCTCTGGGAAGCTTGACCGG 868
DB 182 ATGAGTAGCGGTGTACACAGATCTGCTCAATATCACTGGAAATGTTTACCGGC 241
QY 869 ATAGCATTTGCTTGTGGAAGTGAAGTCAACATGCTCACCAATTCGTCAGACGCTT 928
DB 242 ATCAGCATTTGCTGTGGAAATGAGTCAACATGCGACCAATTCGTCAGATAGCTTG 301
QY 929 GACCATGACCTGATCTGACGACATGCCGCTTTGCAAGTTTGTGCGGGTTCTCAAT 988
DB 302 GATTATGACCTGACCTCCAGCATATCCCTTTTTCAGTCTTTCACGTTTTCAT 361
QY 989 TCCATTAACCTTCATTTATAGGAGAAAGTGAAGTTGATTTCAATGCTAGTCTTG 1048
DB 362 TCAATTACGTTTGTGTTTGAAGAGAAATTAATTTGACCTCTTGCAAGGTTCTC 421
QY 1049 ATCTGTACAGACATTTACTTTTACCCGGTATGCTGTGTCAGAGGTCACATTTGAT 1108
DB 422 ATCAGTTACAGATTTGACGTTTATCCGTATATGCTGTAGGTTAGGTTGAACTGTAT 481
QY 1109 CTGACAGACAATTTGCTATTGTTTTCAGGCGAAAGTGCAGATAGAGCTTGAACATA 1168
DB 482 TTACAGACAATTTGCTATTGTTTTCGAAACCGGAAAGTCCAGATAGAGCATTTAACA 541
QY 1169 ATGGGATCTTGTGTGTTGAGCTGTGTTCCCTTTTATGCTTGTGCTGCTGCAATTTG 1228
DB 542 ATGGGATCTTGTGTGTTGAGCTGTGTTCCCTCTGCTTCTATCTAACCAATTTG 601
QY 1229 CTTGAGGGGTTATGTTGTGCTGTGATGCTGTGTTGTTCCATTCAGACATTTGAG 1288

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DB 602 CCAGA-AAGTTCATGTTTGTCTAAC-ACCTTCGCTGTATACATTCATCA-CATATCCAG 658

QY 1289 TTCTGTTGA 1298

DB 659 GTCTGTTGA 668

Search completed: December 31, 2003, 23:59:24
Job time : 2950.44 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:49:12 ; Search time 95.9683 Seconds
(without alignments)
8894.970 Million cell updates/sec

Title: US-09-857-524B-7

Perfect score: 1934
Sequence: 1 ggcagcagcacaagaftaaaa.....aaaaaaaaaaaaaaaaaaaaa 1934

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/ina/5B COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A COMB.seq: *
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6: /cgn2_6/ptodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	618.4	32.0	1684	2 US-08-831-570-1	Sequence 1, Appl1
2	618.4	32.0	1684	2 US-08-831-575-1	Sequence 1, Appl1
3	618.4	32.0	1685	1 US-08-366-779-4	Sequence 4, Appl1
4	618.4	32.0	1685	1 US-08-789-936-4	Sequence 4, Appl1
5	618.4	32.0	1685	4 US-08-934-254-4	Sequence 4, Appl1
6	555	28.7	1702	4 US-08-934-254-4	Sequence 26, Appl1
7	153	7.9	291	4 US-09-313-294A-1966	Sequence 1966, Ap
8	112	5.8	266	4 US-09-313-294A-3256	Sequence 3256, Ap
9	67	3.5	1443	4 US-09-904-615-21	Sequence 21, Appl1
10	65.4	3.4	1813	5 PCT-US94-12883-3	Sequence 3, Appl1
11	64.6	3.3	931	4 US-08-482-273-31	Sequence 31, Appl1
12	64.2	3.3	1577	3 US-08-821-994-59	Sequence 59, Appl1
13	64.2	3.3	2186	4 US-09-360-545-66	Sequence 66, Appl1
14	64	3.3	731	1 US-08-451-405A-2	Sequence 2, Appl1
15	64	3.3	1733	1 US-08-073-569-1	Sequence 1, Appl1
16	64	3.3	4456	4 US-09-095-443-1	Sequence 1, Appl1
17	63.8	3.3	1898	4 US-08-342-411A-1	Sequence 1, Appl1
18	63.4	3.3	289	1 US-08-341-568-3	Sequence 3, Appl1
19	63.4	3.3	289	4 US-08-911-020-3	Sequence 3, Appl1
20	63.4	3.3	485	4 US-09-996-243-245	Sequence 245, App
21	63.4	3.3	2406	4 US-09-594-506-37	Sequence 37, Appl1
22	62.6	3.2	1037	4 US-09-489-847-112	Sequence 112, App
23	62.4	3.2	4072	3 US-09-245-041-16	Sequence 16, Appl1
24	62.4	3.2	4895	3 US-09-053-866-1	Sequence 1, Appl1
25	62.2	3.2	4895	4 US-09-479-130-1	Sequence 1, Appl1
26	62.2	3.2	4895	4 US-09-472-130A-1	Sequence 1, Appl1
27	62	3.2	1958	4 US-08-665-034A-3	Sequence 3, Appl1

28	62	3.2	2634	4	US-09-463-238-3	Sequence 3, Appl1
29	62	3.2	3715	4	US-09-234-245-1	Sequence 1, Appl1
30	62	3.2	7724	4	US-08-486-049-1	Sequence 1, Appl1
31	61.8	3.2	1166	5	PCT-US96-12129B-1	Sequence 1, Appl1
32	61.2	3.2	1075	3	US-08-400-006B-6	Sequence 6, Appl1
33	61.2	3.2	2184	3	US-08-955-918C-1	Sequence 1, Appl1
34	61.2	3.2	2184	3	US-08-697-766A-1	Sequence 1, Appl1
35	61.2	3.2	2821	4	US-09-702-705-1669	Sequence 1669, Ap
36	61.2	3.2	2821	4	US-09-736-457-1669	Sequence 1669, Ap
37	61	3.2	1201	4	US-09-461-325-36	Sequence 36, Appl
38	60.8	3.1	570	1	US-07-885-970A-10	Sequence 10, Appl
39	60.8	3.1	570	1	US-08-298-687A-10	Sequence 10, Appl
40	60.8	3.1	570	1	US-08-298-829-10	Sequence 10, Appl
41	60.8	3.1	609	1	US-08-530-797-9	Sequence 9, Appl
42	60.8	3.1	609	2	US-08-787-335-9	Sequence 9, Appl
43	60.8	3.1	746	3	US-09-013-810-1	Sequence 1, Appl
44	60.8	3.1	1872	4	US-09-801-052-1	Sequence 1, Appl
45	60.6	3.1	888	3	US-09-188-930-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-831-570-1
Sequence 1, Application US/08831570
Patent No. 5959175
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Number, Andrew N.
TITLE OF INVENTION: A SUNFLOWER ALBUMIN 5' REGULATORY REGION
TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,570
FILING DATE: 09-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DiGioglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10545
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4366
TELEFAX: (516) 743-4366
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1684 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 43..1387
US-08-831-570-1
Query Match 32.0%; Score 618.4; DB 2; Length 1684;
Best Local Similarity 66.5%; Pred. No. 26-128;
Matches 886; Conservative 0; Mismatches 446; Indels 0; Gaps 0;

QY 326 AGAAGTACATTAACCTGAGAGAGCTGAGAGGCTCAACAAGAGAGGAGATTATGATC 385
 DB 58 AAGAAATACATTACTCTGATGAACTCAAGAAACACGATTAACCCGAGATCTATGATC 117
 QY 386 TCAATTCAGAGTAAAGGTGATCAATGTCTCAGATTGGGTCAAGAGACACCTGGTGGTAT 445
 DB 118 TCGATTCAAGGAAAGCCATATGATGTTTGGATGGGTGAAGAACATCCAGGTGGAGC 177
 QY 446 GTTCCATCTCAACCTTGTGCGCCAGATGTCACTGATGATTCATACGATACCATTCT 505
 DB 178 TTTCCTTGAAGAGCTTGTGCTGCTCAAGAGTAACTGATGCTATGTTGCAATTCATCT 237
 QY 506 GGCACAGAGTGTCAACCTTGAAGAAATCTTCACTGGCTCAACCTCAGTACCTTCAAG 565
 DB 238 GCTCTACATGAAAGATCTTGATTAAGTTTTCACCTGGGATTTATCTTAAAGATTACTCT 297
 QY 566 GTCTCTGAGGTGTCCAAAGACTAGAGAAAGCTTGATGATTCGATTCGAAATTTGGTCTT 625
 DB 298 GTTCTGAGGTTCTTAAAGATTATAGGAAGCTTGTGTTGATGTTTCTTAAATGGGTTTG 357
 QY 626 TTGACACCAAGGCGATGTCACTTATGACACCTTGATCTGTGCTTATGTTCTC 685
 DB 358 TATGACAAAAAGGTCATATATATGTTGCACTTGTGCTTATAGCAATGCTGTGCT 417
 QY 686 ATTGACTCTATGAGTCTGAGGTCAGTGTGAGGCTCAATTTGGTTCAGGATG 745
 DB 418 ATGAGTGTATAGGAGTTTGTGTTGAGGAGTGTGTTGATGATTTTCTGAGGCT 477
 QY 746 CTCTAAGGTTCTTTGATGACCAAGTCTTATGAGGCTGATTTGAGGCTACATG 805
 DB 478 TTGATGGGTTCTTTGATGATCAAGTGTGTTGATGACATGATGCTGGGCTATATG 537
 QY 806 GTTATGACAAACATGTTTCAACAAGTGTGACAGATCTCTGAGGAACTGCTTACC 865
 DB 538 GTAGTGTGATTCAGAGCTTAAATGATTTATGTTATGTTGCTGCAAAATGCTTTTCA 597
 QY 866 GGAATTAAGCATTTGCTGTTGAGAGGAGCTCAACATGCTCAACATTTGGGTCAGCAGC 925
 DB 598 GGAATTAAGTATTTGTTGTTGAGAAATGAAACATTAATGACATTCACATTTGCTATATG 657
 QY 926 CTGACCAATGACCTGATCTGACAGCAATGCGGCTTTGACATTTGCTGCGGTTCTC 985
 DB 658 CTGAAATATGACCCGATTTTCAATATATATACATTCCTGTTGTGCTTCAAGTTTCT 717
 QY 986 AATTCATACCTCTCATTTCTATGAGAGAAAGTTGAGTTGATTTATGCTATGCTC 1045
 DB 718 GGTTCACCTACCTCTCATTTCTATGAGAAAGGTTGACTTTTGACTCTTATCAAGATTC 777
 QY 1046 TTGATCTGCTACGACATTTACTTTTACCCTGTAATGTTGTTGCGAGGCTCAACTG 1105
 DB 778 TTGTAAGTTATCAACATTTGACATTTTACCTTATATATGTTGCTGAGGCTCAATATG 837
 QY 1106 TATCTGACAGAAATTTCTGATTTGTTTGAAGGCAAAAGTGCAGATAGACCTTGAAC 1165
 DB 838 TATGTAACATCTTCTATATATGTTGTTGACAAAGAAATGTTCTATCGAGCTAGGAA 897
 QY 1166 AATAAGGAGATCTTGTGTTGACTTGTGCTCTCTTATGATCTTGTGCTGCTCAAT 1225
 DB 898 CTCTTGGAGATCTTGTGCTGATTTGTTGTAACCGTGTGCTGTTCTTGTGTTGCTTAT 957
 QY 1226 TGGCTGAGAGGTTATGTTGTTGCTTGTGCTGCTTGTGTTGTTGTTGTTGTTGTTG 1285
 DB 958 TGGGTTGAAAGATATATGTTGTTATGCAAGTTATATAGTACGATGCAATGCAACAGTT 1017
 QY 1286 CAGTTCTGTTGAATCACTTGTGCTCAATGTAATGTGCGGCTCAACGAGTGGGATGAC 1345
 DB 1018 CAGTTCTGTTGAACCACTTCTCTTCAAGTGTGTTATGTTGAAACCTTAAAGGGAATAT 1077
 QY 1346 TGGTTTGAAGACAGACAAGTGTACATGATATCTTGTGCTCTTGTGATGATGG 1405
 DB 1078 TGGTTTGAAGAAACAAGGATGGGACACTTGTGCTCTGCTCTTGTGATGATGG 1137

QY 1406 TTTTTCGAGCTTGCAGTTTCACTTGTGACATCATTTGTTCCAGGCTACCTCGGTC 1465
 DB 1138 TTTGATGTTGATTTGCAATTCGAATTTGAGCATCATTTGTTCCAGATGCTGATATG 1197
 QY 1466 CAATTGAGGAAGATTTGCGCTTTGTTGTTGATGACCTTTGCAAGAGCATTAATTGCTTAT 1525
 DB 1198 AACCTTGAAGAAATCTGCGCTTACGTTGATGAGTTATGACAAAGAAATTTGCTTAC 1257
 QY 1526 AGAGCTTGTCAATTTTGGAGGCGCAATCAGTGAACAATTTGGAACCTCAGAGCTGTC 1585
 DB 1258 AATTATGATCTTTCTTCAAGGCGCAATGAAATGACACTCGAATTTGAGGAACAAGCA 1317
 QY 1586 CTACACCTAGAGGACTTAAACAACTGCGCTTAAAGATTTGTTGGGAAGCTGTTAAT 1645
 DB 1318 TTGAGGCTAGGGAATATTAACCAAGCCGCTCCGAAAGATTTGATGGAAGCTTCTAC 1377
 QY 1646 ACCATGCTGA 1657
 DB 1378 ACTCATGTTAA 1389

RESULT 2
 US-08-831-575-1
 ; Sequence 1, Application US/08831575
 ; Patent No. 5977436
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; TITLE OF INVENTION: AN OLEOSIN 5'REGULATORY REGION FOR THE
 ; TITLE OF INVENTION: MODIFICATION OF PLANT SEED LIPID COMPOSITION
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/831,575
 ; FILING DATE: 09-APR-1997
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DIGIGLIO, Frank S.
 ; REGISTRATION NUMBER: 31,346
 ; REFERENCE/DOCKET NUMBER: 10203
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1684 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; MOLECULE TYPE: linear
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 43..1387
 ; US-08-831-575-1
 Query Match 32.0%; Score 618.4; DB 2; Length 1684;
 Best Local Similarity 66.5%; Pred. No. 2e-128;
 Matches 886; Conservative 0; Mismatches 446; Indels 0; Gaps 0;

QY 326 AGAAGTACATTAACCTGAGAGAGCTGAGAGGCTCAACAAGAGAGGAGATTATGATC 385
 DB 58 AAGAAATACATTACTCTGATGAACTCAAGAAACACGATTAACCCGAGATCTATGATC 117

QY 386 TCAATTCAGGTAAGTGTACATGCTCAGATTGGGTCAAGAGACACCCGTGTGAT 445
 DB 118 TCGATTCAAGGAAAGGCTATGATGTTGGATTGGGTAAGAACATCCAGGGGACG 177
 QY 446 GTTCCAAATCTCAAACTTGTCTGCGCAGAGATGCTAGATGATTCATAGACATCATCT 505
 DB 178 TTTCCCTTGAAGAGCTTGTGCTGCTCAAGAGGTAATGATGATTTGTGATTCATCT 237
 QY 506 GGACACAGATGTACACCTTGAAAAATCTTCACTGGCTACCACTCAGGACTTCAAG 565
 DB 238 GCTCTACATGAGAAATCTTGATAGATTTTCACTGGGTAATATCTTAAAGATTAATCT 297
 QY 566 GTCTAGAGGTGTCAAGAACTACAGAAAGCTTCATCTGAGTCTCAAAATTTGGTCTT 625
 DB 298 GTTCTCAGGTTTCTAAAGATTAAGAGAGCTTGTGATGATTTCTTAAATGGGTTTG 357
 QY 626 TTGACACCAAGGAGATGTCATTCATGCAACCTTCATCTGTGTGATGTTCTC 685
 DB 358 TATGACAAAAAGGTCATATATATGTTGCAACTTGTGCTTATAGCAATGCTGTTGCT 417
 QY 686 ATTGATCTATAGTGTCTTCAAGGTGCAATGATGTTGGCTCATTTGGGTTCAAGCATG 745
 DB 418 ATGAGTGTATAGGGGTTTGTGTTGAGAGGTGTTTGTGATCAATTTGTTCTGGGTGT 477
 QY 746 CTCTAGAGGTGCTTGTGATGCAAAAGTCTATGTTGGGCAATGATTCGGCATATGTG 805
 DB 478 TTGATGGGGTTTCTTGTGATTCAGAGTGTGATGATGACATGATGCTGGCATTAATAG 537
 QY 806 GTTATGACCAACATGTTTCAACAAAGTTGACAGATTCCTCTCTGGGAACTGCTTGACC 865
 DB 538 GTAGTGTCTATTCAGGCTTAATATAGTTATGGGTATTTTGTGCAAAATGTTCTTCA 597
 QY 866 GGGATAGCATGTTGTGTGGAAGTGAATGATCAATGCTCAACCATTTGGGTGCAACG 925
 DB 598 GGAATAGTATGTTGTGTGGAATGGAACCATATGACATCACTGCTGTAAATAGC 657
 QY 926 CTGACCATACCCGTATCTGACAGACATGCGGCTTGTGAGTTGTGGCGGTTCTC 985
 DB 658 CTGGAATATGACCTGATTTACATATATATACATCTCTGTGTGTCTTCCAGTTTCT 717
 QY 986 AATTCATTAACCTCTCATTTCTATGAGAGAAAGTTGAGTTGATTCATTTGATGAGTTC 1045
 DB 718 GGTTCATCACTCTCTCATTTCTATGAGAAAGTTGATTCATTTGATCAAGATTC 777
 QY 1046 TTGATCTCTACACGACCTTACTTTTACCCTGTAATGTGTGTGTCAGAGGTCACTTG 1105
 DB 778 TTGTATAGTTATCAACATTTGACATTTTACCCTATATGTGTGCTGCTAGGCTCAATATG 837
 QY 1106 TATCTGAGCAATTCGTATATGTTTTCAGAGGAAAGTGAAGTATAGCCTTGAAC 1165
 DB 838 TATGTAATATCTCTCAATATGTTGTGTAACCAAGAAATGTTCTTATGAGCTCAGAGAA 897
 QY 1166 ATATAGGGAATCCTTGTGTGTGACTTGTGCTCTTTTATGATGCTCTGCTGCAAT 1225
 DB 898 CTCTGGGATGCTTCAAGTGTCTGATTTGATACCCGTGTGCTTGTGTTGCTTAAT 957
 QY 1226 TGGCTTGAAGGTTATGTTGTGTGCTTGTGCTGCTGTTGTTTCATTCAGACATTT 1285
 DB 958 TGGGTTGAAGAAATTAATGTTGTATGCAAGTTTATCAGATGAGAAATGCAACAGTT 1017
 QY 1286 CAGTCTGTTGTAATCTTGTGCAAAATGTAATGTGGGCAACCGAGTGGGAATGAC 1345
 DB 1018 CAGTCTCTCTTGAACCACTCTCTCAAGTGTATATGTGAAAGCTTAAAGGGAATAT 1077
 QY 1346 TGGTTTGAAGACAGACAGTGTATGATATCTCTTGTGCTCTTGCATGATTTG 1405
 DB 1078 TGGTTTGAAGAAACAAAGATGAGACACTTGACATTTCTGTCTCTTGTGATGATTTGG 1137
 QY 1406 TTTTTCGTGCTTGAAGTTTCACTTGAAGCATATTTGTTTCCAAAGGCTACCTGCTGC 1465
 DB 1138 TTTTCATGATGATGCAATTCCAATTTGAGATCATTTGTTTCCAAAGATGCTGAATGC 1197

QY 1466 CAATGAGGAAGATTTGCGCTTGTGTAGTACCTTTGCAAGACATTAATTTGCTTAT 1525
 DB 1198 AACCTTAGAAGAAATCTCGCCCTAGATGATGATGATTAAGAAACATTAATTTGCCCTTAC 1257
 QY 1526 AGAGCTGTGATTTTGGAGGCAATCACTGACATTAAGAACCTTCAGAGCTGCTGCC 1585
 DB 1258 AATTATGATCTTCTTCAGAGGCAATGAATGACACTCAGAACTTGAAGAAACACAGCA 1317
 QY 1586 CTACAGCTAGGAGCTTAACAAACCTGCGCTTGAATTTGTTGCGAGAGCTTAAAT 1645
 DB 1318 TTGAGGCTAGGAGATTAACCAAGCGCTCCGAAAGATTTGATGGAGCTTTCAC 1377
 QY 1646 ACCCATGCTGA 1657
 DB 1378 ACTCATGCTTAA 1389

RESULT 3
 US-08-366-779-4
 : Sequence 4, Application US/08366779
 : Patent No. 5614393
 : GENERAL INFORMATION:
 : APPLICANT: Thomas, Terry L.
 : APPLICANT: Reddy, Avutu S.
 : APPLICANT: Nuccio, Michael
 : APPLICANT: Freysinet, Georges L.
 : APPLICANT: Nunberg, Andrew N.
 : TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 : NUMBER OF SEQUENCES: 25
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Scully, Murphy & Presser
 : STREET: 400 Garden City Plaza
 : CITY: Garden City
 : STATE: New York
 : COUNTRY: United States
 : ZIP: 11530
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/366,779
 : FILING DATE: 30-DEC-1994
 : CLASSIFICATION: 800
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Presser, Leopold
 : REGISTRATION NUMBER: 19,827
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (516) 742-4343
 : TELEFAX: (516) 742-4366
 : TELEX: 230 901 SANS UR
 : INFORMATION FOR SEQ. ID NO: 4:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1685 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: both
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA (genomic)
 : US-08-366-779-4

Query Match 32.0%; Score 618.4; DB 1; Length 1685;
 Best Local Similarity 66.5%; Pred. No. 2e-128;
 Matches 886; Conservative 0; Mismatches 446; Indels 0; Gaps 0;

QY 326 AAGAATCACTAATCTCAAGAGGCTGAAGGCTCAACAAGAGGAGATTTATGATC 385
 DB 59 AAGAAATACATTCCTCAAGTGAATCAAGAACAGATTAACCCGAGATCTATGATC 118
 QY 386 TCAATTCAGGTAAGTGTACATGCTCAGATTTGGGTCAAGAGACCCGTGTGAT 445

Db 119 TCGATCAGGAGAAAGCTATGATGTTCCGATGGGTAAGAACATCCAGTGGAGC 178
 Qy 446 GTTCCAACTCAACCTTGTGGCCAGAGATGCACTGATTCATGACATACCACTCT 505
 Db 179 TTTCCTTGAAGAGCTTGTGGTCAGAGGTAACGATGATGATTTGTCATCTCCT 238
 Qy 506 GGCACAGAGATGTCACACCTTGAAGAAATTTCTCACTGGCTACCACTCAGTACTCAAG 565
 Db 239 GGCCTACATGGAAGAAATCTGATAGATTTTCACTGGGATTTATCTTAAAGATTAAGCT 298
 Qy 566 GTCTCTGAGGTGTCAGAAAGCTACAGAAAGCTTGACATGAGTCTCAAAATGGGCTT 625
 Db 299 GTTCTGAGGTTCTTAAAGATTAAGAAAGCTTGATGATTTCTTAAATGGGCTT 358
 Qy 626 TTGACACCAAGGAGATGTCATTCATGCAACCTTGATGCTGCTGATGCTC 685
 Db 359 TATACCAAAAGGTCATATATGTTGCACTTGTGCTTATACATCTGTTGCT 418
 Qy 686 ATGTACTCTATGCTGTCAGGTCACATGCTGTGGCTCATTTGGTTCAGGCAATG 745
 Db 419 ATGAGTGTATGGGCTTTTGTGAGGGTGTGTTGTGACATTTGTTTCTGGGTG 478
 Qy 746 CTCTTAAAGGCTTTGGATSCAAAGTGTGATGAGGCAATGTTGCTGCTACTATG 805
 Db 479 TTGATGGGCTTTCTTGGATCAGAGTGTGATGATGACATGATGCTGGCAATATATG 538
 Qy 806 GTTATGACAAACATGTTTCAACAAGTTGACACAGATCCCTCTGGGAATGCTTGACC 865
 Db 539 GTAGTGTGATGTCAGGCTTAAATGATTAAGTTATGGGATTTTGTGCAAAATGCTTCA 598
 Qy 866 GGGATAGCATTTGCTGGTGAAGTGAAGTGAATGATGATGCTGCAATGCTGCAAGC 925
 Db 599 GGAATAGATTTGCTGGTGAAGTGAAGTGAATGATGATGCTGCAATGCTGCAAGC 658
 Qy 926 CTGACACATGACCTGATCTGACAGACATGCGGCTTGTGAGTTGCTGCGGCTTTC 985
 Db 659 CTGAAATGACCTGATTTACAAATATATACCATCTCTGTGTGCTTCCAAAGTTT 718
 Qy 986 AATTCCAAACCTCTCATTTTCTATGAGAGAAAGTTGAGTTGATTCATGCTAGGTC 1045
 Db 719 GGTTCACCTCCTCATTTCTATGAGAAAGTTGACCTTGTGATCTTATCAAGATTC 778
 Qy 1046 TTGATCTGCTACGACATTTACTTTTACCCTGATATGTTGTTGCCAGGCTCACTTG 1105
 Db 779 TTTGTAAGTATCAACATTTGACATTTTACCTATATATGCTGCTGCTCAAGTATG 838
 Qy 1106 TATCTGACAAATCTGCTATGTTTTCGAGGCAAAAGTGAAGATGAGCTTGAAC 1165
 Db 839 TATGTAACATCTCATATATGTTGTTGACCAAGAAATGTCCTATGAGCTCAGGA 898
 Qy 1166 AATAAGGAGATCTTGTGTTTGAATGCTTCCCTTTAGTCTTGTGCTGCAAT 1225
 Db 899 CTCTGGAGATCTGATGTTCTGCAATTTGTAACCGTGTGCTTGTGTTGCTAT 958
 Qy 1226 TGGCCTGAGAGGTTATGTTGTGCTTCTGACTTGTGCTTGTGTTGCTCAGACAT 1285
 Db 959 TGGGCTGAAGAAATTTATTTGTTTATTCAGATTTATGAGTACGGAATGCAAGAT 1018
 Qy 1286 CAGTTCTGTTGAATCACTTGTGCTGCAATATATGTCGGGCCACCGAGTGGGAATG 1345
 Db 1019 CAGTTCTCTGAAACCACTTCTTCAAGTGTATATGTTGAAAGCTTAAAGGGAATAT 1078
 Qy 1346 TGGTGTGGAAGCAGACAGTGTATGATGATCTCTTGTGCTCTTGCATGATG 1405
 Db 1079 TGGTGTGGAAGCAAAACGATGAGGACCTTGCATTTCTTGTGCTTGCATGATG 1138
 Qy 1406 TTTTTCGTTGCTGCTGCTTCACTTGTGAGATCACTTGTGCTTCAAGGCTCCTGCTG 1465
 Db 1139 TTTCTGTTGATGATGCAATTCATATGACATCTTGTGCTTCCAGATGCTATGATG 1198
 Qy 1466 CAATGAGAAATTTGCTGCTTGTGATGATGCTTGTGCAAGAAACATATTTGCTTAT 1525
 Db 1199 AACCTGAGAAATCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 1258

Qy 1526 AGAGCTTGTCAATTTGGAGGCCAATCAGTGAACAATTAAGAACCTCAGGACTGTGCC 1585
 Db 1259 AATTATGATCTTTCTTCCAAAGCCCAATGAAATGACATCTCAGAACTTGAAGAACAGCA 1318
 Qy 1586 CTACAGCTAGGAGCTTAAACAAACCTGCGCTTAAAGATTTGTTGGGAAGCTTTAAT 1645
 Db 1319 TTGAGGCTAGGAGTATATTAACCAAGCCGCTCCGAAATTTGGATGGAAGCTCTTAC 1378
 Qy 1646 ACCATGGCTGA 1657
 Db 1379 ACTCATGTTAA 1390

RESULT 4
 US-08-789-936-4
 ; Sequence 4, Application US/08789936
 ; Patent No. 5789220
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; APPLICANT: Reddy, Anuth S.
 ; APPLICANT: Nuccio, Michael
 ; APPLICANT: Freysinet, Georges L.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; TITLE OF INVENTION: DELTA 6-DESATURASE
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/789,936
 ; FILING DATE: 28-JAN-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/366,779
 ; FILING DATE: 30-DEC-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 8383EXW
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELE: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1685 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-789-936-4

Query Match 32.0%; Score 618.4; DB 1; Length 1685;
 Best Local Similarity 66.5%; Pred. No. 2e-128;
 Matches 886; Conservative 0; Mismatches 446; Indels 0; Gaps 0;

Qy 326 AAGAATGATTAACCTGAGAGAGCTGAGAGTCAACAAGAGGAGATTATGATC 385
 Db 59 AAGAATGATTAACCTGAGAGAGCTGAGAGTCAACAAGAGGAGATTATGATC 118
 Qy 386 TCAATTAAGGTAAAGTGTCAATGTCTCAGATTGGGTCAAGAGCACCTGTGTGAT 445

Db 119 TCGATTCAGGGAAGGCTATGATGTTGCGATGGGTGAAGACCAATCCAGTGGAGC 178
 Qy 446 GTTCCAAATTCGAACCTTGTGGCCAGGATGTCATGATTCATAGCATACCACTT 505
 Db 179 TTTCCTTGAAGAGCTTGTGGTCAGAGGTAACATGATGATTTGGCAATTCATCCT 238
 Qy 506 GGCACAGCATGTCACACCTTGAAGAAATCTTCACTGGCTACCACTCAGTACCTCAAG 565
 Db 239 GCGCTACATGGAAGAACTTGAATAGTTTTCATGGGTATATATCTTAAGAAATTAATCT 298
 Qy 566 GTCTCTGAGGTGTCAGAAAGATCAAGAAAGTTGCACTGATGTTCTCAAAATGGGTCT 625
 Db 299 GTTCTGAGGTTCTAAAGATTAATAGAAAGCTGTGTTGATGTTCTAAATGGGTCTG 358
 Qy 626 TTGACACCAAGGGAATGTCATTCATGCAACCTTGATCTGTGCTGATGTTCTC 685
 Db 359 TATACCAAAAGGTCATATATGTTGCAACTTGTGCTTAATAGCAATGCTGTGCT 418
 Qy 686 ATGTACTCTATGTTGTTGAGGTGCACTAGTGTGGGCTCATTTGGGTTGAGCATG 745
 Db 419 ATGAGTGTATAGGGTTTGTGTTGAGAGGTGTTTGTGATCAATTTCTTCTGGGT 478
 Qy 746 CTCTTAAAGGTCTTTGAGTCAAGAGTCTTATGTTGGCCATGATCTGCGCACTATG 805
 Db 479 TTGATGGGTTCTTTGATTCAGAGTGTGATGATGATGATGATGATGATGATGATG 538
 Qy 806 GTTATGACCAATGTTTCAAGAGTTCACAGATCTCTCTGGGAATGCTTGAC 865
 Db 539 GTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 598
 Qy 866 GGGATTAAGCATTTGTTGGTGAAGTGAAGTCAATGCTCACCATTGCGTGAACAGC 925
 Db 599 GGAATTAAGTATGTTGGTGAAGTGAAGTCAATGCTCACCATTGCGTGAACAGC 658
 Qy 926 CTGACCAATGACCTGATCTGACAGACATGCGGTCTTTGAGTGTGCTGCGGTCTTC 985
 Db 659 CTGAAATGATGACCTGATCTGACAGACATGCGGTCTTTGAGTGTGCTGCGGTCTTC 718
 Qy 986 AATTCATTAAGTCTGATCTGATGATGATGATGATGATGATGATGATGATGATG 1045
 Db 719 GGTTCACCTGATCTGATCTGATGATGATGATGATGATGATGATGATGATGATG 778
 Qy 1046 TTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1105
 Db 779 TTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 838
 Qy 1106 TATCTGACAGCAATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1165
 Db 839 TATGTAAGTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 898
 Qy 1166 ATTAATGGGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1225
 Db 899 CTCTGGGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 958
 Qy 1226 TGGCTGAGAGGTTATGTTGCTGCTGATCTGATCTGATCTGATCTGATCTGATCTG 1285
 Db 959 TGGGTTGAAGAAATGATGTTGATGATGATGATGATGATGATGATGATGATGATG 1018
 Qy 1286 CAGTCTGTTGATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1345
 Db 1019 CAGTCTGTTGATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1078
 Qy 1346 TGGTTTGAAGAGCAAGTGTATCATGATGATCTGATCTGATCTGATCTGATCTG 1405
 Db 1079 TGGTTTGAAGAGCAAGTGTATCATGATGATCTGATCTGATCTGATCTGATCTG 1138
 Qy 1406 TTTTTCGTTGATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1465
 Db 1139 TTTTTCGTTGATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1198
 Qy 1466 CAATTAAGAGATGTTGCTGTTGATGATCTGATCTGATCTGATCTGATCTGATCTG 1525
 Db 1199 AACCTTAAGAGATGTTGCTGTTGATGATCTGATCTGATCTGATCTGATCTGATCTG 1258

Qy 1526 AGAGCTTGTCAATTTGGAGGCAATCAGTGAATAGGACCTCAGGACTGTGCC 1585
 Db 1259 AATTATGATCTTCTTCAGAGCCCAATGATGATGATGATGATGATGATGATG 1318
 Qy 1586 CTACAACTTGAAGGACCTTAACAAACCTGCGCCCTTAAGATTTGTTGGGAAGCTTTAAT 1645
 Db 1319 TTGAGGCTTGGATTAATTAACCAAGCCGCTCCGAAGAAATTTGGTATGGGAAGCTTCAAC 1378
 Qy 1646 ACCATGCTGA 1657
 Db 1379 ACTCATGTTAA 1390

RESULT 5
 US-08-934-254-4
 ; Sequence 4, Application US/08934254
 ; Patent No. 6355861
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; TITLE OF INVENTION: DELTA 6-DESATURASE.
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/934,254
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 8383ZYXWVU
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1685 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-934-254-4

Query Match 32.0%; Score 618.4; DB 4; Length 1685;
 Best Local Similarity 66.5%; Pred. No. 2e-128;
 Matches 886; Conservative 0; Mismatches 446; Indels 0; Gaps 0;

Qy 326 AAGAAGTCACTTAACCTTCAGAGGCTGAAGGTCACAAACAAGAGAGATTTATGATC 385
 Db 59 AAGAATTAACCTTAACCTTCAGAGGCTGAAGGTCACAAACAAGAGAGATTTATGATC 118
 Qy 386 TCAATTAAGAGTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATG 445
 Db 119 TCAATTAAGAGTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATG 178
 Qy 446 GTTCCAAATTCGAACCTTGTGGCCAGGATGTCATGATGATGATGATGATGATGATG 505
 Db 179 TTTCCTTGAAGAGCTTGTGGTCAGAGGTAACATGATGATGATGATGATGATGATG 238
 Qy 506 GGCACAGCATGTCACACCTTGAAGAAATCTTCACTGGCTACCACTCAGTACCTCAAG 565

Db 239 GCGCTACATGAGAAATCTGATTAAGTTTCTACCTGGGTATTAATCTTAAGATTAAGTCT 298
 Qy 566 GTCTCTAGAGTGTCCAAAGACTACAGAAAGCTTGATGTGCTCAAAATGGGCTT 625
 Db 299 GTTCTGTAGGTTTCTAAAGATTAAGAAAGCTTGTGTAGTTCTTAAATGGGTTG 358
 Qy 626 TTGACACCAAGGCAATGTCATCTTCATGCAACCCCTGATCGTTGCTGTAATGTTCTC 685
 Db 359 TATACCAAAAGGCTATTAATGTTGCAACTTGTGCTTATTAAGCAATCTGTTGCT 418
 Qy 686 ATGTACTATAGTGTCTGAGTGCACTAGTGTGGCTCAATTTGGGTTCAAGCAG 745
 Db 419 ATGAGTGTATAGGGGTTTGTGTGAGGGTGTGTTGTAACATTTGTTTCTGGGGT 478
 Qy 746 CTCTTAGGGTCTTTGGATGCAAAAGTCTTATGTGGCCATGATTTGGCCACTATGTG 805
 Db 479 TTGATGGGTTTCTTTGATTCAGAGTGTGATGACATGATGCTGGGCATTTATATG 538
 Qy 806 GTTATGACCAACCAATGGTTTCAACAGGTTGACAGATCTCTCTGGGAGCTGGTGAC 865
 Db 539 GTAGTGTCTGATTAAGGCTTAATTAAGTTTATGGGTATTTTGTCTGCAATTTGCTTCA 598
 Qy 866 GGGATTAAGCATTTGCTGTGGAAGTGAAGTCAATGCTCAACATTCGCTGCAAGC 925
 Db 599 GGAATTAAGTATTTGGTGTGAATGGAACATATGACATTCATTTGCTGTAATAGC 658
 Qy 926 CTGATCAATGACCTGATCTGACAGACATGCCGGTCTTTGCAATTTGCTGGGTTCTC 985
 Db 659 CTGAAATATGACCTGATTTCAATATATATACATTCCTGTTGTGTTCTTCAAGTTT 718
 Qy 986 AATTCATTAACCTCTCATTTCTATGGGAGGAAGTTGAGTTGATTTGATTTGCTAGGTC 1045
 Db 719 GGTCTACTACCTCTCATTTCTATGAGAAAGTTGACTTTTGTACTTTTATCAAGATTC 778
 Qy 1046 TTGATCTGCTACAGACATTTACTTTTACCCTGATATGTGTGTCAGGATCAACTTG 1105
 Db 779 TTGTAAGTTATCAACATTTGACATTTTACCTTATATGTTGCTGCTAAGCTCAATAG 838
 Qy 1106 TATCTGACAGCAATTTGCTATTTGTTTGGAGCGAAAGTGCAGATAGAGCTTGAC 1165
 Db 839 TATGTACATCTCTCATATATGTTGTGACCAAGAAATGTCTTATCGAGCTCAGAA 898
 Qy 1166 AATAAGGAGATCTTGTGTTTGGACTGTTGCCCTTTAGTGTCTTGTGCTGCAAT 1225
 Db 899 CTCTTGGATGCTTATGTTCTCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 958
 Qy 1226 TGCCCTGAGAGGTTATGTTGTGCTGCTAGCTTGTGCTTGTGTTGTTGTTGTTGTT 1285
 Db 959 TGGGGTGAATAATTTATTTGTTATTCAGATTTATCAGTGAAGTGAATCAACAAGTT 1018
 Qy 1286 CAGTTCTGTTGAATCACTTTGCTGCAATATATATGTGGGCCACCGAGTGGAGTAC 1345
 Db 1019 CAGTTCTCTTGAACCACTTCTCTTCAAGTTTATATGTGAAAGCTTAAAGGGAGTAT 1078
 Qy 1346 TGGTTTGAGAGCAAGAGTGTATCTGATTAATCTTGTGCTCTTGTGATGATTTG 1405
 Db 1079 TGGTTTGAGAAACAACGAGTGGACCTTGAATTTTGTCTCTCTTGTGATGATTTG 1138
 Qy 1406 TTTTTCGTTGCTGCAATTTCACTTGAAGTCAATTTGTTTCCAAAGCTACTCGTGC 1465
 Db 1139 TTTTATGTTGATTTGCAATTTCAATTTGAGCATCTTTGTTTCCAAATATGCTAGATGC 1198
 Qy 1466 CAATTTGAGAAATTTGCTCTTGTGTTAGTACCTTTGCAAGAAAGCAATTTTGGCTTAT 1525
 Db 1199 AACCTTGAAGAAATCTCGCTTACGTGATCGATTTATCAAGAAACATATTTGCTTAC 1258
 Qy 1526 AGAGCTTGTATTTTGGAGGCAATGAGTGAACATTAAGACCTTGAAGTGTGCC 1585
 Db 1259 AATTAATGATTTTCTCAAGGCAATATAATGACATCAAGAACTTGAAGAAACAGACA 1318
 Qy 1586 CTACAGCTAGGAGCTTAACAAACCTTGCCTTAAAGATTTGTTGTGGAGCTGTAT 1645

Db 1319 TTGAGGCTAGGATATATACCAAGCCGCTCCGAAAGATTTGTATGGAGACTTTCAC 1378
 Qy 1646 ACCCATGGCTGA 1657
 Db 1379 ACTCATGTTAA 1390
 RESULT 6
 US-08-934-254-26
 ; Sequence 26, Application US/08934254
 ; Patent No. 635861
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; TITLE OF INVENTION: DELTA 6-DESATURASE
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/934,254
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Preser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 83832YXWU
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1702 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 48..1406
 ; NAME/KEY: CDS
 ; LOCATION: 48..1406
 ; US-08-934-254-26
 Query Match 28.7%; Score 555; DB 4; Length 1702;
 Best Local Similarity 64.8%; Pred. No. 2,5e-114; Indels 12; Gaps 4;
 Matches 889; Conservative 0; Mismatches 470;
 Qy 321 AGGAGAAAGATACATTAACCTCAGAGAGCTGAAGGCTCAACAAGAGGAGATTAT 380
 Db 58 AAGCTAAGAGTATATACACGCGGAGGAGCTCCGCCCAACAAGATCCGGGATCTCT 117
 Qy 381 GGATCTCAATTCAGAGTAAAGTGTACAAATGTCTTCAATTTGGGTCAAGAGACCTCTGTG 440
 Db 118 GGATCTCAATTCAGAGGCAAGGTCTACATGCTCTCGGTGGCGCGAGAGACCCCGCG 177
 Qy 441 GTGATGTTCAATCTCAACCTTGTGCGCAGAGTGTCACTGATGATTTATATACATACC 500
 Db 178 GCGAGGTCCGCTCTTAAGTGTGCGCGCAGAGGTACCGAGCCCTTATTCGTAACC 237
 Qy 501 ATCTGACAGCATGCTACACCTTGAGAAATTTCTCACTGG--CTACCACTCAAGTG 557

Db	238	ACCCGGGACGCGGCGGCGCATCTGGATCCGCTCTTCAACGGGTAACTAATCACTCAACG	297
Oy	558	ACTTCAAGTCTCTAAGGTGTCCAAAGACTACAGAAAGTTGCATCTGACTTCAAAAT	617
Db	298	ACTTGAAGTGTCCGAGATCTTCAAGGACTTACCGAGGCTTTTGAACGAGATGTGCGGT	357
Oy	618	TGGGTCTTTTGAACCAAGGGGACATGTCATCTTCANGCACCTTGATCTGTGTGCTTGA	677
Db	358	CCGGATCTTGCAGAGAGAGGSCACCATATATGTGACGTTGCTGTGCGCTTGCGGTCA	417
Oy	678	TGTTCTCATGTACTTATGTTGTCTGAGGTGACATAGTGTGTGCTCATTTGGGTT	737
Db	418	TGATGGCGGCAATCGTCTACGCGGTGTGGCGCTCGGAGTCCGTGGAGTTTCAATGCTCT	477
Oy	738	CAGCATGCTCTTAGGGTTGCTTTGGATGCAAAAGTCTTATGTGGCCATGATTTGGCC	797
Db	478	GCGGGCACTGTGTGGCTTGTGTGTGATTCAAAGCCGCTATGTGGGCATGATCTCGGCG	537
Oy	798	ACTATGTGTTATGACCAACAAATGTTTCAACAAAGTTGACAGATCCCTCTGGGAAT	857
Db	538	ATTACAGGTGATGCCAACCCGTGATACACAGATACAGCACTCATAGAGGCAACA	597
Oy	858	GCTTGACCGGATTAAGCATTTGCTGTGGAGTGAAGTCACTACATGCTACACCATTTGGT	917
Db	598	TCCTAACGGGATACGATTCGCTGTGTGGAATGGAACCAACGCCACACACTCGCTCT	657
Oy	918	GCAACAGCTTTGACCATATACCTGTATCTGCAGACATACGCCGCTTTTGCAATTTGTCGC	977
Db	658	GCAACAGCTCGACTACACACCCCGCACTCAAGCATATCCGATATCCCGCTCAACCC	717
Oy	978	GGTCTTCAATTCCTAACCTCTCATTTCTATGGAGGAAGTTGAGATTTTCATTTG	1037
Db	718	GACTTTCACTCACTCACTCTGCTTCTATGGCGGATCTGAAATTCAGCAAGAGTG	777
Oy	1038	CTAGGTTCTTGATCTGCTACACGACTTTCATTTTACCCGGTATATGTGTGTCAGAG	1097
Db	778	CACGGTCTTGTGTGATCAACGACTGGAAGCTTACCCGCTATGATCTTTCGGCCAG	837
Oy	1098	TCAACTGTATCTGCAGCAAAATCTGTATGTTTTCGAGGCGAAAGTGCAGATPAG	1157
Db	838	TCAACCTTTCATCCAGACTTTTATATGTCTTCAACAGGGCGACGTCCCTGACCGG	897
Oy	1158	CCTTGAATATATGGGGATCCCTGTGTTTGGACTTGTGTCCTCTTTTATGTCTTGCC	1217
Db	898	CTTAACTTATATGGGATATCCGGTCTTCTGACGTGTGTCCCGCTCTTGATCTTTC	957
Oy	1218	TGCCAAATTTGACCTAGAGGGTATATGTGTGCTTGAAGTATATGTCGGGCAACGAGTG	1277
Db	958	TCCGAACTGGCTTACGCGTTCCGGTCTGTCTCATGACCTTTCGGGTCAACGGGATCC	1017
Oy	1278	AGCACTTCAAGTCTGTTTGAATCATCTTGTGCTCAAAATGATATGTCGGGCAACGAGTG	1337
Db	1018	AGCAGCTCAAGTTACGCTCAACACTTCTCCGGGACAAATAGCTGGGCCCCCAAG	1077
Oy	1338	GGAATGACTGTTTGAAGAGCAGACAAAGTGTACTTGGATATCTCTGTGCTCTTGA	1397
Db	1078	GCGCAACTGTGTTCCAGAGAGCAGAAAGGACATGATATACGTCGCCACAGCTGGA	1137
Oy	1398	TGATATGTTTTCGGTGGCTTGACGTTTCAAGCTTGAACATATTTGTTCCAGGGCTAC	1457
Db	1138	TGAGATGTTCTTTGTGTGGCTGCACTTTCAGTTGTGAGACACACTTGTTCCTTGAAGCTGC	1197
Oy	1458	CTGGGTGCCAATGAGAAAGATTTTCGCTTGTGTATGACTTTTGCAGAAAGCAATAAT	1517
Db	1198	CGCGTGGGACATTAGAAAGATTTGGCTTGCGCTTGCGGACTTGTGTAAAGACACGGGA	1257
Oy	1518	TGCTTATAGAGCTTGTCAATTTTGG---GAGGCCAATCAGTGACAAATTAAGACCTTCA	1574
Db	1258	TGCGGTATAGAGCTTTCGGGTTTGTGGAGCAGACGCTTAATGTCAAGCAAAATTCGACGCTGA	1314
Oy	1575	GGACTGTGCTTACAGCTAGGACCTTAA---CAAAACCTGCCCCCTTAAGAA---TTTGT	1628
Db	1318	GGGATGCGCGGCTTACGGCGGTGACCTTAAATTCGGCCCCGTGCTTAAAGAACTTGGGT	1377

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      1629  TGTGGAGAGCTGTATATACCAATGCGCTAGCGCATTTGGAGTTTAAAGTT 1679
      1378  ATGGGAAAGCTTATACACCAATGCTGTATGTGTGTTTGTGTGGTT 1428

RESULT 7
US-09-313-294A-1966
; Sequence 1966, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Laljudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 1966
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700551823H1
; NAME/KEY: unsure
; LOCATION: 256
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-1966

Query Match          7.9%; Score 153; DB 4; Length 291;
Best Local Similarity 71.3%; Pred. No. 3e-25;
Matches 201; Conservative 0; Mismatches 81; Indels 0; Gaps 0

Qy      1198  CCTCTTTAGTGTCTGCTGCCAAATTGGCGCTGAGAGGGTATATGTTGTGCTGTAG 125
Db      2      CCGGTGCTGTGTGCTTCCCTGCGCAATTGGTGGGAGAGGGTCCGTTTGTGCTTTGAG 61
Qy      1258  CTTTGCTGTGTGCTTCATCCAGACATTCAGTTCGTGTTGAATCACTTTGCTGCAATGT 131
Db      62      CTTACCACTGCGGGGATTCAGACAGTCCAAATTCCTGCAACCACTTCGTCGAGCT 121
Qy      1318  ATATGTCGGGCAACCGAGTGGGAATGACTGTGTTGAGAAAGCAGACAGATGGTACATTGGA 137
Db      122  GTATGTCGGGCAACCGAGGCAATGACTGTGTTGAGAAAGCAGACAGGCAAGCCTGCA 181
Qy      1378  TATCTCTGTGCTCTTCGATGATGTGTTTGTGCGTGTGACAGTTTCAGCTTGAGCA 143
Db      182  CATCTGTGCTCTCTCTTGATGATGTGTTTCCAGGCTGCGCTGCAAGTTGAGCA 241
Qy      1438  TCATTTGTTTCCAAAGCTACTCGGTGCCAATTGAGAAAT 1479
Db      242  CCATCTGTTCCTCCNCCCTACTAGGTGCACCTCGTAAGTT 283

RESULT 8
US-09-313-294A-3256
; Sequence 3256, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Laljudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 3256
; LENGTH: 266

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Query Match          3.4%; Score 65.4; DB 5; Length 1813;
Best Local Similarity 78.8%; Pred. No. 1.5e-05;
Matches 78; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy      1836  TGCAGTTATATGCTTGTCATCATACAAATTCATATCATGTATATGCCAAAAAAAAAAAAA 1895
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1706  TCCTCTTCTCTGCTTTATTTAATTAATAAACTAATAAACAGAAAAAAAAAAAAAAAAAA 1765
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

Qy      1896  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1934
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1766  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1804
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 11
US-09-482-273-31
; Sequence 31, Application US/09482273

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Patent No. 6534631
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: P2030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,922
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 31
LENGTH: 931
TYPE: DNA
ORGANISM: Homo sapiens
US-09-482-273-31

Query Match 3.3%; Score 64.6; DB 4; Length 931;
Best Local Similarity 67.4%; Pred. No. 1.8e-05;
Matches 91; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1800 GTGTGCTGTAACAATGATGTGATCCAGATGTACTGCAATTCATGCTTGTGATCA 1859
DB 783 GCGGGGGGTGGGGGGGTATCCAGATGTGTAATTCATTCATTCATTCATTCATTCAT 842
QY 1860 TACAATTCATCATCATGATGATCCAAAAA 1919
DB 843 CACAAACAGACCTCAA 902
QY 1920 AAAAAAAAAAAAAAAAAA 1934
DB 903 AAAAAAAAAAAAAAAAAA 917

RESULT 12
US-08-821-994-59
Sequence 59, Application US/08821994A
Patent No. 6228643
GENERAL INFORMATION:
APPLICANT: Greenland, Andrew J
APPLICANT: Thomas, Didier RP
TITLE OF INVENTION: Promoters
FILE REFERENCE: PPD 50108
CURRENT APPLICATION NUMBER: US/08/821,994A
CURRENT FILING DATE: 1997-03-22
EARLIER APPLICATION NUMBER: PCT/GB97/00729
EARLIER FILING DATE: 1997-03-18
EARLIER APPLICATION NUMBER: GB 9606062.9
EARLIER FILING DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 59
LENGTH: 1577
TYPE: DNA
ORGANISM: Brasica napus
US-08-821-994-59

Query Match 3.3%; Score 64.2; DB 3; Length 1577;
Best Local Similarity 64.4%; Pred. No. 2.6e-05;
Matches 96; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1786 TAACTTTTGTAGTGTGCTGTAACAATGATGTGATCCAGATGTACTGCAATTCAT 1845
DB 1428 TGATTTACTTATTAAGCTGTGTTGGAATATGATATAGTCTTATTTGATGATATACA 1487
QY 1846 GTGCTTGATCAATACAAATTCATCATGATGATCCAAAAAAAAAAAAAAAAAAAAA 1905

DB 1488 AACTTTGATTCATAAAGGTACTTGACGACACATTAATAAAAAAAAAAAAAAAAAA 1547
QY 1906 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1934
DB 1548 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1576

RESULT 13
US-09-360-545-66
Sequence 66, Application US/09360545
Patent No. 6429014
GENERAL INFORMATION:
APPLICANT: Crocneau, Rodney B
APPLICANT: Bohlmann, Jorg
APPLICANT: Steele, Christopher L
APPLICANT: Phillips, Michael A
TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
FILE REFERENCE: wu13885
CURRENT APPLICATION NUMBER: US/09/360,545
CURRENT FILING DATE: 1999-07-26
EARLIER APPLICATION NUMBER: 60/052,249
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: PCT/US98/14528
EARLIER FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 66
LENGTH: 2186
TYPE: DNA
ORGANISM: Abies grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (34)..(1923)
US-09-360-545-66

Query Match 3.3%; Score 64.2; DB 4; Length 2186;
Best Local Similarity 60.7%; Pred. No. 2.9e-05;
Matches 105; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1762 CTTTCAGATGGCTTTGAATTTAATTTTGTAGTGTGCTGATCAAAATGATGCT 1821
DB 1978 CATGTCATGCTCTGATGATTAAGTGTATGCGGTGATGATTAATAATGAGGT 2037
QY 1822 GATCCAGATGTACTGCAATGATGCTTGTGATCAATCAAAATTCATGATGCT 1881
DB 2038 TACTCGTCTCTCATGATGATGATGAGTGTGCAAAATTCCTCAAAAAAAAAA 2097
QY 1882 CAAA 1934
DB 2098 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2150

RESULT 14
US-08-451-405A-2
Sequence 2, Application US/08451405A
Patent No. 5736358
GENERAL INFORMATION:
APPLICANT: FASEL, NICOLAS JOSEPH
APPLICANT: REYMOND, CHRISTOPHE DOMINIQUE
TITLE OF INVENTION: DICTYOSTELID EXPRESSION VECTOR AND
TITLE OF INVENTION: METHOD FOR EXPRESSING A DESIRED PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE WEBB LAW FIRM
STREET: 700 KOPPERS BUILDING, 436 SEVENTH AVENUE
CITY: PITTSBURGH
STATE: PENNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 15219-1818
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK
COMPUTER: Midwest Micro 486-50

OPERATING SYSTEM: DOS
 SOFTWARE: WORDPERFECT 6.1
 CURRENT APPLICATION DATA: 6.1
 APPLICATION NUMBER: US/08/451.405A
 FILING DATE: 26-MAY-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/965,273
 FILING DATE: 15-JAN-1993
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 731
 TYPE: NUCLEIC ACID
 STRANDEDNESS: SINGLE
 TOPOLOGY: UNKNOWN
 US-08-451-405A-2

Query Match 3.3%; Score 64; DB 1; Length 731;
 Best Local Similarity 55.6%; Pred. No. 2.3e-05;
 Matches 148; Conservative 0; Mismatches 110; Indels 8; Gaps 1;
 Oy 1669 TTTTGAAGTTAGGATTTTGTCAAGTCTTTTGTGTTTCTTTAAAGAA 1728
 Db 51 TTGATTTAGTATGTTTTTTTCTTTTATTTTATTTTATTTTAAAAA 110
 Oy 1729 AAAAAATCTCATGTGATTTTGTCAAGCCCATTTCCAGATTGGCTTGAATTAA 1788
 Db 111 TAAAAATTAAGATTAATAATTTT-----CTATTGAAGAGATTATTTTATTTAA 162
 Oy 1789 CTTTGTAGGTGTGTGTACAAATGATGTGATCCAGATGTACTGCAATTGATGTG 1848
 Db 163 AATTATATTAAACATAGTGAACCTAAATAGATTGTGACGATATATGATAGAAATT 222
 Oy 1849 CTTTGCAATCAATCAATTCATATCATGTATGCCAAAAAATTTTAAAAA 1908
 Db 223 CTAATAAATAAATTCAGATTAATTTTGGATTGGAACAACAAAAAATTTTAAAAA 282
 Oy 1909 AAAAAAATTTTAAAAAATTTTAAAAA 1934
 Db 283 AAAAAAATCAAAAAAATTTTAAAAA 308

RESULT 15
 US-09-073-569-1
 Sequence 1, Application US/09073569
 Patent No. 6084088
 GENERAL INFORMATION:
 APPLICANT: Sheppard, Paul O.
 APPLICANT: Grossmann, Angelika
 TITLE OF INVENTION: NOVEL TUMOR ANTIGENS
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZymoGenetics, Inc.
 STREET: 1201 Eastlake Avenue East
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/073,569
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Sawiak, Deborah A
 REGISTRATION NUMBER: 37,438

REFERENCE/DOCKET NUMBER: 97-14
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6672
 TELEFAX: 206-442-6678
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1733 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURES:
 NAME/KEY: Coding Sequence
 LOCATION: 34...1344
 OTHER INFORMATION:
 US-09-073-569-1

Query Match 3.3%; Score 64; DB 3; Length 1733;
 Best Local Similarity 73.2%; Pred. No. 3e-05;
 Matches 82; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
 Oy 1823 ATCCAGATGTTACTGCAATTCATGTCTTGCATCAATCAAAATTCATATCATGTATGCC 1882
 Db 1573 ATGTATCTGATTAATACAGACCTGTCTTCTCCAAAAAATTTTAAAAA 1632
 Oy 1883 AAAAAAATTTTAAAAAATTTTAAAAA 1934
 Db 1633 AAAAAAATTTTAAAAAATTTTAAAAA 1684

Search completed: January 1, 2004, 00:05:29
 Job time : 98.9683 secs

Qy	31	GGTTGTGGAAGAGGAAGTGCATPACTCAGAGAGCTGAAGGTACACAAGGA	369
Db	3	GGCGAAGAGACGGAGAAAAGTACATTACAGACGAAGCTTAAAAACACACAAATTC	62
Qy	370	GGGAGATTATGATCTCAATTCAAGTAAAGGTGTACATGTCTCAGATTGGGTCAAGA	429
Db	63	TGAGATCTATGATTCGGGATTCAAGGCACAGTCTTCAACAGTCTCGGATTGGATTAAAC	122

QY 430 GCAACCTGTGTGATGTTCCAACTTCTGAGGAGATGTCATGAT 489
 DB 123 TCATCCCGAGGCGACACGGTGTCTCAATCTGTGTGTCAGACGTCCATGCTTT 182
 QY 490 CATAGCATACCATCTGGACACAGATGTCACACCTTGAAATTTCTCACTGGCTACA 549
 DB 183 CATGACATTTCAATCCGGAAACGGCTTGGACACATCTGCACCATCTTCAACGGTTACA 242
 QY 550 CCTCAGTACTTCAAGGTCCTGAGGTGTCGAAAGATACAGAAAGTTTCATCTGATG 609
 DB 243 CATCAGAGATTTCCAAATCTCCGAAAGTCTACGGGATTTACCGTGTGATGCGAGTT 302
 QY 610 CTGAAATTTGGTCTTTTGAACCAAGGAGATGTCATCTTCACTGACCTTGCATCTGT 669
 DB 303 TCGTAACCTGGTCTCTTCAAAAACAAAGTCACTTACTCTACACTCTTACCTTCTGT 362
 QY 670 TGCTGTATGTTCTCTCAATGTAATGATGTTCTGAGTGTCACTAGTGTGGCTCA 729
 DB 363 CGCGCGCATGTTCTCGGAGTGTCTAGGGTGTGTTGGCTGTATCCTCGCTTCTGCTCA 422
 QY 730 TTGGGTTGAGGATGCTCTTAGGGTCTTGGATGCAAAAGTCTTATGTGGCCATGA 789
 DB 423 CCAAAATCGCGCGCTCTCGCTCTCTGATCCAGAGCGCTTACATAGGTCAAGA 482
 QY 790 TTCTGGCCATATGTGTGTAACAACCAAGTGTCAACAAGTGTGACAGATCTCTC 849
 DB 483 TTCTGGCATTTAGTTATCTGTCGAAACAAATCTTAAACAGATTCGCTCAAGCTTCTCTC 542
 QY 850 TGGGAATGCTTGAACCGGAGTAAGCATTTGTTGTGAGAGTGAAGTCAACATGCTCA 909
 DB 543 CGGTAACTGTCTACCGGAATCTCAATCGGTGTGAAATGAGCTCAATGCTCATCA 602
 QY 910 CATGTGTCGAACAGCTTGAACCATGACCTGATCTGACAGACATGCGGTCTTGTGAGT 969
 DB 603 TCTAGCTTGAACAGCTTCAATCAAGTCAAGATCTCAACACATCTCTCTCGCGCT 662
 QY 970 TTGTGCGGCTTCTCAATTCATTAACCTCTCATTTCTATGGGAGAAATGAGTTGA 1029
 DB 663 CTCACCAAAATTTCTTCTCTCATTTGACCTTGAAGATTTTACATGCGAACTCACGTTTGA 722
 QY 1030 TTTCATTTGCTAGTGTCTGATCTGCTCAACAGACTTTTACTTTTACCAGGTAATGTGT 1089
 DB 723 TCAGATGCGAGATTTCTAGCTATCAACACTTTACTATATATCAGTATATGTCTT 782
 QY 1090 TGCAGAGGTCAACTGTATCTGACAGAAATTTGCTATTTTTCAGAGGAAAGTGA 1149
 DB 783 TGGAAAGATCAATCTCTTCAATCAAAAGTTCCTTCTCTCCAAAGTGAAGTACC 842
 QY 1150 GGATAGAGCTTGAACATTAAGGGGATCTGTGTTTGTGAGATTTGCTCTCTTGTAGT 1209
 DB 843 AGATCTGCTTTAACTTCCCGGAACTTATGCTTGTGAGCTTGTCCACTTGTAGT 902
 QY 1210 GTCTTGTCTGCAAAATTTGCTGAGAGGTTATGTTGCTTGTCTGCTAGTTTGTCTTTG 1269
 DB 903 CTATGCTTCAAAACGCTGAGATTTCTTCTTGTCTTCAACAAGCTTCAACCGTCA 962
 QY 1270 TTCCATTCAGACATTCATTTGTTGAATCACTTTGCTGCAATGTATATGTGGGCC 1329
 DB 963 GGGGCTTCAACACATTCATTTCAAGCTTAACTTTGCTGATGATTTCAAGTGTGCTC 1022
 QY 1330 ACCGAGTGGGAATGAGCTGTTTGAAGAGACAGAAAGTGTGAACTTGTATCTTGTGTC 1389
 DB 1023 ACCACCGGAGGAGCTGTTTGAAGAGCAAGCGCGGAAACATTCATTTCTTGTAG 1082
 QY 1390 CTCTTGATGATGATGTTTTCGTTGCTTGAAGTTCAGTTTCACTTGAAGCATATTTGTTCC 1449
 DB 1083 ATCATATCATGATGATGTTTCTTGTGATTAACGTTTCACTTGAAGCATATTTGTTCC 1442
 QY 1450 AAGGCTACTGAGTCAATTTGAAGAAAGATTTGCTTGTGATGATCTTTGCAAGAA 1509
 DB 1143 TCGCTTACTGTTGCTATCTCGGAAAGTTCCTCGGTGTGTTCAAGAGCTTTGCAAGAA 1202

QY 1510 GCATTAATTTGCTTATAGAGAGCTTGTCTATTTTGGAGGCCAATCAGTGAACATTTAGAC 1569
 DB 1203 GCATTAATTTTCCGTATATAGAGATGTGTGTGTTGAAGCAAAATGTGTGACATTTAACAC 1262
 QY 1570 CTTGAGGACTGTGCTTACAGCTTACAGCTTAAACAAACCTTGGCCCTTAAGATTTGTT 1629
 DB 1263 TTTGAAGACAGAGCTTATATCACTAGACAGCTGCTTAAATCCGTGTGTTAAGAACTTGT 1322
 QY 1630 GTGGAAAGCTGTATATACCATGCTGA 1657
 DB 1323 TTGGAGACTTTGAATATCTATGCTTA 1350

RESULT 2

US-10-029-756-4

Sequence 4, Application US/10029756

Publication No. US20020108147A1

GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.

TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A

DELTA 6-DESATURASE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/029, 756

FILING DATE: 21-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934, 254

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Presser, Leopold

REGISTRATION NUMBER: 19,827

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1685 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-029-756-4

Query Match

Best Local Similarity 66.5%; Pred. No. 2,9e-136;

Matches 886; Conservative 0; Mismatches 446; Indels 0; Gaps 0;

QY 326 AAGAAGTACATTAACCTGACAGAGCTGAAAGGTCACACACAGAGGAGATTTATGATC 385
 DB 59 AAGAATATACATTAACCTGACAGATGAATCAAGAACACAGATTAACCCGAGATCTATGATC 118
 QY 386 TCAATTCAGAGTATGATGATATGCTGATGTTGATGATGATGATGATGATGATGAT 445
 DB 119 TCATTCAGAGGAAACCTATGATGTTGATGATGATGATGATGATGATGATGATGAT 178
 QY 446 GTTCCATCTCAAACTTGTGCTGCGAGATGTCATGATGATGATGATGATGATGATGAT 505

Db 179 TTTCCTTGAAAGAGCTTGCTGCTCAAGAGTAACAGATGATTTGTCATTCATCCT 238
 QY 506 GGCACAGCATGTCACACCTTGAAATTTCTTCACTGCTACCACTGATGACTTCAAG 565
 Db 239 GCCTTACATGGAAGATCTTGATTAAGTTTTCACCTGGGATTAATCTTAAGATTTCTCT 298
 QY 566 GTCTCTGAGGTGTCAGAAAGCTACAGAAAGCTTGATCTGAGTTCTCAAAATTTGGTCTT 625
 Db 299 GTTCTGAGGTTTCTAAAGATTAAGAGAGCTTGTTGATGATTTCTAAATAGGGTTTG 358
 QY 626 TTGGAACCAAGAGGATGTCATTCATGACCCCTTGACCTGTGCTGTATGTTCTTC 665
 Db 359 TATGACAAAAAGATCATATTAATGTTGCAACTTTGTGCTTTATGACAAAGCTGTGCT 418
 QY 686 ATGTACTCATGCTGTTGAGTGCACACTAGTGTGGGCTGATTTGGGTTGAGGATG 745
 Db 419 ATGAGCTTTATGGGTTTGTGTTGAGGGGTTGTTGATACATTTGTTCTGGGCTG 478
 QY 746 CTCTTAAAGGTTGCTTGATGCAAGTGTCTTATGTGGCCATGTTCTGGCCACTATGTG 805
 Db 479 TGTATGGGGTTTCTTGGATTCAGAGTGGTTGATTTGACATGATGCTGGGCAATTATAG 538
 QY 806 GTTATGACCAACATGTTTCAACAAGGTTGCAAGATCTCTCTGGGAACTGCTTGACC 865
 Db 539 GTAGTGTCTGATTCAGAGGCTTAATTAAGTTATGGGTAATTTGCTCAAAATGCTTTCA 598
 QY 866 GGGATAGCATGCTTGAGTGAAGTGAAGTCAACATGCTCAGCAATGCTGCAACAGC 925
 Db 599 GGAATTAAGTATGTTGGTGAAGTGAAGTCAACATGCAATGCAATGCTGTTAATAGC 658
 QY 926 CTTGACATGACCCCTGATCTGACGACATGCGGCTTTGCACTTTGCTGCGGCTTCTTC 985
 Db 659 CTGGAATGATGACCCCTGATTTACATATATATATCATCTCTGTTGCTGCTTCAAGTTT 718
 QY 986 AATTCCATACTCTCAATTTCTATGAGAGAGTTGAGATTTGATTTGATGCTAGGCTTC 1045
 Db 719 GGTTCACATCACTCTCAATTTCTATGAGAAAGTTGACCTTTGATCACTTTATCAAAATTC 778
 QY 1046 TTGATGCTGACAGCACTTACTTTTTCACCGGTATGTTGCTGCGGCTGCAACTTG 1105
 Db 779 TTGTGAAGTATTAACAATGAGACATTTTACCTATTAATGTGCTGCTGAGGCTCAATATG 838
 QY 1106 TATCTGACAGCAATTTGCTATATGTTTTCAGAGCGCAAAAGTGCAGATAGAGCTTGAAC 1165
 Db 839 TATGTACATCTCTCATATATGTTGTTGACCAAGAAATGTCTATGAGCTCAGGAA 898
 QY 1166 ATTAATGGAGATCTTGTGTTTGAAGTGTGCTCTTTTATGTTGCTGCTGCAAT 1225
 Db 899 CTCTTGGAGATGCTGATGTTCTGATTTGGTACCCGTTGCTGTTCTTGTGTTGCCAAT 958
 QY 1226 TGGCCCTGAGAGGTTATGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1285
 Db 959 TGGGGTGAAGAAATTAATGTTTGTATTTGCAAGTTTATCACTGATGCAAGCAAGAT 1018
 QY 1286 CAGTTCTGTTTGAATCACTTTGCTGCAAAATGATATGTGCGGACACCGAGTGGAAATGAC 1345
 Db 1019 CAGTTCTGCTGCAACATTTCTTCAAGTGTATGTTGAAAGCTTAAAGGAAATTAAT 1078
 QY 1346 TGGTTTGAAGAGCAACAAGTGTATGATATCTCTTGTGCTCTTGTGATGATGATG 1405
 Db 1079 TGGTTTGAAGAAACAACAAGTGTGAGACATTTCTTGTCTCTCTGCTGATGATGATG 1138
 QY 1406 TTTTGTGGTGGCTTGAGATTTGAGATCACTTTGTTTTCAGAGGCTACTCGGTGC 1465
 Db 1139 TTTCAATGAGTGAATTTCAATTTGCAATTTGACATCAATTTGTTTCCAAAGATCTGATG 1198
 QY 1466 CAATTGAGAGAAATTTGACCTTTGTTAGTGAACCTTTGCAAGAAATTAATTTGCTTAT 1525
 Db 1199 AACCTTAGAATAATCTGCGCTTACGATGATGATGATGATGATGATGATGATGATGAT 1258
 QY 1526 AGGAGCTTGTCAATTTGGAGGCAATCACTGACAAATTAAGCACTCTGAGAGCTGTGCTC 1585
 Db 1259 AATTATGATCTTCTTCCAAAGGCAATGAATGACACTGAGAACATTTAGGAGAACAGCA 1318

QY 1586 CTACAGCTAGGAGACTTAACAACCTGCGCCCTAAGAAATTTGTTGGAGAGCTGTTAT 1645
 Db 1319 TTGACAGCTAGGAGATTAACAAGCCGCTCCGAGAAATTTGTTAGGAGAGCTTTTAC 1378
 QY 1646 ACCATGCTGA 1657
 Db 1379 ACTCATGTTAA 1390
 RESULT 3
 US-10-029-756-26
 ; Sequence 26, Application US/10029756
 ; Publication No. US20020108147A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; DELTA 6-DESATURASE
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/029,756
 ; FILING DATE: 21-Dec-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/934,254
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; REFERENCE/DOCKET NUMBER: 83832YXWVU
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1702 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 48..1406
 ; NAME/KEY: CDS
 ; LOCATION: 48..1406
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 ; US-10-029-756-26
 Query Match 28.7%; Score 555; DB 14; Length 1702;
 Best Local Similarity 64.8%; Pred. No. 3, 3e-121;
 Matches 889; Conservative 0; Mismatches 470; Indels 12; Gaps 4;
 QY 321 AGAGAGAAAGTATCACTCAAGAGAGCTGAGAGGTCACAACAAGAGAGGATTTAT 380
 Db 58 AAGCTTAGAAGTATCAAGAGAGGAGACCTCGCCGCAACAACAAGTCCGGGATCTCT 117
 QY 381 GGAATCTCAATTAAGTATGATCAATGCTCAAGATTTGGTCAAGAGCAACCTGTG 440
 Db 118 GGAATCTCAATCAAGGCAAGTCTACGACTGCTGCTGGTGGGCGGAGACACCCGGGG 177

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Qy 441 GTGATGTTCCAACTCTCAAACTTGTGCTGGCCAGATGTCATGATGATTCATAGCATACC 500
Db 178 GCGAGGTCCTGCTCTCAAGTCGTGGCCGCGCAGAGCTCACCGAGCCCTTCAATTCGTAAC 237
Qy 501 ATCTGGCAGCAGATGTCACACTTGGAAAATTTCTACTGG--CTACCACTCATG 557
Db 238 ACCGGGCGACGGCGTGGCGGATCTGATCCGCTTTCACCGGACTACTACTCAAG 297
Qy 558 ACTTCAAGTCTCTGAGTGTCCAAAGATCAGAAAGCTTGATGATCTGAATCTCAAAAT 617
Db 298 ACTTCGAAGTGTGGAATCTCCAAAGACTACCGAGGCTTTTGAACGAATGTGCGGT 357
Qy 618 TGGGCTTTTTCACCAAGGCGATGTCATTCATGACACCTTGCATCTGTGCTGTA 677
Db 358 CCGGAACTTCGAGAAAGAGGCGCACCACTCATGATGAGTTCTGTGGGCTTGGCTCA 417
Qy 678 TGTTCCTCATTTACTCTATGTTGTTCTGAGTGCATGATGTGTGGCTCATTTGGGTT 737
Db 418 TGATGGCGCAATGCTTACGCGGTCTGGGCTCGAGTCCGAGTTCACATGCTCT 477
Qy 738 CAGGCAATGCTTGAAGTGTCTTGTGATGCAAGTGTGATGAGGCGATGATTTGGCC 797
Db 478 GCGGCGCATGCTGGGCTTGTGATGCAAGCGGATGTGGGCGCATGACTCCGGCC 537
Qy 798 ACTATGTTTATGACAAACCAATGTTTCAAGGTTGACAGATCTCTCTGGGAACT 857
Db 538 ATTCACAGTGTATGCAACCGCGTGTATACAAAGATCAGCACTATAGCAGGCAACA 597
Qy 858 GCTTGAACCGGATTAAGCATGCTTGTGTGAGTGAAGTGAACATGCTCACCAATTCGT 917
Db 598 TCCTAACCGGAATCAGATCGCGGTGGAGTGAAGTGAACCAACGCGCAACCTGCGCT 657
Qy 918 GCAACAGCTTGAACATGACCTGATGTGAGCAGATGCGGCTTGTGCACTTTCGTCGC 977
Db 658 GCAACAGCTTGAACATGACCTGATGTGAGCAGATGCGGCTTGTGCACTTTCGTCGC 977
Qy 978 GATTTCTTCAATTCATTAACCTCTCATTTATGAGGAGAAAGTTGATTTGATTTATG 1037
Db 718 GACTCTTCAATTCATTAACCTCTCATTTATGAGGAGAAAGTTGATTTGATTTATG 777
Qy 1038 CTAGGTTCTTGAATCTGCTACAGCACTTATTTTACCGGATTAAGTGTGTGCCAGG 1097
Db 778 CAGGTTCTTGAATCTGCTACAGCACTTATTTTACCGGATTAAGTGTGTGCCAGG 837
Qy 1098 TCACATTTGATCTGCAACAATCTGCTATTTTGTGAGGCGCAAAAGTGCAGATAGAG 1157
Db 838 TCACATTTGATCTGCAACAATCTGCTATTTTGTGAGGCGCAAAAGTGCAGATAGAG 897
Qy 1158 CTTTGAACATTAATGAGGATCTTGTGTTTGAACCTTGTCCCTCTTTTATGTTGCTGCC 1217
Db 898 CTCTAAACTTAATGAGGATCTTGTGTTTGAACCTTGTCCCTCTTTGTATCTTGTTC 957
Qy 1218 TGGCAATTTGAGGCTGAGAGGATTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1277
Db 958 TCCGAACTGAGGCTGAGAGGATTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1017
Qy 1278 AGACATTCAGTTCTGTTTGAATCATTGCTGCAATGATATGTGTGCGCCACCGAGTG 1337
Db 1018 AGACATTCAGTTCTGTTTGAATCATTGCTGCAATGATATGTGTGCGCCACCGAGTG 1077
Qy 1338 GGAATGCTGTTTGAAGAGCAGACAGTGTACATGATGATCTCTGTCCTCTTGA 1397
Db 1078 GGAATGCTGTTTGAAGAGCAGACAGTGTACATGATGATCTCTGTCCTCTTGA 1137
Qy 1398 TGAATGTTTTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1457
Db 1138 TGAATGTTTTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1197
Qy 1458 CTGCGTGCATTTGAGGAGATTTGCGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1517
Db 1198 CTGCGTGCATTTGAGGAGATTTGCGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1257

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Qy 1518 TGGCTTAATAGAGCTTGTGATTTGG---GAGGCCAATGATGACAAATTAGAACCTTCA 1574
Db 1258 TGGCTTAATAGAGCTTGTGATTTGG---GAGGCCAATGATGACAAATTAGAACCTTCA 1317
Qy 1575 GGAATGCTGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGA 1628
Db 1318 GGAATGCTGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGA 1377
Qy 1629 TGTGGAAGCTGTTAATACCATGCTGAGGAGCTTGAAGAGCTTGAAGAGCTTGAAGAG 1679
Db 1378 ATGGGAAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGA 1428

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RESULT 4

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US-09-770-149-494/c
; Sequence 494, Application US/09770149
; Patent No. US200205963A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Moessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davies, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,506
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 494
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-149-494

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Query Match 13.9%; Score 269.4; DB 9; Length 657;
Best Local Similarity 67.2%; Pred. No. 1,2e-53;
Matches 381; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

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Qy 1152 ATGAGCTTGAACATTAATGAGGATCTGTTGTTTGAACCTTGTCCCTTTTATGTT 1211
Db 657 ATGAGCTTGAACATTAATGAGGATCTGTTGTTTGAACCTTGTCCCTTTTATGTT 598
Qy 1212 CTGCTGCAATTAATGAGGATCTGAGAGGATTAATGTTGCTGCTGCTGCTGCTGCTGCT 1271
Db 597 CATGCTTACCAATGAGGATCTGAGAGGATTAATGTTGCTGCTGCTGCTGCTGCTGCTGCT 538
Qy 1272 CCATCCAGACATTCAGTTCTGTTTGAATCATTGCTGCAATGATATGTGCGCCAC 1331
Db 537 CGCTTCAACATTCATTCAGCTTACCAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 478
Qy 1332 CGAGTGGATGATCTGTTTGAAGAGCAGACAGATGCTATGATGATCTTGTGCGCT 1391
Db 477 CCACCGTGGAGCTGTTTGAAGAGCAGACAGATGCTATGATGATCTTGTGAGAT 418
Qy 1392 CTTCGATGATGATGTTTTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1451

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Db 417 CATACATGATGGTGTCTTGTGATGATTAAGATTGACGTTGAGCATCATTTGTCCTC 358
Qy 1452 GGGTACCTGGTGGCCATTTAGAGAAATTTCCCTTTGTTAGTACCTTTGCAAGAAC 1511
Db 357 GCTTACCTGCTGGCCTCCGGAAGATTTCTCGGGGTTTCAAGACCTTTGCAAGAAC 298
Qy 1512 ATATATTCCTTATAGAGAGCTGTCATTTTGGAGGCCATTCAGTGAATTTAGAACCC 1571
Db 297 ATATATTCCTTATAGAGAGTATGTCGTTTGAAGCAATTTGTTAGACCTTTTACCTT 238
Qy 1572 TCAGAGCTGCTGCTCAAGAGCTTAAGGACCTTAACAAACCTGCTTACAGATTTGTTG 1631
Db 237 TGAAGACAGAGCTTATCAAGAGCTAGAGACGTCGCTATCCGGTGTGAAGACCTGGTTT 178
Qy 1632 GGAAGCTGTTATACCAAGCTGAGGAGCATTTGAGTTTATAGATTGATTTGTC 1691
Db 177 GGAAGCTTGAATACCATGCTTAATGATTTTAAACAAATATGCTTTGTTT 118
Qy 1692 AAGTCTTTTCTTTTCTCT 1718
Db 117 GGGTAAATTTGATGCTGTTTAT 91

RESULT 5

US-09-878-574-15653
; Sequence 15653, Application US/09878574
; Patent No. US2002010548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21 (15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 15653
; LENGTH: 267
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701070356H1
US-09-878-574-15653

Query Match 13.2%; Score 256; DB 10; Length 267;
Best Local Similarity 99.6%; Pred. No. 1,1e-50;
Matches 267; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 50 GGGTAAAGGGTATAGATCTTGAACAGATCAAAATCTGCTTATGGG 109
Db 1 GGGTAAAGGGTATAGATCTTGAACAGATCAAAATCTGCTTATGGG 60
Qy 110 TTGTGAAAAAACAATACATTTGTTGCTGTAAGGGGATTCCTTATGATTTG 169
Db 61 TTGTGAAAAAACAATACATTTGTTGCTGTAAGGGGATTCCTTATGATTTG 120
Qy 170 TTGTCATGAGAGAACAGATACCCATTTATGTTCTTATCATCTATCTAT 229
Db 121 TTGTCATGAGAGAA-ACCAGATACCCATTTATGTTCTTATCATCTATCTAT 179
Qy 230 TCTATTTATCTTCTTATTTAGTTCTCATTTGCTGATTTCAAGTATTTGTTGTTT 289
Db 180 TCTATTTATCTTCTTATTTAGTTCTCATTTGCTGATTTCAAGTATTTGTTGTTT 239
Qy 290 TTGTTAACAGAGATGAGGTTGTTG 317
Db 240 TTGTTAACAGAGATGAGGTTGTTG 267

RESULT 6

US-09-770-444-39
; Sequence 39, Application US/09770444
; Patent No. US20020023280A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maya
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurlan, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2027 (PARA-016PRV)
; CURRENT APPLICATION NUMBER: US/09/770,444
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,502
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(476)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-444-39

Query Match 10.7%; Score 206.4; DB 9; Length 476;
Best Local Similarity 65.5%; Pred. No. 9,1e-39;
Matches 300; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

Qy 458 AACCTGCTGCGCCAGATGCTAGTATGATTCATGATACCATCTGACAGCATGG 517
Db 18 AATCTGTTGGTGAAGACGTCACGATGCTTATGATTCATCCGGAAACGGTTGG 77
Qy 518 TCACACCTTGAATAATTTCTTACTGCTACACCTCAGTACTTCAAGTCTTGAGTG 577
Db 78 CACCATCTGACCATCTTCAACCGGTACACATCAGATTTCCAAAGTCTCGAATC 137
Qy 578 TCAGAGCTAGAGAGAGCTGATGATGCTCAAAATTTGGGCTTTTGAACCAA 637
Db 138 TCAGAGATTAACCGTGATAGTGTGCGAGTTGTAATCGGCTCTTGAACCAA 197
Qy 638 GGGCATGCTCATTCATGACACCTTGCATCTGTTGCTTATGTTCTCATTTACTAT 697
Db 198 GGTCAAGTTACTCTACACTGTAAGCTTGTCGCGCATGTTCTCGGAGTTCTTAC 257
Qy 698 GGTGTTCTGAGTGACATAGTGTGGGCTCATTTGGGTTCAAGCATGCTTAAAGGTTG 757
Db 258 GGTGTTTGGCTTGTACTCCGCTTCGCTACCAATGCGCCGCGGCTTCGCGTTC 317
Qy 758 CTTGATGCAAGAGCTTATGAGGCAATGTTCTGGCCATGAGTTGATGACAAC 817
Db 318 CTTGATGCAAGAGCTTATGAGTCAAGATTTGTCATTTACGTTATCATGATGAC 377
Qy 818 AATGTTTCAAGAGTTGACAGATCTCTGGAACCTGTTGACCGGATTAAGCAT 877
Db 378 AATCTTATTAAGATTCGCTGACGTTCTCTNNGTAACTGCTCACCGGAATCTAATC 437

Qy 878 GCTTGTGAAGTGGCTCACAATGTCACCAATTCG 915
 Db 438 GCGTGTGAATGACTCACAATGCTCATCATCTAGC 475

RESULT 7

US-09-878-574-3260
 ; Sequence 3260, Application US/09878574
 ; Patent No. US20020110548A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Byrum, Joseph R.
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Thompson, Michael D.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(15401)B
 ; CURRENT APPLICATION NUMBER: US/09/878,574
 ; PRIOR FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: 09/333,535
 ; PRIOR FILING DATE: 1999-06-14
 ; NUMBER OF SEQ ID NOS: 15775
 ; SEQ ID NO 3260
 ; LENGTH: 287
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION (1): (287)
 ; OTHER INFORMATION: unsure at all n locations
 ; OTHER INFORMATION: Clone ID: LIB028-013-Q1-B1-H6
 ; US-09-878-574-3260

Query Match 9.7%; Score 188.4; DB 10; Length 287;
 Best Local Similarity 78.4%; Pred. No. 1.3e-34;
 Matches 225; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 1183 GTTTGAGCTGTGCTCCCTCTTTAGTGTCTTGTGCTGCGCAATTTGCGTGAAGGCTTAT 1242
 Db 1 GTTTGAGCTGTGCTCCCTCTTTAGTGTCTTGTGCTGCGCAATTTGCGTGAAGGCTTAT 60
 Qy 1243 GTTTGCTGTGCTAGCTTTGCTGTTTGTTCATCAGACATTCAGTTCTGTTGAATCA 1302
 Db 61 GTTTGCTGTGCTAGCTTTGCTGTTTGTTCATCAGACATTCAGTTCTGTTGAATCA 120
 Qy 1303 CTTTGTGCAATATATATATGTCGCGCCACGAGTGGGAATATCTGTTTGAAGCAGAC 1362
 Db 121 TTTGCGACGATGTATATGAGGCCCAACCAATGGCAATGATGTTTGAAGCAAAC 180
 Qy 1363 AAGTGTACATTTGATATCTCTTGTGCTCTTCATGATGATTTTTCGTTGCTTGA 1422
 Db 181 TGTGTGCACTTGAACATCTTTTCTTCAATGATGATTTGTTTTCGTTGCTTGA 240
 Qy 1423 GTTTCACTTGAGCATATTTGTTTCCAAAGGCTACCTCGTGCAT 1469
 Db 241 ATTCACTTGAGCATATTTGTTTCCCTTANGCTCCCAAGCACAAT 287

RESULT 8
 US-09-924-035A-370/c
 ; Sequence 370, Application US/09924035A
 ; Patent No. US20020142319A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Grlach, Jm
 ; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 ; FILE REFERENCE: 2011US
 ; CURRENT APPLICATION NUMBER: US/09/924,035A
 ; PRIOR FILING DATE: 2000-08-11
 ; PRIOR APPLICATION NUMBER: US 60/148,784
 ; PRIOR FILING DATE: 1999-08-13
 ; NUMBER OF SEQ ID NOS: 900
 ; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 370
 ; LENGTH: 480
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-924-035A-370

Query Match 8.6%; Score 166.2; DB 10; Length 480;
 Best Local Similarity 67.4%; Pred. No. 3.2e-29;
 Matches 234; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

Qy 1372 ATTGATATCTCTTGGCCCTTTCATGATTTGTTTTCGTCGCTTGCATTTACGT 1431
 Db 480 AATCGATATCTCTTGGATATGATGATTTGTTTTCGTCGCTTGCATTTACGT 421
 Qy 1432 TGAGCATATTTTTCGAAGGCTACCTGCTGCAATTTGAGGAGATTTGCTTGT 1491
 Db 420 TGAGCATATTTTTCGCTGCTTACCTGCTGCAATTTGAGGAGATTTGCTTGT 361
 Qy 1492 TAGTACCTTTGCAAGAGCATATTTGCTTATAGAGCTTGTCAATTTGAGGCA 1551
 Db 360 TCAAGAGCTTTGCAAGAGCATATTTGCTTATAGAGATTTGCTTGTGAGCA 301
 Qy 1552 TCAAGAGCATATTTGAGGCTGCTGCAATTTGAGGAGATTTGCTTGTGAG 1611
 Db 300 TGTGTGACCATTTAGCATTTTGAAGAGCATTTATCAAGCTTGAAGAGCTGCTATTC 241
 Qy 1612 TGCCCTTGAAGATTTGTTGAGGAGCTTATATCCATGCTGAGGATTTGAGATT 1671
 Db 240 GGTGTTTGAAGATTTGTTGAGGAGCTTATATCTGATTTATATTTTATCA 181
 Qy 1672 TTAGATTTAGATTTTGTCAAGGCTTTTGTGTTTGTCTCT 1718
 Db 180 AACAAATATGCTTTTGTGTTGTTGTTTGAATTTGATTTGTTTAT 134

RESULT 9

US-09-878-574-9255
 ; Sequence 9255, Application US/09878574
 ; Patent No. US20020110548A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Byrum, Joseph R.
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Thompson, Michael D.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(15401)B
 ; CURRENT APPLICATION NUMBER: US/09/878,574
 ; PRIOR FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: 09/333,535
 ; PRIOR FILING DATE: 1999-06-14
 ; NUMBER OF SEQ ID NOS: 15775
 ; SEQ ID NO 9255
 ; LENGTH: 263
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; OTHER INFORMATION: Clone ID: 701102270H1
 ; US-09-878-574-9255

Query Match 8.1%; Score 156.2; DB 10; Length 263;
 Best Local Similarity 78.7%; Pred. No. 5.4e-27;
 Matches 199; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

Qy 825 TCAACAAAGTTGACAGATCTCTCTGGAAGTGTGACCGGAGTATGAGATTGCTTGT 884
 Db 12 TCAGCGGCTGAGCAATCTTTGTGCAATTTGCAATGCTGAGATGAGATTGCTTGT 71
 Qy 885 GGAAGTGAATCAATATGCTTACACATTTGCTGCAACAGCTTGAACATGACCTGATC 944
 Db 72 GGAAGTGAATCAATATGCTTACACATTTGCTGCAACATGATTTGATGATGATGAT- 130
 Qy 945 TGAGCATATGCGGCTTTTGAAGTTTGTGCGGCTTTCAATTTCAATTAACCTTAT 1004
 Db 131 TCAGCATATGCTTGTGCTTGTGCGGCTTGTGCAAGGCTTTCAATTAACCTTAT 190

QY 1005 TCTATGAGAGAGATTGAGATTGATTGCTAGTCTTGTGCTTACAGACT 1064
 |||||
 DB 191 TCTATGAGAGAGATTGAGATTGATTGCTATTCATCAAGCTTCTCATCAGCTACAGACT 250
 |||||
 QY 1065 TTACTTTTACC 1077
 |||||
 DB 251 TCACATCTTACC 263
 |||||

RESULT 10

US-09-923-876-5116
 ; Sequence 5116, Application US/09923876
 ; Patent No. US20020013958A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Laligudi, Raghunath V.
 ; APPLICANT: Kamigaki, Laura Y. (Ito)
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
 ; FILE REFERENCE: PL-0012-1 CON
 ; CURRENT APPLICATION NUMBER: US/09/923,876
 ; PRIOR FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: 09/298,329
 ; PRIOR FILING DATE: 1999-04-21
 ; PRIOR APPLICATION NUMBER: 60/085,331
 ; PRIOR FILING DATE: 1998-05-05
 ; NUMBER OF SEQ ID NOS: 6332
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 516
 ; LENGTH: 265
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20020013958A1 700456385H1
 ; US-09-923-876-5116

Query Match 4.9%; Score 94.8; DB 9; Length 265;
 Best Local Similarity 62.0%; Pred. No. 2e-12;

Matches 150; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 911 ATTGCTGCAACAGCTTGAACCATGACCTGATCTGAGACATGCGGCTTTGAGATT 970
 |||||
 DB 1 ATGCGCTGCAACAGCTTGAACCATGACCTGATCTGAGACATGCGGCTTTGAGATT 60
 |||||
 QY 971 TCGTGGGCTTCTCAATTCATTAACCTCTCATTTTCTAGGAGAGAGTTGAGTTGAT 1030
 |||||
 DB 61 TCCCAAGCTGTTGGGCAACATATGCTCTTCTACCAAGGAGACCTGCGCTTCGAC 120
 |||||
 QY 1031 TTCAATGCTAGGTTCTTGAATGCTGACCAAGCTTTACTTTTACCGGTAATGTGTT 1090
 |||||
 DB 121 GCCGCTCGAATTTCTCTCATCACTGACCAAGCTTCTTCAACCGGTAATGTGATC 180
 |||||
 QY 1091 GCCAGGTCACACTTGTATCTGACAGCAATTTCTCTATTTTTCGAGGCGAAAGTGAC 1150
 |||||
 DB 181 GCCAGATTAATCTTCTGCGGAGCGTCCGCTGTCTGTCTCTGACCAAGAGAGGTCGCG 240
 |||||
 QY 1151 GA 1152
 |||||
 DB 241 CA 242
 |||||

RESULT 11

US-09-923-876-5116
 ; Sequence 5116, Application US/09923876
 ; Publication No. US20030237110A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Laligudi, Raghunath V.
 ; APPLICANT: Kamigaki, Laura Y. (Ito)
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
 ; FILE REFERENCE: PL-0012-1 CON
 ; CURRENT APPLICATION NUMBER: US/09/923,876

; CURRENT FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: 09/298,329
 ; PRIOR FILING DATE: 1999-04-21
 ; PRIOR APPLICATION NUMBER: 60/085,331
 ; PRIOR FILING DATE: 1998-05-05
 ; NUMBER OF SEQ ID NOS: 6332
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 516
 ; LENGTH: 265
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030237110A9 700456385H1
 ; US-09-923-876-5116

Query Match 4.9%; Score 94.8; DB 12; Length 265;
 Best Local Similarity 62.0%; Pred. No. 2e-12;

Matches 150; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 911 ATTGCTGCAACAGCTTGAACCATGACCTGATCTGAGACATGCGGCTTTGAGATT 970
 |||||
 DB 1 ATGCGCTGCAACAGCTTGAACCATGACCTGATCTGAGACATGCGGCTTTGAGATT 60
 |||||
 QY 971 TCGTGGGCTTCTCAATTCATTAACCTCTCATTTTCTAGGAGAGAGTTGAGTTGAT 1030
 |||||
 DB 61 TCCCAAGCTGTTGGGCAACATATGCTCTTCTACCAAGGAGACCTGCGCTTCGAC 120
 |||||
 QY 1031 TTCAATGCTAGGTTCTTGAATGCTGACCAAGCTTTACTTTTACCGGTAATGTGTT 1090
 |||||
 DB 121 GCCGCTCGAATTTCTCTCATCACTGACCAAGCTTCTTCAACCGGTAATGTGATC 180
 |||||
 QY 1091 GCCAGGTCACACTTGTATCTGACAGCAATTTCTCTATTTTTCGAGGCGAAAGTGAC 1150
 |||||
 DB 181 GCCAGATTAATCTTCTGCGGAGCGTCCGCTGTCTGTCTCTGACCAAGAGAGGTCGCG 240
 |||||
 QY 1151 GA 1152
 |||||
 DB 241 CA 242
 |||||

RESULT 12

US-10-369-27824
 ; Sequence 27824, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052) B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; PRIOR FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 27824
 ; LENGTH: 1098
 ; TYPE: DNA
 ; ORGANISM: Neurospora crassa
 ; US-10-369-27824

Query Match 4.6%; Score 89.6; DB 12; Length 1098;
 Best Local Similarity 53.1%; Pred. No. 7.9e-11;

Matches 191; Conservative 0; Mismatches 169; Indels 0; Gaps 0;


```
US-09-814-353-11141/c
; Sequence 11141, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-0068
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11141
; LENGTH: 299
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 146, 163, 175, 190, 191, 192, 195, 198, 199, 201, 202, 203,
; LOCATION: 206, 213, 214, 217, 222, 224, 225, 226, 229, 232, 233, 239,
; LOCATION: 246, 247, 249, 254, 255, 256, 264, 268, 274, 284, 286
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-11141

Query Match          3.9%; Score 74.6; DB 13; Length 299;
Best Local Similarity 52.2%; Pred. No. 1.4e-07;
Matches 119; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 1707 TTGTTTCTCTTAAGAAAAAATCTCATGTGATTTGCTAGCCCACTTTT 1766
    |||||
DB 299 TTTTNTTTTNNAAAAAATTTTNNCCATTTTNNNTTTTNNNGATTTT 240
    |||||

QY 1767 CCAGATTGGGCTTGAATTTTCTTTGTTAGTGTGTGTAACAATGATGATCC 1826
    |||||
DB 239 NAAAAAANNCNTTNNNTTTTNTTNNTTTNNAAANNNGNATNANNNTTTT 180
    |||||

QY 1827 AGATGTACTGCATGTGCTTTGCATCAATACAAATTCATATCATGATGCCAAA 1886
    |||||
DB 179 TTTTNNAAAAAAGGATTTTNTTTTNTTNNAAAAAATTTTNTTTT 120
    |||||

QY 1887 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1934
    |||||
DB 119 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 72
    |||||
```

Search completed: January 1, 2004, 05:19:34
Job time : 484.374 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 16.9369 Seconds
(without alignments)
2555.128 Million cell updates/sec

Title: US-09-857-524B-8
Perfect score: 2449
Sequence: 1 MEVVEKEKKYITSEELKGNH.....RDLTPAPAKLMEAVVTHG 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r.76:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1943	79.3	449	2	hypotheetical prote
2	1902	77.7	449	2	delta-8 sphingolip
3	1887	77.1	449	2	delta-8 sphingolip
4	1801	73.5	458	2	delta8 sphingolip
5	684.5	28.0	523	2	linoeoyl-CoA desa
6	451.5	18.4	444	2	linoeoyl-CoA desa
7	441.5	18.0	444	2	linoeoyl-CoA desa
8	401	16.4	472	1	linoeoyl-CoA desa
9	373.5	15.4	447	1	linoeoyl-CoA desa
10	361	14.7	454	1	linoeoyl-CoA desa
11	221.5	9.3	345	2	proteain T13f2.1 [1
12	202.5	8.0	359	2	probable Deltae fa
13	189.5	7.7	368	2	Deltae fatty acid
14	180	7.3	365	2	linoeoyl-CoA desa
15	179	7.3	427	2	hypotheetical prote
16	159	6.5	982	1	probable dea33 pro
17	156.5	6.4	137	2	nitrate reductase
18	154.5	6.3	134	2	cytochrome b5 - r1
19	152.5	6.2	134	2	cytochrome b5 - w1
20	151.5	6.2	573	1	cytochrome b5 [imp
21	149.5	6.1	121	2	L-lactate dehydrog
22	149.5	6.1	134	2	probable Cytochrom
23	146.5	6.0	147	2	cytochrome b5 At2g
24	146	6.0	905	1	probable heme bind
25	144.5	5.9	139	2	nitrate reductase
26	144	5.9	134	1	cytochrome b5 - co
27	143.5	5.9	541	2	cytochrome b5, mic
28	143	5.8	120	2	hypotheetical prote
29	143	5.8	133	1	cytochrome b5 - ye

30	142.5	5.8	135	2	cytochrome b5 - co
31	140.5	5.7	140	2	cytochrome b5 [imp
32	140	5.7	370	2	conserved hypothe
33	139	5.7	141	2	probable cytochrom
34	137	5.6	112	2	cytochrome b5 - p1
35	137	5.6	926	1	nitrate reductase
36	136.5	5.6	98	1	nitrate reductase
37	136.5	5.6	129	2	cytochrome b5, ery
38	136	5.6	384	1	probable cytochrom
39	136	5.6	894	2	probable fatty aci
40	134	5.5	864	1	nitrate reductase
41	133.5	5.5	134	1	nitrate reductase
42	133	5.4	134	1	cytochrome b5, mic
43	133	5.4	211	2	cytochrome b5, mic
44	132.5	5.4	135	1	hypotheetical prote
45	131	5.3	134	1	cytochrome b5, out

ALIGNMENTS

RESULT 1									
A84900 hypotheetical protein At2g46210 [imported] - Arabidopsis thaliana									
C/Species: Arabidopsis thaliana (mouse-ear cress)									
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001									
C/Accession: A84900									
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N									
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.J.									
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.									
Nature 402, 761-768, 1999									
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.									
A/Reference number: A84420; MUID:20083487; PMID:10617197									
A/Accession: A84900									
A/Status: preliminary									
A/Molecule type: DNA									
A/Residues: 1-449 <STO>									
A/Cross-references: GB:AB002093; NID:G3702328; PIDD:AA062885.1; GSPDB:GN00139									
C/Genetics:									
A/Genes: At2g46210									
A/Map position: 2									
Query Match									
Best Local Similarity 79.3%; Score 1943; DB 2; Length 449;									
Matches 346; Conservative 41; Mismatches 59; Indels 0; Gaps 0;									
QY	5	EKEKKYITSEELKGNKGGDLWISIQKVVNSDVKENPGDVPISNLAGDVTDAFIA	64						
DB	4	QTKKRYVTSDDLKKNKPGDLWISIQKVVNSDVKENPGDVPISNLAGDVTDAFIA	63						
QY	65	YHGTAMSHLEKFTGTHLSDPKVSESKDYRLKLSFSLGLPDTKGYTSCILASVAV	124						
DB	64	YHGTAMSHLEKFTGTHLSDPKVSESKDYRLKLSFSLGLPDTKGYTSCILASVAV	123						
QY	125	MPILVLYGVLRCTSVMAHLASGMLGLIMQASVYVGDSDGHVYVMTNGNPKVAQILSGN	184						
DB	124	MLAAVLXGVLAQTSIRNAHLISAVLISLWIOSAVYVGDSDGHVYVMTNGNPKVAQILSGN	183						
QY	185	CLTGISIAWKKWTHNAHIAICNSLDHDPDLQHPVPVASSRFPNSITSHFVGRKLEDFI	244						
DB	184	CLTGISIAWKKWTHNAHIAICNSLDHDPDLQHPVPVASSRFPNSITSHFVGRKLEDFI	243						
QY	245	ARPLISYQHTTFYPVNCVGRINLFIQTFLLFSGKRAHPDALLIAGLVMTWTFPLLVSF	303						
DB	244	ARPLISYQHTTFYPVNCVGRINLFIQTFLLFSGKRAHPDALLIAGLVMTWTFPLLVSF	303						
QY	305	LPMWPERVMPVLASFVACSIOHIOFCINHPAAVYVGPSPGNDMPFKOTSGTIDISCASS	364						
DB	304	LPMWPERVMPVLASFVACSIOHIOFCINHPAAVYVGPSPGNDMPFKOTSGTIDISCASS	363						
QY	365	MDWFFGGLQOLBHHLPFRLPRCOLRKISPLVSLDCKKNLPRYSLSFWMEANQMTIRTLR	424						
DB	364	MDWFFGGLQOLBHHLPFRLPRCOLRKISPLVSLDCKKNLPRYSLSFWMEANQMTIRTLR	423						

QY 425 TAAQARADLTNPAPKNLWEAVNTHG 450
DB 424 NAAIQARDATNPVLKNLWEAVNTHG 449

RESULT 2

T47950
delta-8 sphingolipid desaturase (EC 1.14.99.-) [validated] - Arabidopsis thaliana
N.Altimate names: protein F2A19.180
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 20-Apr-2000 #sequence_rev1510 20-Apr-2000 #text_change 02-Sep-2000
C/Accession: T47950
R/De Haan, M.; Maarse, A.C.; Grievell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quest submitted to the Protein Sequence Database, January 2000
A/Reference number: Z24480
A/Accession: T47950
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-449 <DEH>
A/Cross-references: EMBL:AJ132962; PIDN:CA871088.1
A/Experimental source: cultivar Columbia; BAC clone F2A19
R/Sperling, P.; Zaehring, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A/Title: A sphingolipid desaturase from higher plants. Identification of a new cytochrome
A/Reference number: Z22986; MUID:99003197; PMID:9786850
A/Accession: T51848
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-449 <SPE>
A/Cross-references: EMBL:AJ224161; PIDN:CA11858.1
A/Experimental source: cultivar Columbia; mainly green parts, some flowers, few roots
C/Genetics: sld1
A/Map position: 3
A/Note: F2A19.180
C/Function:
A/Description: (EC 1.14.99.-); delta-8 sphingolipid desaturase [validated, MUID:99003197
C/Keywords: oxidoreductase, unsaturated fatty acid biosynthesis

Query Match 77.7%; Score 1902; DB 2; Length 449;

Best Local Similarity 74.9%; Pred. No. 3.9e-157;

Matches 334; Conservative 54; Mismatches 58; Indels 0; Gaps 0;

QY 5 EKEKKITSEELKGNKEDLWISIQKYYNVDWVKEHGGDVPISNLAGDVTDAFTA 64
DB 4 ETEBKITTEDLKKHNSGDLWIAIQKYYNVDWVKEHGGDVTILNLVGDVTDAFTA 63
QY 65 YHPTAMSHLEKFTGYHLSDFKVSSEVSKDYRKLAESFSLGLFDTKGHVTSCCTLASVAV 124
DB 64 FHPGTAMRHLDHLEFTGYHLSDFKVSSEVSKDYRKLAESFSLGLFDTKGHVTSCCTLASVAV 123
QY 125 MELIYVGLRCTSVWALHSGMGLGLMWQSAVYGHDSGHVYVMTNGFNKVAQILSGN 184
DB 124 MELIYVGLRCTSVWALHSGMGLGLMWQSAVYGHDSGHVYVMTNGFNKVAQILSGN 183
QY 185 CLTGSIAMWKTTHNHNHIAACNSLDHDPDLOHMPVAVSRRFNSITSHFYGRKLEFDFI 244
DB 184 CLTGSIAMWKTTHNHNHIAACNSLDHDPDLOHMPVAVSRRFNSITSHFYGRKLEFDFI 243
QY 245 AEFLLCYQHFTFYVWCVARVNLVLTILLFRRKRVQDRALNMGILVFWTFPPLVSC 304
DB 244 AEFLLCYQHFTFYVWCVARVNLVLTILLFRRKRVQDRALNMGILVFWTFPPLVSC 303
QY 305 LPPWPERVWFLVSLAVCSIQHIOFCLNHPANVYVGPSSGNDWFEKOTSGTLDISCAS 364
DB 304 LPPWPERVWFLVSLAVCSIQHIOFCLNHPANVYVGPSSGNDWFEKOTSGTLDISCAS 363
QY 365 NMWFGGLOFQLEHNLFPRLPRCOLRKISPLVSDCKKNLPRYSLSPEANQWTRTLR 424
DB 364 NMWFGGLOFQLEHNLFPRLPRCHLRGVSPPVQELCKKNLPRYSLSPEANQWTRTLR 423
QY 425 TAAQARADLTNPAPKNLWEAVNTHG 450

DB 424 TAAQARADVNPVKNLWEALNTHG 449

RESULT 3

T50555
delta-8 sphingolipid desaturase (imported) - rape
C/Species: Brassica napus (rape)
C/Date: 21-Jul-2000 #sequence_rev1510 21-Jul-2000 #text_change 15-Sep-2000
C/Accession: T50555
R/Sperling, P.; Zaehring, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A/Title: A sphingolipid desaturase from higher plants. Identification of a new cytochrome
A/Reference number: Z22986; MUID:99003197; PMID:9786850
A/Accession: T50555
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-449 <SPE>
A/Cross-references: EMBL:AJ224160; PIDN:CA11857.1
A/Experimental source: cultivar Drakkar
C/Genetics: sld1
A/Map position: 3
A/Note: F2A19.180
C/Function:
A/Description: (EC 1.14.99.-); delta-8 sphingolipid desaturase [validated, MUID:99003197
C/Keywords: oxidoreductase, unsaturated fatty acid biosynthesis

Query Match 77.1%; Score 1887; DB 2; Length 449;

Best Local Similarity 74.7%; Pred. No. 7.7e-156;

Matches 333; Conservative 52; Mismatches 61; Indels 0; Gaps 0;

QY 5 EKEKKITSEELKGNKEDLWISIQKYYNVDWVKEHGGDVPISNLAGDVTDAFTA 64
DB 4 ETEBKITTEDLKKHNSGDLWIAIQKYYNVDWVKEHGGDVTILNLVGDVTDAFTA 63
QY 65 YHPTAMSHLEKFTGYHLSDFKVSSEVSKDYRKLAESFSLGLFDTKGHVTSCCTLASVAV 124
DB 64 FHPGTAMRHLDHLEFTGYHLSDFKVSSEVSKDYRKLAESFSLGLFDTKGHVTSCCTLASVAV 123
QY 125 MELIYVGLRCTSVWALHSGMGLGLMWQSAVYGHDSGHVYVMTNGFNKVAQILSGN 184
DB 124 MELIYVGLRCTSVWALHSGMGLGLMWQSAVYGHDSGHVYVMTNGFNKVAQILSGN 183
QY 185 CLTGSIAMWKTTHNHNHIAACNSLDHDPDLOHMPVAVSRRFNSITSHFYGRKLEFDFI 244
DB 184 CLTGSIAMWKTTHNHNHIAACNSLDHDPDLOHMPVAVSRRFNSITSHFYGRKLEFDFI 243
QY 245 AEFLLCYQHFTFYVWCVARVNLVLTILLFRRKRVQDRALNMGILVFWTFPPLVSC 304
DB 244 AEFLLCYQHFTFYVWCVARVNLVLTILLFRRKRVQDRALNMGILVFWTFPPLVSC 303
QY 305 LPPWPERVWFLVSLAVCSIQHIOFCLNHPANVYVGPSSGNDWFEKOTSGTLDISCAS 364
DB 304 LPPWPERVWFLVSLAVCSIQHIOFCLNHPANVYVGPSSGNDWFEKOTSGTLDISCAS 363
QY 365 NMWFGGLOFQLEHNLFPRLPRCOLRKISPLVSDCKKNLPRYSLSPEANQWTRTLR 424
DB 364 NMWFGGLOFQLEHNLFPRLPRCHLRGVSPPVQELCKKNLPRYSLSPEANQWTRTLR 423
QY 425 TAAQARADLTNPAPKNLWEAVNTHG 450
DB 424 TAAQARADVNPVKNLWEALNTHG 449

RESULT 4

S6358
delta-8 sphingolipid desaturase (EC 1.14.99.-) [similarity] - common sunflower
C/Species: Helianthus annuus (common sunflower)
C/Date: 15-Feb-1997 #sequence_rev1510 13-Mar-1997 #text_change 21-Jul-2000
C/Accession: S6358
R/Sperling, P.; Schmidt, H.; Heinz, E.
Eur. J. Biochem. 232, 798-805, 1995
A/Title: A cytochrome-b(5)-containing fusion protein similar to plant acyl lipid desaturase
A/Reference number: S6358; MUID:96028121; PMID:7588718
A/Accession: S6358
A/Status: preliminary
A/Molecule type: mRNA

A:Residues: 1-458 <SEP>
 A:Cross-references: EMBL:X87143; NID:G1040728; PIDN:CAA60621.1; PID:G1040729
 C:Superfamily: cytochrome b5 core homology
 C:Keywords: heme; iron; metalloprotein; oxidoreductase
 F:16-90/Domain: cytochrome b5 core homology <CBS>
 F:51.74/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 73.5%; Score 1801; DB 2; Length 458;
 Best Local Similarity 71.6%; Pred. No. 2.3e-148;
 Matches 317; Conservative 55; Mismatches 71; Indels 0; Gaps 0;

QY 8 KKITTSEELKHNKGGDMISIQKVVYVSDWKVKEHPEGDVPIISNLAGQVDTAFIAYHP 67
 D 16 KKYYTSKELKGNPNNDIMISILKVVYVTEMAKEHPGSDAPLINALGQVDTAFIAYHP 75
 QY 68 GTANSHLEKFTGYHLSDFKYSVSKDYRKLASSESKGLPDTGHTVTSCLASVAVMFL 127
 D 76 GTANKHLDKLFYTHLNDYQVSDISRDYRKLASSEPAKAGMEKGGHYISLCVSLLS 135
 QY 128 ILYGVLRCTSVMAHLGSGMLLGLLMQSAVYVGHSDGHVYVMTTNGFNKVAQILSGNCLT 187
 D 136 ACYGVLYSGSFVHMLSGALLGLAMQIAYLGHDAHYOMATRGNNKAFGIFIGNCIT 195
 QY 188 GISIAMKWTNNAHIAACNSLDHDPDLOHMPFAVSSRFENSTSHFYGRKLEDFIARF 247
 D 196 GISIAMKWTNNAHIAACNSLDYDPDLOHLPMAVSSKLFNSITSVFYGRQLEDFIARF 255
 QY 248 LICQHFTEFYVPMGVARNVLYLOTLLLFSSRKQODRALNMGILFVFTWPRPLVSCLPN 307
 D 256 FVSQHYLYPYIMCVARNVLYLOTLLLFSSRKIPDRGLNLTGLTFWTPRPLVSRLPN 315
 QY 308 WPERVMEVLASFVACSIOHIOFCINHPAANYVGPSPGNDMEFEKOTSGTLDISCASSMDW 367
 D 316 WPERVAVLVSCYCTGTOHIOFTLNHPBGDYYVGRPKDMMFEKOTGTITDIACSSMDW 375
 QY 368 FFGGLQFQLEHNLPRPLRCQKRIISPLVSDCKKHNLPYRSLPWEANQWITRTAA 427
 D 376 FFGGLQFQLEHNLPRPLRCRLRISPIRCLCKKYNLPYSLFYDANVTTLKTLRTAA 435
 QY 428 LQARDLNPAPKQLMEAVNTHG 450
 D 436 LQARDLNPAPKQLMEAVNTHG 458

RESULT 5

JG7556
 1:linoleoyl-CoA desaturase (EC 1.14.19.3) - Mucor rouxii
 N:Alternate names: delta6-desaturase
 C:Species: Mucor rouxii
 C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Jun-2002
 C:Accession: JG7556
 R:Biochem. K.; Mammontarac, R.; Tanticaroen, M.; Cheevadhanarak, S.
 Biochem. Biophys. Res. Commun. 279, 17-22, 2000
 A:Title: Delta6-desaturase of Mucor rouxii with high similarity to plant delta6-desaturase
 A:Reference number: JG7556; MUID: 20563795; PMID:11112411
 A:Accession: JG7556
 A:Molecule type: DNA
 A:Residues: 1-523 <LAO>
 A:Cross-references: GB:AF290983
 A:Experimental source: strain ATCC 24905
 C:Comment: This enzyme, a membrane-bound key enzyme, is responsible for the transformation of oxido-reductase; transformation

Query Match 28.0%; Score 684.5; DB 2; Length 523;
 Best Local Similarity 28.5%; Pred. No. 2.1e-51;
 Matches 147; Conservative 86; Mismatches 200; Indels 83; Gaps 7;

QY 6 KEKKYITSEELKHNKGGDMISIQKVVYVSDWKVKEHPEGDVPIISNLAGQVDTAFIAY 65
 D 17 RSSNIVTEKQELIKQSDSVFYEQKVVYVNTFMARPGGSAARSLGRDVTDEIRTM 76
 QY 66 HPGTAMHLEKFTGYHLSDF----- 86

D 77 HPGQVY---EKLINLYCIGDYMEDVIRPASMKQOHTFKPKEDKPVLTATWEGFTVOAY 133
 QY 87 -----KVSEVSKD-----YRKLASSESKGLPDTGHTVTSCLAS 121
 D 134 DDAIQDLHKHSHDLIDAVLQKDLNDQIRNAYRKLEAEIYAKGLF-----KCYWK 186
 QY 122 VA-----VMFLVLYGVLRCTSVMAHLGSGMLLGLLMQSAVYVGHSDGHVYVMTTNGF 174
 D 187 YARGCYRTLLIFLSLFTLKGTETHTYMAAFAFMFMQLVETADAGNEITGSEI 246
 QY 175 NKVAQILSGNCLTGISIAMKWTNNAHIAACNSLDHDPDLOHMPFAVSSRFENSTSHF 234
 D 247 DHTVGIANFIIGLSIGMKNDNNVHIVTNEHEDPDLOHPEFMAITTKFFNNISTY 306
 QY 235 YGRLEDFPIARFLICYQHFTEFYVPMGVARNVLYLOTLLLFSSRKQODRALNMGILVF 294
 D 307 YKRVLPDPAASRFVNRQHLVLYLISFGFNLRLSFAVLLTKANVTRTLBELVGTFF 366
 QY 295 WTPRPLVSCLPWPERVMEVLASFVACSIOHIOFCINHPAANYVGPSPGNDMEFEKOTS 354
 D 367 FVWFGLSLSTLPNTNIRIAYIMVSYMLTFPLHQITLSHFGMSTEDRGPD-EPPAKMLR 425
 QY 355 GTLDISCASSMDWFFGGLQFQLEHNLPRPLRCQKRIISPLVSDCKKHNLPYRSLPWE 414
 D 426 TTMVDVDCPEMHDMFHGGLQYQAVHILPRPLRPNRLRQCVLPKFCDEVGILHYVMYFST 485
 QY 415 ANQWITRTLTALQARDLNPAPKQL-MEAVNTH 449
 D 486 GNGVLTGLKSVADQVGFNMEVAKSNAEIVANDKEH 521

RESULT 6

JG0180
 Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
 C:Accession: JG0180
 R:Biochem. T.; Shmida, Y.; Inagaki, K.; Higashimoto, H.; Kawamoto, S.; Shigeta, S.; Ono, K.;
 Biochem. Biophys. Res. Commun. 255, 575-579, 1999
 A:Title: Molecular cloning and functional characterization of rat delta-6 fatty acid desaturase
 A:Reference number: JG0180; MUID:99160394; PMID:10049752
 A:Accession: JG0180
 A:Stacus: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-444 <AKI>
 A:Cross-references: DDBJ:AB021980; NID:94514721; PIDN:BA475496.1; PID:94514722
 C:Superfamily: cytochrome b5 core homology
 C:Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid biosynthe
 F:18-94/Domain: cytochrome b5 core homology <CBS>
 F:53.76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 18.4%; Score 451.5; DB 2; Length 444;
 Best Local Similarity 28.5%; Pred. No. 2.9e-31;
 Matches 126; Conservative 62; Mismatches 157; Indels 97; Gaps 15;

QY 14 BELKGNKGGDMISIQKVVYVSDWKVKEHPEGDVPIISNLAGQVDTAFIAYHGTAMSH 73
 D 24 BELQHNLRTRDMLVIDRKVVNTKMSQRHPGGHVLGHVSGEATAPAFRAF-----H 76
 QY 74 LEKFTGYHLSDF-----KVSEVSKDYRKLASSESKGLPDTGHTVTSCT 118
 D 77 LDDDFVKKFLKPLRIGLAPBEPBLDGKSSQITEDRALKKTAEKNNLFRKTNLFFFL 136
 QY 119 LASVAVMFLVLYGVLRCTSVMAHLGSG-----MLGLLMQSAVYVGHSDGHVYVMT 170
 D 137 LSHIIVMESIAMF-----ILSYFGMGWIPVTATVLTATSQAOQMLQHDYGLSVYK 189
 QY 171 TNGNKKVAQILSGNCLTGISIAMKWTNNAHIAACNSLDHDPDLOHMPFAVSSRFENSI 230
 D 190 KSLVNNHIVHKFVYGLHLSGASANNMNRHHPQHHAKENPFHKQPDKSLHVFVLE--WQPL 247
 QY 231 TSHFYGRK---LEDFIARFLICYQHFTEFYVPMGVARNVLYL--QTLLLFSSRKQODR 284

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Db      248 E-----YGRKKLKYLPYN-----HHEHYEFLIGPRLIPMYFOYQIMTMRIRRWVDL 296
QY      285 A-----LIMIGILVFWTWPRLVSLCPNMPERMPFLASFAVCSIOHI- 327
Db      297 AMAISTARFFYYIIPYGLGALVFLNFIRFLES---HW-----VTQNMHIW 344
QY      328 -QCLNHPAANYVGPSPGNDWEFKQTSGLTIDISCSAMDWFFGQLQFQLEHHLFRLPLR 386
Db      345 MEIDLDDHY-----RDMFSSQLAATCNVEQSPFNDFSGHLNFQLEHHLFPTMPR 393
QY      387 CQKRTSPVSLDCKKNLPIYR 408
Db      394 HNLKIALPLVKSLLCAKHGIEYQ 415

RESULT 7
T13155
linoleoyl-CoA desaturase (EC 1.14.19.3) [validated] - human
N/Alternate names: Delta6 fatty acid desaturase; protein DKFZps86C201.1
C/Species: Homo sapiens (man)
C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 03-Jun-2002
C/Accession: T13155; T08765
R/Cno, H.P.; Nakamura, M.T.; Clarke, S.D.
J. Biol. Chem. 274, 471-477, 1999
A/Title: Cloning, expression, and nutritional regulation of the mammalian Delta-6 desatu
A/Reference number: 217612; MUID:99085046; PMID:9867867
A/Accession: T13155
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-444 <CHO>
A/Cross-references: EMBL:AF126799; NID:94406527; PID:94406528; PIDN:AMD20018.1
R/Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
A/Reference number: Z16471
A/Accession: T08765
A/Molecule type: mRNA
A/Residues: 'RTRG', 138-428, 'D', 430, 'W', 432-444 <WAM>
A/Cross-references: EMBL:AL050118
A/Experimental source: adult uterus; clone DKFZps86C201
C/Genetics:
A/Gene: GDB:FADS6
A/Cross-references: GDB:9956652
A/Note: DKFZps86C201.1
C/Superfamily: cytochrome b5 core homology
C/Keywords: cytochrome b5 core homology; heme; iron; metalloprotein; oxidoreductase; unsaturated fatty
F/18-94/Domain: cytochrome b5 core homology <CBS>
F/53,76/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match      18.0%; Score 441.5; DB 2; Length 444;
Best Local Similarity 28.1%; Pred. No. 2.2e-30;
Matches 128; Conservative 65; Mismatches 171; Indels 91; Gaps 16;

QY      14 EELKHNKEDLMISIGKYYNVSVDWYKEHFGDVPISNAGDVTDAFLAHPGTAMSH 73
Db      24 EEIQKHLRTDRMLVIDRKYYNITKMSIQHGGGQVIGHAGBDATAPAFHDLFF- 81
QY      74 LEKFTGYHLSDF-----KVSEVSKDYRLASEFSEKLGFPDKGHVTSGLASVA 123
Db      82 VGKFLKPLLIGELAPESPDSODHGNSKITEDPRLARTADDMNLFKN-----H 130
QY      124 VMFLVLVYGLVRLCTSV-W-----AHLSG-----MLGLLMMQSAVGHDSGHVVMVT 171
Db      131 VFLLLLLAHIALESIMFVYFGNGWITPLTIAFLATSOQAAGLQCHDYGLSLYRK 190
QY      172 NGENKVAQILSGNCTGISIAMWKTNNAHIACNLSDHDPDLOHMPFVAVSSRFNSIT 231
Db      191 PKNMHLVHKVEVIGHLKASAMWNRHAFQHAKEINI FHKD PDVMTLHVFLGE--WQPIE 248
QY      232 SHFVGRK-----LEPDFIARFLICYGHFTYRVMCAVAVNLVL--QTLLLSFRKQDRA 285
Db      249 ---YGRKKLKYLPYN-----HHEHYEFLIGPRLIPMYFOYQIMTMRIRRWVDL 297
QY      286 -----LIMIGILVFWTWPRLVSLCPNMPERMPFLASFAVCSIOHIQF 329

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Db      298 MAVSYIRFFITYIPYGLIGALLFLNFIRFLES---HW-----VTQNMHIW 345
QY      330 CLNHFAANYVGPSPGNDWEFKQTSGLTIDISCSAMDWFFGQLQFQLEHHLFRLPLR 389
Db      346 EIDQEAAY-----RDMFSSQLAATCNVEQSPFNDFSGHLNFQLEHHLFPTMPR 396
QY      390 RKISPLVSLDCKKNLPIYRSLSFWEANQWIRTLR 424
Db      397 HKIAPLVKSLCAKHGIEYQEKPLRLALDITRSK 431

RESULT 8
T26280
linoleoyl-CoA desaturase (EC 1.14.19.3) W08D2.4 - Caenorhabditis elegans
N/Alternate names: Delta6 fatty acid desaturase
C/Species: Caenorhabditis elegans
C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 03-Jun-2002
C/Accession: T26280; T37238
R/Swinburne, J.; Alnecough, R.
submitted to the EMBL Data Library, March 1996
A/Reference number: Z20188
A/Accession: T26280
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-473 <WIL>
A/Cross-references: EMBL:Z70271; PIDN:CA94233.1; GSPDB:GN00022; CESP:W08D2.4
A/Experimental source: clone W08D2
R/Napier, J.A.; Hey, S.J.; Lacey, D.J.; Shewry, P.R.
Biochem. J. 330, 611-614, 1998
A/Title: Identification of a caenorhabditis elegans Delta6-fatty-acid-desaturase by heter
A/Reference number: Z21637; MUID:98149727; PMID:9480865
A/Accession: T37238
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-38,69-430, 'V', 432-473 <NAP>
A/Cross-references: EMBL:AF031477; NID:93088519; PIDN:AAC15586.1; PID:G3088520
C/Genetics:
A/Gene: CESP:W08D2.4
A/Map position: 4
A/Intons: 13/3; 39/2; 234/3; 277/3; 378/1; 413/3
C/Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C/Keywords: alternative splicing; oxidoreductase; unsaturated fatty acid biosynthesis

Query Match      16.4%; Score 401; DB 1; Length 473;
Best Local Similarity 25.3%; Pred. No. 7.6e-27;
Matches 124; Conservative 77; Mismatches 187; Indels 102; Gaps 18;

QY      20 NKEGDLMISIGK-VYNVSDWYKEHFGDVPISNAGDVTDAFLAHPGTAMSH-----LEKFF-----TGYHL 83
Db      6 NAG-LRMVVDGKMLVSEELVYKHPGAVIEQYSIPLNKNIETRGITTRGSSNALDI 64
QY      53 ---LAQDVTDAFLAHPGTAMSH-----LEKFF-----TGYHL 83
Db      65 LYFRRNSDATHIFAHVHBSQAYKQDLKKHGEHDEFLERLKDVDINVAAYDV 124
QY      84 SDPKVSEVSKDYRLASEFSEKLGFPDKGHV-----SGLTASVVMFLVLVYGLVRLCT 137
Db      125 SVAQEKVSEFSEKLGKQKLDHDDLM--KANETVFLFKAIISTISIMFAAYLYLG----- 177
QY      138 SVVAHLGSGMLLGLLMMQSAVGHDSGHVVMVTNNGFNVAQILSGNCTGISIAMWKTN 197
Db      178 -W-YITSACLALANAOQGMLTHERCHQOPTKNRPLNTITSLFENFLQGSFSDMKOK 234
QY      198 HNAHITACNSLDHDPDLOHMPFVAVSSRFNSITSHFYGRKLEPDFIARFLICYGHFTY 257
Db      235 HNTHTAATVVIDHDGDIDALPLFAF-----IPGDLCKYKASFEXAILIKIVYQHLVFT 287
QY      258 PWCVCARVNLVYQITILLFSRRKYQDRA-----LIMIGILVFWTWPRLVSLCPNMP 308
Db      288 AMLPMLRFSWTGSGVQVFEKNQMEYKYVQRNAFWEOATIVG--HWAVFQQLFLPLPTW 344
QY      309 PERVMEVLAS--FAVCSIOHIQFCLNHPAANYVGPSPG--NDWEFKQTSGLTIDISCS 363

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Db 345 PLRAVAFISQMGGLTAHV-VTFNNSVDKY--FANSRLINNEPALQIITTRMTSP 401
Qy 364 SMDVFEGLQSOLEHLPRLPRCOLKISPLVSDLCCKHLLPFRSLSFMEANQMTITL 423
Db 402 FIDWIMGGGLNQLIEHLPFRRCNLNACMKYKXCKENMLPYLVDDYFDGYANMLQOL 461
Qy 424 RTAA--LQAR 431
Db 462 KNMAEHIQAK 471

RESULT 9
T43319
Deltas5 fatty acid desaturase (EC 1.14.99.-) T13F2.1 (validated) - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C:Accession: T43319; T24875
R:Michaelson, L.V.; Napier, J.A.; Lewis, M.; Griffiths, G.; Lazarus, C.M.; Stobart, A.K.
FEBS Lett. 439, 215-218, 1998
A:Title: Functional identification of a fatty acid deltas desaturase gene from *Caenorhabditis elegans*
A:Reference number: Z22422; MUID:99059458; PMID:9845325
A:Accession: T43319
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-447 <MIC>
A:Cross-references: EMBL:AF078796; NID:g4003522; PIDN:AAC95143.1; PID:g4003523
R:Swindburne, J.
Submitted to the EMBL Data Library, October 1996
A:Reference number: Z19947
A:Accession: T24875
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-197, 'VSHIFNN', 198-447 <WIL>
A:Cross-references: EMBL:Z81122; PIDN:CAB03352.1; GSPDB:GN00022; CESP:T13F2.1
A:Experimental source: clone T13F2
C:Genetics:
A:Gene: CESP:T13F2.1; des-5
A:Map position: 4
A:Introns: 43/3; 80/3; 197/3; 295/3; 318/2; 349/1; 384/3
C:Superfamily: *Caenorhabditis elegans* Delta6 fatty acid desaturase
C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 15.3%; Score 373.5; DB 1; Length 447;
Best Local Similarity 24.7%; Pred. No. 1.7e-24;
Matches 112; Conservative 78; Mismatches 198; Indels 65; Gaps 14;

Qy 26 WISIQGVNVSDWV-KEHFGDVPISNLAGQVTDFAIVHPT---AW-SHLEK--- 76
Db 12 FIKIDGKMCQIDDAVLRSHPGSA-ITTYKMDATVTFHFTGSKAYQWLTCLKKCP 70
Qy 77 -----FTGYHLSDFKVSVDYKRLASEFSGKLGFDTKGHVTS 116
Db 71 TOBEIPIDIDDPKIGIDVNMGTFFNISSEKSAQINSLFTDLRMRVBAEGLMD--GSPLEF 128
Qy 117 CTLASVAMFPLIVLYGVLRCTSVANHLGSGMLGLMMQSAVYVGDGHVYVMTTNGPNK 176
Db 129 YIRKILFTITFLPAFLQHTY--YLPASALMGVAMQGLMLHEPRAHQDLFKRRYYND 186
Qy 177 VAQILSGNCLTGISIAWKKTNHAIACNSLDHDPDLQHPVPVASSRFPNSITSHFYG 236
Db 187 LASYFVGNFLQGFSSGCKEQHNVHATVNGRGDLDLVPFAVTAVEHLNNSQ----- 242
Qy 237 KLEPDIARFLICYQHTFYPMCVARVNLVLTILL-----FSRRVQDRAL 286
Db 243 -----DSWVMTLFRWQHVTMFLPRLSLWLSQIIFVSQMPHYDYVYRNTAIYEQ-- 295
Qy 287 NIMGLVFWTPPLVSLCPNMPBRVWFVLSFAVCS--IHIQFCNLHFAANYVGPSP 344
Db 296 --VGLSLHMAWSLQGLYFLPDMSTRIMFPLVSHLVGGFLSHV-VTFNHYSEKFA--LS 350
Qy 345 GN---DWFEKQTSGLTIDISCASSMDWFFGLQFQLEHLPRLPRCOLKISPLVSDLC 401

Db 351 SNINSNVACIQIMTRMRPGRPIDWMLGGLNVOIEHNLPEPTMRHNLNTVPLVKEFAA 410
Qy 402 KENLPYRSLSPWEANQMTITRLTPRALQARDLT 434
Db 411 ANGLPYNVDYFTTGFMLEIEQFRNIANVAKLT 443

RESULT 10
H88791
protein T13F2.1 (imported) - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: H88791
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: See websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: H88791
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-454 <STO>
A:Cross-references: GB:chr_IV; PIDN:CAB03352.1; PID:g3879828; GSPDB:GN00022; CESP:T13F2.1
A:Gene: T13F2.1
A:Map position: 4
C:Superfamily: *Caenorhabditis elegans* Delta6 fatty acid desaturase

Query Match 14.7%; Score 361; DB 2; Length 454;
Best Local Similarity 24.3%; Pred. No. 2.1e-23;
Matches 112; Conservative 78; Mismatches 198; Indels 72; Gaps 15;

Qy 26 WISIQGVNVSDWV-KEHFGDVPISNLAGQVTDFAIVHPT---AW-SHLEK--- 76
Db 12 FIKIDGKMCQIDDAVLRSHPGSA-ITTYKMDATVTFHFTGSKAYQWLTCLKKCP 70
Qy 77 -----FTGYHLSDFKVSVDYKRLASEFSGKLGFDTKGHVTS 116
Db 71 TOBEIPIDIDDPKIGIDVNMGTFFNISSEKSAQINSLFTDLRMRVBAEGLMD--GSPLEF 128
Qy 117 CTLASVAMFPLIVLYGVLRCTSVANHLGSGMLGLMMQSAVYVGDGHVYVMTTNGPNK 176
Db 129 YIRKILFTITFLPAFLQHTY--YLPASALMGVAMQGLMLHEPRAHQDLFKRRYYND 186
Qy 177 VAQILSGNCL-----TGISIAWKKTNHAIACNSLDHDPDLQHPVPVASSRFPNS 229
Db 187 LASYFVGNFLQVSHIFNNGFSSGCKEQHNVHATVNGRGDLDLVPFAVTAVEHLNNSQ 246
Qy 230 ITSHFPRKLEPDIARFLICYQHTFYPMCVARVNLVLTILL-----FSRR 279
Db 247 YSQ-----DSWVMTLFRWQHVTMFLPRLSLWLSQIIFVSQMPHYDYVYRNT 297
Qy 280 KVQDRALNIMGLVFWTPPLVSLCPNMPBRVWFVLSFAVCS--IHIQFCNLHFAANY 337
Db 298 AIYVQ-----VGLSLHMAWSLQGLYFLPDMSTRIMFPLVSHLVGGFLSHV-VTFN 352
Qy 338 VYVGPBSGN---DWFEKQTSGLTIDISCASSMDWFFGLQFQLEHLPRLPRCOLKISP 394
Db 353 KFA--LSSNINSNVACIQIMTRMRPGRPIDWMLGGLNVOIEHNLPEPTMRHNLNTVMP 410
Qy 395 LVSDLCCKHLLPFRSLSFMEANQMTITRLTPRALQARDLT 434
Db 411 LVKEFAANGLPYVVDYFTGFMLEIEQFRNIANVAKLT 450

RESULT 11
T36617
Probable Delta6 fatty acid desaturase (EC 1.14.99.-) SCH35.42c [similarity] - *Streptomyces*
C:Species: *Streptomyces coelicolor*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C:Accession: T36617
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, June 1999

A/Reference number: Z21610

A/Accession: T36617

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-345 <OL1>

A/Cross-references: EMBL:AL078610; PIDN: CAB44385.1; GSPDB: GNO0070; SCOEDB: SCH35.42C

A/Experimental source: strain A3(2)

C/Genetics:

A/Genes: SCOEDB: SCH35.42C

C/Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 9.0%; Score 221.5; DB 2; Length 345;

Best Local Similarity 24.7%; Pred. No. 2e-11;

Matches 89; Conservative 58; Mismatches 158; Indels 55; Gaps 14;

94 DYKLAASEFKLGFDTKG-----HTSCSLASVAVMFLVLYGVLRCTSVMAHLSGML 148

16 DFARLSKRVADAGILGRPGYTLRTAVTGLVAAAGAAFLVG-----ASMTLAIAP 70

149 IGLIMQSAVYVGHDSGHVYVMTTNGFNKVAQIISGNCLTGISTAMKWTNNAHIIACNSL 208

71 LAWYGVAVVAADHMAKQVFRRRASBELSGRIAGAST-GMSYGWODKTRHIANPTE 129

209 DHDPDLQHMVFAY-SSRFNSITSHFYGRKLEDFIARFLICYHFTFYVVCVARVNL 267

130 DLDPDIG--PDLVWSPDQARAATG-----LPRLLGRMQAFLFFPLTLBSGNL 176

268 YLQTLILFRRKXQDRAIMIGILVFWTWPFLIVSCLPMPERVMFLASFAVCISIQHI 327

177 HVASGRAMARR-LKRRLD--GAL-----LHACAV-YLTALFWLPPGMAIAPLAV 225

328 QFCL-----NHPAANYVGP-----SGNDWFEKQSGTILDISCASSMDPFGGLQFOL 376

226 HQCLFGYLYLSAFAFN-HKGNPILITADDPDLKROVLTSTNVNGCLFTDLALGGLNHQI 284

377 EHHLPRLPRCQRLKISPLVSDLCCKNLPYRSLSFWEANQWITRTIATLQARDLTPN 436

285 EHHLPMPSPNLRKARATIRRYCRDLGVY-----AETGLVASRLALTLSDAGTP 337

RESULT 12

Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - Synecocystis sp.

C/Species: Synecocystis sp.

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000

C/Accession: S35157; S76243

R/Reddy, A.S.; Nuccio, M.L.; Gross, L.M.; Thomas, T.L.

Plant Mol. Biol. 22, 293-300, 1993

A/Title: Isolation of a Delta(6)-desaturase gene from the cyanobacterium Synecocystis S

A/Reference number: S35157; MUID: 9328363; PMID: 8389613

A/Accession: S35157

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-359 <RSD>

A/Cross-references: GB:J1421; NID:9349562; PIDN:AAA27286.1; PID:9349563

R/Kanejo, T.; Sato, S.; Kocani, H.; Tanaka, A.; Asamiizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shingo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-116, 1996

A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis

S.

A/Reference number: S74322; MUID: 97061201; PMID: 8905231

A/Accession: S76243

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-359 <KAN>

A/Cross-references: EMBL:D90914; GB:AB001339; NID:G1653477; PIDN:BA18502.1; PID:d101923

A/Experimental source: PCC 6803

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C/Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 8.3%; Score 202.5; DB 2; Length 359;

Best Local Similarity 23.6%; Pred. No. 9.2e-10;

Matches 79; Conservative 47; Mismatches 120; Indels 89; Gaps 15;

125 MFLIVYGVLRCTSVAAH-----LGSMLGLIMQSAVYVGHDSGHVYVMTTN 172

40 MYLKTIIIVMLFSAMAFULFAPVIFPVVLLGCMVLAIALAASFVNGDANNAVSSNP 99

173 GFNKVAQIISGNCLTGISTAMKWTN-AMHIIACNSLDH-----PDLQHMPV 219

100 HINRVLGMTYD--FVGLSFLMRRYRNHYLHHTYTINILGHDEIHGDGAVRMSPEQGHVGI 157

220 FAVSSRFNSITSHFYGRKLEDFIARFLICYHFTFYVVCVARVNLVLOTILLFSRR 279

158 Y-----RF-----QQFYIWL-----YLFIPFY-----WFLYDVYLVING 188

280 KYQDRAL-----NIMGILVFWTWPFLIVSCLP-----NMPF-----RVMFLASPA 320

189 KIHDKIIPPEPPELASSLIGIKLMLGY--VFGLPAGFSLPEVLIGASVYMTYGYV 245

321 VCSIOHIOFCLNHPAANYVGPSPG-----NDWFEKQSGTILDISCASSM-DWFEGLQ 373

246 VCTI-----FMAHVLSTEFITPDGSGAIDDEMAICQRTTANPATNPPMNMWFCGGLN 301

374 FQLEHLPRLPRCQRLKISPLVSDLCCKNLPYR 408

302 HQVTHLFPNICHINHYPOLENIKDYCOBGEVEYK 336

RESULT 13

S54809

linoleoyl-CoA desaturase (EC 1.14.19.3) - Spirulina platensis

N/Alternate names: Delta6-desaturase

C/Species: Spirulina platensis

C/Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 03-Jun-2002

A/Accession: S54809

R/Tanaka, Y.

submitted to the EMBL Data Library, May 1995

A/Reference number: S54809

A/Accession: S54809

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-368 <TAS>

A/Cross-references: EMBL:X67094; NID:G809109; PIDN:CAA60573.1; PID:G809110

C/Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 7.7%; Score 189.5; DB 2; Length 368;

Best Local Similarity 24.2%; Pred. No. 1.3e-08;

Matches 80; Conservative 56; Mismatches 116; Indels 79; Gaps 19;

115 TSCTLASVAVMFLIVYGVLRCTSVAAHLSGMLGLIMQSAV-VGHDSGHVYVMTTN 173

45 TAILIMVVSAMTFVFGP---DVLMMKLLGICVLFSGVSAVGFNISHDGNH-----GG 95

174 ENKVAQI--LSGNCLT---GISAMKWTNNA-HHIIACNSLDHDDLPQHMVFAVSSRF 226

96 YSKYQWVNYLSG--LTHDAIGVSSYLKMRHNVLHHTYTINILGHDEIHGDELVRMSR-- 151

227 FNSITSHFYGRKLEDFIARFLICYHFTF---YPMW---CYARVNLVLOTILLFSRR 279

152 --SMERYWYR-----YQHWTFVYPRPIPYWISADY---QTLFLF--KR 189

280 KYQDR-----ALNIMGILVFWTWPFLIVSCLPMPERVMFLASFAVCSIO 325

190 QYHDEIIPSTWADIATLLAFKAGAVFLI-IPINAVGSP-----LEAVIGASIVYMTN 243

326 HIOFCLNHPAANY-----YVGPSP---GNDWFEKQSGTILDISCASS-NDWFEGLQFOL 376

244 GLVACVFMIAHVEBAEFLDPDNLHIDDEMAIAQVKTVDFAPNPIINWYVGLNYQT 303

377 EHHLPRLPRCQRLKISPLVSDLCCKNLPY 407

304 VHHLFPNICHINHYKIAPIIAVECBEGVNY 334

RESULT 14

A86390

hypothetical protein Trx7.28 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001

C/Accession: A86390

R/Theologian: A.; Becker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Hultzer, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzalli, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A86141; MUID:21016719; PMID:11130712

A/Accession: A86390

A/Status: Preliminary

A/Molecule type: DNA

A/Residues: 1-135 <STO>

A/Cross-references: GB:A8005172; NID:g9797763; PTDN:AA98581.1; GSPDB:GN00141

C/Genetics:

A/Map position: 1

C/Superfamily: cytochrome b5; cytochrome b5 core homology

C/Keywords: heme; iron; metalloprotein

F/40,64/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match

Best Local Similarity 7.3%; Score 180; DB 2; Length 135;

Matches 50; Conservative 23; Mismatches 44; Indels 10; Gaps 6;

Db

Qy

Db

Qy

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Qy

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Search completed: January 1, 2004, 06:39:43
Job time : 18.9369 secs

121 WRYTHNFVHHKTYTNILGMDDDVGXGMLRVTRDQWRKRNIENFVWNTI-----LAIG 172
243 FIAFLICYOHFFFPVWCARVNLVYQITLLFSRRKQDRAINIGILVF--WTMEPL 300
173 F--EWGVALQHLKIGIKFKGRADREAKTRLREPSAK-----AGROVFQDYAFPA 221
301 LVSLCP-----NMPRVMEVLASFAVCSIOHIOFCINHEPANVYVGPSPGNDWFE 350
222 LTSLSPGATYRSTLTAVVANVIRNWSNNAVIFCGHFPDGAEXKPTKTDWIGEPKG-QWYL 280
351 KQTSGLTDISCASMDWFFEGLOFQLEHLFPRLPQCLRKISPLVSDCKGNLPYRSL 410
281 ROMLSANFNAGPALRFMSGNLCHQIEHHLVFDLPNRLHEISVREVECDRYDLPYTTG 340
411 SFWEANQWTRTLRTAL---QARDLTNPAPK 439
341 SFLVQYKTRWTLAKUSLPDKRYLRDNADDAPE 372

RP MUTANTS.
 RC STRAIN=74-OR23-1A / FGSC 987;
 RX MEDLINE=93241176; PubMed=8479443;
 RA Okamoto P.M., Garrett R.H., Marzluf G.A.;
 RT "Molecular characterization of conventional and new repeat-induced
 mutants of nit-3, the structural gene that encodes nitrate reductase
 in Neurospora crassa.";
 RL Mol. Gen. Genet. 238:81-90(1993).
 RN (4)
 RP MUTAGENESIS.
 RX MEDLINE=93360901; PubMed=8355655;
 RA Okamoto P.M., Marzluf G.A.;
 RT "Nitrate reductase of Neurospora crassa: the functional role of
 individual amino acids in the heme domain as examined by
 site-directed mutagenesis.";
 RL Mol. Gen. Genet. 240:221-230(1993).
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
 step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NADPH(+) + H(2)O = nitrate + NADPH.
 CC -1- COFACTOR: EACH SUBUNIT CONTAINS 1 EQUIVALENT OF FAD, HEME IRON,
 AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME GROUP IS
 CALLED CYTOCHROME B-557.
 CC -1- PATHWAY: Nitrate assimilation (denitrification).
 CC -1- SUBUNIT: Homodimer.
 CC -1- INDUCTION: ITS EXPRESSION IS HIGHLY REGULATED AND RESPONDS RAPIDLY
 TO NITRATE INDUCTION AND TO NITROGEN REPRESSION.
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
 C-TERMINAL DOMAIN.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X61303; CAA43600.1; -.
 DR HSP, P00171; 1R03.
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR001834; Cyt_B5_reductase.
 DR InterPro; IPR000572; Euk_Mb_oxred.
 DR InterPro; IPR005066; Mo-Co_dimer.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR Pfam; PF03404; Mo-co_dimer; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR Pfam; PF00174; oxidored_molzb; 1.
 DR PRINTS; PR00406; CYB5RDPTASE.
 DR PRINTS; PR00363; CYTOCHROMEBS.
 DR PRINTS; PR00407; EMOPTERIN.
 DR PRODOM; PD000612; Cyt_B5; 1.
 DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
 DR Oxidoreductase; Flavoprotein; FAD; NADP; Heme; Molybdenum;
 Nitrate assimilation.
 KM METAL 240 240
 FT METAL 240 240
 FT METAL 295 295
 FT DISULFID 499 499
 FT DOMAIN 621 691
 FT METAL 652 652
 FT METAL 675 675
 FT METAL 675 675
 FT METAL 675 675
 FT NP_BIND 952 961
 FT MUTAGEN 652 652
 FT MUTAGEN 675 675
 SO SEQUENCE 982 AA; 108432 MW; B7838C031B19687F CRC64;

Query Match 6.5%; Score 159; DB 1; Length 982;
 Best Local Similarity 41.0%; Pred. No. 2e-05;
 Matches 32; Conservative 15; Mismatches 31; Indels 0; Gaps 0;
 QY 3 VVEKKTITSEELKHNKGGDLWISIGKYVNSDWKHPGQDVPISNLAGQVDTAF 62
 DB 612 VDEKVTLLTLEELRHHGDEEPFVNVGQVYNGTPIFLEHGGMASTGAAGQVDTDF 671
 QY 63 IAYHGTAMSHLEKFTFG 80
 DB 672 LAHSNKAKMPTVYHIG 689
 RESULT 4
 ID_CVBS_ORYSA STANDARD; PRT; 137 AA.
 AC P49100;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Callus;
 RX MEDLINE=94325476; PubMed=8049375;
 RA Smith M.A., Stobart A.K., Shewry P.R., Napier J.A.;
 RT "Robacco cytochrome b5: cDNA isolation, expression analysis and in
 vitro protein targeting".
 RL Plant Mol. Biol. 25:527-537(1994).
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 carrier for several membrane bound oxygenases (By similarity).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE. BOUND TO THE
 CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X75670; CAA53366.1; -.
 DR PIR; S46307; S46307.
 DR HSP, P00171; 1R03.
 DR Glemene; P49100; -.
 DR InterPro; IPR001199; Cyt_B5.
 DR Pfam; PF00173; heme_1; 1.
 DR PRODOM; PD000612; Cyt_B5; 1.
 DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 DR Electron transport; Transmembrane; Heme; Iron; Microsome.
 KM TRANSMEM 108 128
 FT METAL 41 41
 FT METAL 65 65
 FT METAL 65 65
 SO SEQUENCE 137 AA; 15296 MW; 4260C9D633B60FPA CRC64;
 QY 8 KKYITSEELGHNKGGDLWISIGKYVNSDWKHPGQDVPISNLAGQVDTAF 66
 DB 6 KKYITTELVAKHNSKDDCWLLIGKYVNSKFLBHPGGDVLISYTGKATDDFEDVGH 65
 QY 67 PGTAMSHLEKFTFG 80
 Query Match 6.4%; Score 156.5; DB 1; Length 137;
 Best Local Similarity 41.9%; Pred. No. 3.3e-06;
 Matches 31; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

Db 66 TTTARANMDEYYVG 79

RESULT 5
CYB5_BRAOL STANDARD; PRT; 134 AA.
AC P40934;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome b5.
GN CYB5.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 6-47 AND 75-89.
RC STRAIN=cv. Cauliflora;
RA Kearns E.V., Keck P., Somerville C.R.;
RT "Nucleotide sequence of cDNA for cytochrome b5 from cauliflower
(Brassica oleracea L.)."
RL Plant Physiol. 99:1254-1257(1992).
CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
carrier for several membrane bound oxygenases.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

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or send an email to license@sib-sib.ch).

CC EMBL; M87514; AAA32990.1; -;
CC PIR; T1454; T1454.
CC HSSP; P00171; 1EHB.
CC InterPro; IPR001199; Cyt_B5.
CC Pfam; PF00173; heme_1; 1.
CC PRINTS; PR00363; CYTOCHROMEBS.
CC ProDom; PD000612; Cyt_B5; 1.
CC PROSITE; PS00191; CYTOCHROME_B5_1; 1.
CC PROSITE; PS50255; CYTOCHROME_B5_2; 1.
CC Electron transport; Transmembrane; Heme; Iron; Microsome.
KW TRANSMEM 107 127 POTENTIAL.
FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT VARIANT 5 5 K -> N
SQ SEQUENCE 134 AA; 15062 MW; 764DC24ACDD591 CRC64;

Query Match 6.3%; Score 154.5; DB 1; Length 134;
Best Local Similarity 4.3%; Pred. No. 4.8e-06;
Matches 31; Conservative 15; Mismatches 28; Indels 1; Gaps 1;

QY 7 EKRTTSEELKGNKGGDLWISIQKRYNVSDWYKEHPGDDVPSINLAGDVTDAF-IAY 65
DB 4 EKRVLGESEVSOHNKTKDCLWISIGKYVDVTPFMDHDPGDEVLSTGDAATDFEDVG 63
QY 66 HPGTAMSHLEKFTG 80
DB 64 HSDTARDMEKTYIG 78

RESULT 6
CY51_ARATH STANDARD; PRT; 134 AA.
AC Q42342; Q9S805;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b5 isoform 1.
GN ATSG53560 OR MNC6.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=99097071; PubMed=9880378;
RA Fukuchi-Mizutani M., Mizutani M., Tanaka Y., Kusumi T., Ohta D.;
RT "Microsomal electron transfer in higher plants: cloning and
heterologous expression of NADH-cytochrome b5a5 reductase from
Arabidopsis.";
RL Plant Physiol. 119:353-361(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=99087489; PubMed=9872454;
RA Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VII.
RT Sequence features of the regions of 1,013,767 bp covered by sixteen
physically assigned pl and TAC clones.";
RL DNA Res. 5:297-306(1998).
RN [3]
RP SEQUENCE OF 1-113 FROM N.A.
RC STRAIN=cv. Columbia;
RA Cooke R., Laudie M., Raynal M., Delseny M.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
carrier for several membrane bound oxygenases (By similarity).
CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

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or send an email to license@sib-sib.ch).

CC EMBL; AB007801; BA74839.1; -;
CC EMBL; AB015476; BAB09732.1; -;
CC EMBL; F20001; CAA23377.1; -;
CC PIR; T52469; T52469.
CC HSSP; P00171; 1EHB.
CC InterPro; IPR001199; Cyt_B5.
CC Pfam; PF00173; heme_1; 1.
CC PRINTS; PR00363; CYTOCHROMEBS.
CC ProDom; PD000612; Cyt_B5; 1.
CC PROSITE; PS00191; CYTOCHROME_B5_1; 1.
CC PROSITE; PS50255; CYTOCHROME_B5_2; 1.
CC Electron transport; Transmembrane; Heme; Iron; Microsome;
KW Multigene family.
FT TRANSMEM 107 127 POTENTIAL.
FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT CONFLICT 1 3 MSS -> ARA (IN REF. 3).
SQ SEQUENCE 134 AA; 15084 MW; 9CC01C60F7C873FD CRC64;

Query Match 6.2%; Score 152.5; DB 1; Length 134;
Best Local Similarity 37.2%; Pred. No. 7e-06;
Matches 29; Conservative 19; Mismatches 29; Indels 1; Gaps 1;

QY 4 VEREKYITSEELKGNKGGDLWISIQKRYNVSDWYKEHPGDDVPSINLAGDVTDAF-62
DB 1 MSSDRVLSFESEVSKNKTKDCLWISIGKYVDVTPFMDHDPGDEVLSTGDAATDFE 60

QY 63 IAHPTGTAWSHLEKFTG 80
 DB 61 DVGHSPTARDMDXKFIG 78

RESULT 7
 CYB2_HANAN STANDARD; PRT; 573 AA.
 ID CYB2_HANAN
 AC P09437;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b2, mitochondrial precursor (EC 1.1.2.3) (L-lactate dehydrogenase [Cytochrome] (L-lactate ferricytochrome c oxidoreductase) (L-LCR).
 GN CYB2.
 OS Hansenula anomala (Yeast) (Candida pelliculosa).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.
 NCBI_TaxID=4927;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90045973; PubMed=2813072;
 RA Kaiser Y., Tesson M., Gervais M.;
 RT "Nucleotide sequence of the Hansenula anomala gene encoding flavocytochrome b2 (L-lactate:cytochrome c oxidoreductase).";
 RL Nucleic Acids Res. 17:8381-8381(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90088451; PubMed=2688640;
 RA Black M.T., Gunn F.J., Chapman S.K., Reid G.A.;
 RT "Structural basis for the kinetic differences between flavocytochromes b2 from the yeasts Hansenula anomala and Saccharomyces cerevisiae.";
 RL Biochem. J. 263:973-976(1989).
 RN [3]
 RP SEQUENCE OF 80-163.
 RX Hamont P.-Y., Thomas M.-A., Labeyrie F., Lederer F.;
 RT "Amino-acid sequence of the cytochrome-b5-like heme-binding domain from Hansenula anomala flavocytochrome b2.";
 RL Eur. J. Biochem. 169:539-546(1987).
 RL Eut. J. Biochem. 169:539-546(1987).
 CC -1- CATALYTIC ACTIVITY: (S)-lactate + 2 ferricytochrome c = pyruvate + 2 ferrocyclochrome c.
 CC -1- SUBUNIT: Homotetramer.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial intermembrane space.
 CC -1- MISCELLANEOUS: THIS ENZYME BINDS FMN AND PROTOHEME IX PROSTHETIC GROUPS.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -1- SIMILARITY: TO SPINACH GLYOXALATE OXIDASE (33% IDENTITY), TO P. PUTIDA S-MANDELATE DEHYDROGENASE, AND TO M. SMEGMATIS LACTATE 2-MONOOXYGENASE.
 CC -----
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 CC -----
 CC EMBL: X16051; CAA34183.1; -.
 CC PIR: S06600; S06600.
 CC HSSP: P00175; ILCO.
 CC InterPro: IPR001199; Cyt B5.
 CC InterPro: IPR003009; FMN enzyme.
 CC InterPro: IPR000262; FMN_hydroxycac_hh.
 CC Pfam: PF01070; FMN_dh; 1.
 CC Pfam: PF00173; heme_1; 1.
 CC PRINTS: PR00363; CYTOCHROMEBS.
 CC PRODOM: PD000612; Cyt_B5; 1.
 CC PROSITE: PS00191; CYTOCHROME_B5_1; 1.

DR PROSITE: PS00255; CYTOCHROME_B5_2; 1.
 DR PROSITE: PS00557; FMN HYDROXY ACID DH; 1.
 KW Electron transport; Respiratory chain; Oxidoreductase; Flavoprotein;
 KW FMN; Heme; Mitochondrion; Transit peptide.
 FT TRANSIT 1 73
 FT CHAIN 74 573
 FT DOMAIN 80 163
 FT METAL 115 115
 FT METAL 138 138
 FT ACT_SITE 432 432
 FT ACT_SITE 435 435
 FT ACT_SITE 435 435
 FT SEQUENCE 573 AA; 64202 MW; 83EEF645C580BC8 CRC64;
 SO

Query Match 6.2%; Score 151.5; DB 1; Length 573;
 Best Local Similarity 35.9%; Pred. No. 4.5e-05;
 Matches 33; Conservative 18; Mismatches 36; Indels 5; Gaps 3;

QY 11 ITSEELGNHKEGDLWISIQKVVNSDVKVHFGDVPISNLGQVDTAFIAVHGT 70
 DB 83 LTPETVSGHNKQDLWVVLNGQVYDLPFPHNGGQKIIIRVAGKATKIFVHPD 142

QY 71 WSHLEKFP-TGYHLSDFKVSBSKDYKRLASE 101
 DB 143 ---IEKFIPEKHLGFL-VGFEQEELSLDE 170

RESULT 8
 CY52_ARATH STANDARD; PRT; 134 AA.
 ID CY52_ARATH
 AC O48845;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable cytochrome b5 isoform 2.
 GN ATG32720 OR F24L7.14.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 CC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V., Buehl C.R., Ketchum K.A., Lee J.J., Romling C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhagen G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";
 RL Nature 402:761-768(1999).
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron carrier for several membrane bound oxygenases (By similarity).
 CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -----
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 CC -----
 CC EMBL: AC003974; AAC04491.1; -.
 CC PIR: T00796; T00796.
 CC HSSP: P04166; 1B5M.

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DR InterPro: IPR001199; Cyt_B5.
DR Pfam: PF00173; heme_1; 1_B5.
DR PRINTS: PR00363; CYTOCHROMB5.
DR ProDom: PD000612; Cyt_B5; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS0255; CYTOCHROME_B5_2; 1.
DR Electron transport; Transmembrane; Heme; Iron; Microsome;
KW Multigene family;
FT TRANSMEM 107 127 POTENTIAL.
FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY)
FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY)
SQ SEQUENCE 134 AA; 15016 MM; B405F5430F5716C1 CRC64;

Query Match 6.1%; Score 149.5; DB 1; Length 134;
Best Local Similarity 40.0%; Pred. No. 1.2e-05;
Matches 30; Conservative 15; Mismatches 25; Indels 1; Gaps 1;

QY 7 EKKYITEELKGNHKEGDLMTISIOGKVVNVDWKEHGVPIISNLGADVTAF-TAY 65
Db 4 EAKFTLSEVSEHNQADHCWLVINKYVNVKFLPDHKGSDVLLSTGKATDDFEDVG 63
QY 66 HPGTAWSHLEKFTG 80
Db 64 HSESAREWMEQYVG 78

RESULT 9
YDAA SCHPO STANDARD; PRT; 147 AA.
ID YDAA SCHPO
AC Q10352;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein ClF12.10c in chromosome I.
GN SPAC1F12.10C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21849401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
RA Soudou V., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jurgels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Voicakert G., Aert R., Robben J., Grymoult P.,
RA Weltsch J., Vanstreels E., Rieger M., Schaefer M., Muller-Auer S.,
RA Gebel C., Fuchs M., Fritz C., Holzer E., Moesli D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Weller H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu S., Dreano S., Gloux S., Lelaute V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Huret S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
RA Cerruti L., Lowe T., McCombie W.K., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Useery D., Bartell B.G., Nurse P.,
RT The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC EMBL; Z69944; CA93814.1; -.
DR PIR; S67453; S67453.
DR HSP; P00175; IUTD.
DR Genedb_Spomb; SPAC1P12.10c; -.
DR InterPro; IPRO01199; Cyt_B5.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR ProDom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Hypothetical protein; Heme.
FT METAL 106 106
FT METAL 129 129 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 147 AA; 16667 MW; E874859F52B1AFD CRC64;

Query Match 6.0%; Score 146.5; DB 1; Length 147;
Best Local Similarity 41.3%; Pred. No.2.5e-05;
Matches 31; Conservative 13; Mismatches 24; Indels 7; Gaps 2;

QY 11 ITSEELKGNHKEGDLWISIGKRYNNSDWKVEHPGCDVPSINLAGODVDAFLAHPGTA 70
Db 74 VTKEELAKHKTKECDWAIKRGKYNSAVYLPYHAGCKRILDYAGRDATVIFMKFH--A 130
QY 71 WSH---LLEKFTGY 81
Db 131 WNEEALLKTSFVGF 145

RESULT 10
NIA_FUSOX STANDARD; PRT; 905 AA.
AC P39863;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase (NADPH) (EC 1.7.1.3) (NR).
GN NIA.
OS Fusarium oxysporum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocrematocetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxId=5507;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FOM24;
RX MEDLINE=93380674; Pubmed=8370541;
RA Dioler A., Langin T., Gerlinger C., Brygoo Y., Delbousi M.-J.;
RT "The nia gene of Fusarium oxysporum: isolation, sequence and
RT development of a homologous transformation system.";
RL Gene 131:61-67(1993).
CC CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NADP(+) + H(2)O = nitrate + NADPH.
CC -1- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
CC AND ONE MOLYBDENUM ATOM.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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CC -----

DR EMBL; Z22549; CAAB0270.1; .

DR PIR; JN0803; JN0803.

DR HSSP; P04166; 1EUE.

DR InterPro; IPR001199; Cyt_B5.

DR InterPro; IPR001834; Cyt_B5_reductase.

DR InterPro; IPR000572; Euk_Mb_oxred.

DR InterPro; IPR001709; FPN_Cyt_redctse.

DR InterPro; IPR005066; Mo-co_dimer.

DR InterPro; IPR001433; Oxred_FAD/NAD(P).

DR Pfam; PF00970; FAD_binding_6; 1.

DR Pfam; PF00173; heme_1; 1.

DR Pfam; PF03404; Mo-co_dimer; 1.

DR Pfam; PF00175; NAD_binding_1; 1.

DR Pfam; PF00174; oxidored_molayb; 1.

DR PRINTS; PR00406; CYTB5BDTASB.

DR PRINTS; PR00363; CYTOCHROME5.

DR PRINTS; PR00407; EUMOPTERIN.

DR PRINTS; PR00371; FPNCR.

DR PROSITE; PS000612; Cyt_B5; 1.

DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.

DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.

DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.

DR Oxidoreductase; Flavoprotein; FAD; NADP; Heme; Molybdenum; Nitrate assimilation.

KM DOMAIN 3

FT METAL 179 179 POLY-THR.

FT METAL 230 230 MOLYBDENUM-PTERIN (POTENTIAL).

FT DISULFID 428 428 MOLYBDENUM-PTERIN (POTENTIAL).

FT DOMAIN 550 620 INTERCHAIN (POTENTIAL).

FT METAL 581 581 HEME-BINDING (BY SIMILARITY).

FT METAL 604 604 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

FT DOMAIN 645 905 FLAVIN-BINDING DOMAIN (BY SIMILARITY).

FT NP_BIND 875 884 NADP (BY SIMILARITY).

SEQ SEQUENCE 905 AA; 101898 MW; D5D8E23F971ACDA CRC64;

Query Match 6.0%; Score 146; DB 1; Length 905;

Best Local Similarity 36.3%; Pred. No. 0.00022;

Matches 33; Conservative 14; Mismatches 32; Indels 12; Gaps 1;

QY 2 EVEKE-----KYYTSEELKGNKEGDLWISIOGKYVNSDWYKEHGGDVP 49

DB 528 EVVYKEPEKQICMTNPQINRKITTEELKAGSGEPEPVVAGVYDGPVLSGHPGGA 587

QY 50 ISNLAGQDVTAFIAYHPGTAWSHLEKFTG 80

DB 588 IFGAAGQDATEEFMAHSENAKAMLPYHIG 618

RESULT 11

CYB5_RABIT STANDARD; PRT; 133 AA.

AC P00169; Q28726; .

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Cytochrome b5.

GN CYB5.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCI_TaxID=9986;

RN (1)

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=8912816; PubMed=322252;

RA Darluah N., Fisher C.W., Steggle A.W.;

RT "The nucleotide sequence of rabbit liver cytochrome b5 mRNA.";

RL Protein Seq. Data Anal. 1:351-353(1988).

RN (2)

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC STRAIN=New Zealand white;

RX MEDLINE=92328788; PubMed=1627141;

RA Takamatsu H., Kozusumi Y., Suzuki A., Kawasaki T.;

RT "Molecular cloning of rabbit cytochrome b5 genes: evidence for the occurrence of two separate genes encoding the soluble and microsomal forms.";

RL Biochem. Biophys. Res. Commun. 185:845-851(1992).

RN (3)

RP SEQUENCE OF 8-45 AND 49-90.

RX MEDLINE=69108767; PubMed=5709273;

RA Tawgita A., Kobayashi M., Kajihara T., Hagihara B.;

RT "Primary structure of rabbit liver cytochrome b5.";

RL J. Biochem. 64:727-730(1968).

RN (4)

RP SEQUENCE OF 6-7 AND 46-48.

RX MEDLINE=70289989; PubMed=5272324;

RA Tawgita A., Kobayashi M., Tani S., Kyo S., Rashid M.A., Yoshida Y., Kajihara T., Hagihara B.;

RT "Comparative study of the primary structures of cytochrome b5 from four species.";

RL Proc. Natl. Acad. Sci. U.S.A. 67:442-447(1970).

RN (5)

RP SEQUENCE OF 4-97.

RX MEDLINE=71001482; PubMed=5506260;

RA Ozols J.;

RT "Amino acid sequence of rabbit liver microsomal cytochrome b5.";

RL J. Biol. Chem. 245:4863-4874(1970).

RN (6)

RP SEQUENCE OF 91-133.

RX MEDLINE=80049603; PubMed=500581;

RA Kondo K., Tajima S., Sato R., Narita K.;

RT "Primary structure of the membrane-binding segment of rabbit cytochrome b5.";

RL J. Biochem. 86:1119-1128(1979).

RN (7)

RP SEQUENCE OF 98-133.

RX MEDLINE=80115672; PubMed=7354043;

RA Takagaki Y., Geher G.B., Nihel K., Khorana H.G.;

RT "Amino acid sequence of the membranous segment of rabbit liver cytochrome b5. Methodology for separation of hydrophobic peptides.";

RL J. Biol. Chem. 255:1536-1541(1980).

RN (8)

RP SEQUENCE OF 1-10.

RX MEDLINE=89323209; PubMed=2752049;

RA Ozols J.;

RT "Structure of cytochrome b5 and its topology in the microsomal membrane.";

RL Biochim. Biophys. Acta 997:121-130(1989).

RN (9)

RP STRUCTURE BY NMR OF 6-99.

RX MEDLINE=20117684; PubMed=10651812;

RA Banci L., Bertini I., Rosato A., Scacchiari S.;

RT "Solution structure of oxidized microsomal rabbit cytochrome b5 factors determining the heterogeneous binding of the heme.";

RL Eur. J. Biochem. 267:755-766(2000).

CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND OXYGENASES.

CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM.

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named Isoforms=2;

CC Name=1; Synonyms=liver, Membrane-bound;

CC IsoId=P00169-1; Sequence=Displayed;

CC Name=2; Synonyms=Brylncocyte, Cytoplasmic;

CC IsoId=P00169-2; Sequence=VSP_001244, VSP_001245;

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

CC -----

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CC EMBL; M24844; AAB03878.1; -
 CC EMBL; D10901; BAA01712.1; -
 DR PIR; J03373; CERB5.
 DR PIR; J03373; CERB5.
 DR PDB; 1D09; 20-MAR-00.
 DR InterPro; IPR001199; Cyt B5.
 DR Pfam; PF00173; heme 1; 1.
 DR Prodom; PD000612; Cyt B5; 1.
 DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME B5_2; 1.
 DR Electrom transport; Transmembrane; Heme; Iron; Microsome; Acetylation;
 KM Alternative splicing; 3D-structure.
 FT INIT MET 0 0
 FT MOD RES 1 1 ACETYLATION.
 FT DOMAIN 1 90 HEME-BINDING.
 FT METAL 43 43 MEMBRANE-BINDING.
 FT METAL 67 67 IRON (HEME AXIAL LIGAND).
 FT METAL 97 97 IRON (HEME AXIAL LIGAND).
 FT VARSPPLIC 97 97 T -> P (in isoform 2).
 FT VARSPPLIC 97 97 /FTid=VSP_001244.
 FT VARSPPLIC 98 133 Missing (in isoform 2).
 FT CONFLICT 61 61 /FTid=VSP_001245.
 FT CONFLICT 103 103 N -> D (IN REF. 3 AND 5).
 FT CONFLICT 103 103 D -> N (IN REF. 6).
 SQ SEQUENCE 133 AA; 15218 MW; 2848AEC0BC39720 CRC64;

Query Match 5.9%; Score 144; DB 1; Length 133;
 Best Local Similarity 28.6%; Pred. No. 3.6e-05;
 Matches 36; Conservative 25; Mismatches 65; Indels 0; Gaps 0;

QY 5 EKEKYYTSELKGNKEGDLWISIOGKVVNSPDWVEHFGDVPISNLGQVTDPAFIA 64
 DB 5 DKVQKYYTLEIKKHNKSKTWLHKKVVDLTFLEHGGSEVLRBOGSGDATEMFED 64
 QY 65 YHGTAWSHLEKFFTYGHLSDPKVSEVSKDYRKLAESFSLGLFTDKGHTVSTCLASVAV 124
 DB 65 VGHSTDAEELSKFTIIGELHAPDDRSLKSLKPMETLITVDNSNSWMTWVIPAISALVAL 124
 QY 125 MELIVL 130
 DB 125 MYRLYM 130

RESULT 12
 CYB5_YEAST STANDARD; PRT; 120 AA.
 AC P40312;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5.
 GN CYB5 OR YNL111C OR N1949.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FL100;
 RX MEDLINE=94237477; PubMed=8181746;
 RA Tuan G., Epinat J.-C., Rougulle C., Cullin C., Pompon D.;
 RT Cloning and characterization of a yeast cytochrome b5-encoding gene
 which suppresses ketoconazole hypersensitivity in a NADPH-P-450
 reductase-deficient strain.";
 RL Gene 142:123-127 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97245296; PubMed=9090055;
 RA de Antoni A., D'Angelo M., Dal Pero F., Sartorello F., Pandolfo D.,
 RA Pallavicini A., Lanfranchi G., Valle G.;
 RT "The DNA sequence of cosmid 14-13b from chromosome XIV of

RT Saccharomyces cerevisiae reveals an unusually high number of
 RT overlapping open reading frames.";
 RL Yeast 13:261-266 (1997).
 CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases. It plays a role in
 CC fatty-acid desaturation and is also involved in several steps of
 CC the steroid biosynthesis pathway, particularly in the 4-
 CC demethylation of the 4,4'-dimethyl zymosterol.
 CC -1- SUBCELLULAR LOCATION: MICROSOmal MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -----
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 CC or send an email to license@lsb-sib.ch).
 CC -----
 DR EMBL; L22494; AAA67468.1; -
 DR EMBL; Z69382; CAA93396.1; -
 DR EMBL; Z71387; CAA95990.1; -
 DR PIR; S63052; S63052.
 DR HSSP; P04166; 1EUE.
 DR SGD; S0005055; CYB5.
 DR GO; GO:0005792; Cytochrome b5.
 DR GO; GO:0016126; Steroid biosynthesis; IDA.
 DR InterPro; IPR001199; Cyt B5.
 DR Pfam; PF00173; heme 1; 1.
 DR PRINTS; PR00363; CYTOCHROME B5.
 DR Prodom; PD000612; Cyt B5; 1.
 DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME B5_2; 1.
 KM Electrom transport; Transmembrane; Heme; Iron; Microsome.
 FT TRANSHEM 98 118 POTENTIAL.
 FT METAL 37 37 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 61 61 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT CONFLICT 17 17 E -> Q (IN REF. 1).
 SQ SEQUENCE 120 AA; 13297 MW; 598EF2A6730CAD19 CRC64;

Query Match 5.8%; Score 143; DB 1; Length 120;
 Best Local Similarity 29.9%; Pred. No. 3.8e-05;
 Matches 38; Conservative 25; Mismatches 52; Indels 12; Gaps 3;

QY 9 KYITSELKGNKEGDLWISIOGKVVNSPDWVEHFGDVPISNLGQVTDPAFIY-HP 67
 DB 3 KVTSGVEAHNPPENFWIIDDKVTDSQFKDEHFGDEIIMDLGGQDATESFVIGHS 62
 QY 68 GTAWSHLEKFFTYGHLSDPKVSEVSKDYRKLAESFSLGLFTDKGHTVSTCLASVAVML 127
 DB 63 DEALRLKGLYIG-----DVDKTSERVSE--KVTSEKSGSGGLVLAIVLML 111
 QY 128 IYLYGV 134
 DB 112 GVAVYVL 118

RESULT 13
 CYB5_TOBAC STANDARD; PRT; 135 AA.
 AC P49099;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5, seed isoform.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotae;
 OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=cv, Samsun; TISSUE=Seed;
RX MEDLINE=96009039; PubMed=7580860;
RA Napier J.A., Smith M.A., Stobart A.K., Shewry P.R.;
RT "isolation of a cDNA encoding a cytochrome b5 specifically expressed
in developing tobacco seeds."
RL Planta 197;200-202(1995).
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
OXYGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY
DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH IN
THE DEVELOPING SEED IS UTILIZED FOR MEMBRANE SYNTHESIS AND IN THE
DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE
LIPIDS.
CC -1- SUBCELLULAR LOCATION: MICROSOAL MEMBRANE. BOUND TO THE
CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING SEEDS.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC -----
DR EMBL; X80008; CAA56318.1; -.
DR PIR; S49200; S49200.
DR HSSP; P00171; ICTO.
DR InterPro; IPR001199; Cyt_B5.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME B5_2; 1.
KM Electron transport; Transmembrane; Heme; Iron; Microsome;
KM Multigene family.
FT TRANSSEM 107 127
FT METAL 40 40
FT METAL 64 64
FT METAL 64 64
FT METAL 64 64
SQ SEQUENCE 135 AA; 14669 MW; A36CCN081A72EBC6 CRC64;
Query Match 5.8%; Score 142.5; DB 1; Length 135;
Best Local Similarity 36.0%; Pred. No. 4.8e-05;
Matches 27; Conservative 17; Mismatches 30; Indels 1; Gaps 1;
QY 7 EKKYITSEELKGNKGGDLWISIQKVVNVSDWKEHGGVDPISNLAGOVDTAFIAY - 65
DB 4 QSKVFTLAEVSQHNNAKDCWLIVISGKYVNTKFLDHPGGDEVLLSATGKDATDFFDVG 63
QY 66 HPGTAMSHLEKFTFG 80
DB 64 HSSSRAMLDYVYG 78
RESULT 14
CYB5_TOBAC
ID CYB5_TOBAC STANDARD; PRT; 136 AA.
AC P49096;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b5.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=94325476; PubMed=8049375;
RA Smith M.A., Stobart A.K., Shewry P.R., Napier J.A.;
RT "Tobacco cytochrome b5: cDNA isolation, expression analysis and in

RT vitro protein targeting."
RL Plant Mol. Biol. 25;527-537(1994).
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
OXYGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY
DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH IN
THE DEVELOPING SEED IS UTILIZED FOR MEMBRANE SYNTHESIS AND IN THE
DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE
LIPIDS. IS INVOLVED IN THE REDUCTION OF CYTOCHROME P-450 AND
MAY THEREFORE BE INVOLVED IN FLAVONOID BIOSYNTHESIS IN THE PETALS.
CC -1- SUBCELLULAR LOCATION: MICROSOAL MEMBRANE. BOUND TO THE
CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: IS HIGHLY EXPRESSED IN DEVELOPING SEEDS.
CC MODERATELY EXPRESSED IN FLOWERS, AND IS EXPRESSED AT LOW
LEVELS IN THE LEAF.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC -----
DR EMBL; X71441; CAA50575.1; ALT_INIT.
DR EMBL; X68140; CAA48240.1; -.
DR HSSP; P04166; IB5M.
DR InterPro; IPR001199; Cyt_B5.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME B5_2; 1.
KM Electron transport; Transmembrane; Heme; Iron; Microsome;
KM Multigene family.
FT TRANSSEM 107 127
FT METAL 40 40
FT METAL 64 64
FT METAL 64 64
FT CONFLICT 10 11
FT CONFLICT 105 105
SQ SEQUENCE 136 AA; 14979 MW; DACE9EA695B2835F CRC64;
Query Match 5.8%; Score 142.5; DB 1; Length 136;
Best Local Similarity 37.3%; Pred. No. 4.9e-05;
Matches 28; Conservative 16; Mismatches 30; Indels 1; Gaps 1;
QY 7 EKKYITSEELKGNKGGDLWISIQKVVNVSDWKEHGGVDPISNLAGOVDTAFIAY - 65
DB 4 ETKVFTLAIVSQHNNAKDCWLIVISGKYVNTKFLDHPGGDEVLLSATGKDATDFFDVG 63
QY 66 HPGTAMSHLEKFTFG 80
DB 64 HSSSRAMLDYVYG 78
RESULT 15
CYB5_HUMAN
ID CYB5_HUMAN STANDARD; PRT; 146 AA.
AC O43169;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b5 outer mitochondrial membrane isoform precursor.
GN CYB5M OR OMB5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Ishibashi K.;
RT "Cytochrome b5 and aquaporins share the last transmembrane amino acids

```

RT sequence."
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
CC OXYGENASES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Mitochondrial outer membrane (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AB009282; BAA23735.1; -
DR HSSP; P04166; 1B5M.
DR InterPro; IPR001199; Cyt_B5.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR PRODOM; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Electron transport; Mitochondrion; Outer membrane; Transmembrane;
KW Heme; Iron.
FT PROPEP 1 11 BY SIMILARITY
FT CHAIN 12 146 CYTOCHROME B5 OUTER MITOCHONDRIAL
FT DOMAIN 12 103 MEMBRANE ISOFORM.
FT TRANSMEM 119 136 HEME-BINDING.
FT METAL 55 55 POTENTIAL.
FT METAL 79 79 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 146 AA; 16332 MW; 2FF7DBA297124E19 CRC64;

Query Match 5.8%; Score 141.5; DB 1; Length 146;
Best Local Similarity 27.6%; Pred. No. 6,4e-05;
Matches 43; Conservative 22; Mismatches 50; Indels 41; Gaps 5;

QY 4 VEKEKYYTSEELKGNKEDLMISIQKYYNVDWYKEHGGDVPISNLAGDVTDAF- 62
DB 16 VETSVYYRLEAEVAKRNSLKEVLVIHGRVYDVTPLNEHGGSEVLLDAQVDASFSFE 75
QY 63 IAHYPTGASHLSEKFTG-YHLSDFKSEVSKDYKXLAESFKLGDPDTKGHTSCTLAS 121
DB 76 DVGHSSDAREMLKQYIIGDIHPBDLKPESGSKDPSQ-----NDT----- 114
QY 122 VAVMFLIVLYGVLCRTSVMAH---LGGSMILGLW 153
DB 115 -----CKSCWAYWILPIIGAVLGLFLY 136

```

Search completed: January 1, 2004, 06:30:56
 Job time : 9.90156 secs

GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: January 1, 2004, 06:29:49 / Search time 40.388 Seconds
(without alignments)
2875.205 Million cell updates/sec

Title: US-09-857-524B-8
Perfect score: 2449
Sequence: 1 MEVVEKEKTYITSEELKGN.....RDLTPAPKNLMWEAVNTHG 450

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_plant:*
- 10: sp_proteome:*
- 11: sp_virus:*
- 12: sp_vertebrate:*
- 13: sp_unclassified:*
- 14: sp_virus:*
- 15: sp_bacteriophage:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1802	77.7	449	10	Q9ZRP7
2	1899	77.5	449	10	Q8LBP6
3	1887	77.1	449	10	Q9ZRP8
4	1801.5	73.6	446	10	Q9FR82
5	1801	73.5	458	10	Q43469
6	1749.5	71.4	446	10	Q9ZRP9
7	1692.5	69.1	446	10	Q8LBP7
8	1670	68.2	448	10	Q8VZ22
9	1656	67.6	448	10	Q9SAU5
10	1655	67.5	448	10	Q04353
11	1653	67.5	448	10	Q8VZ21
12	1597	65.2	449	10	Q8L717
13	1463	59.7	469	10	Q9ZT18
14	688.5	28.1	523	3	Q9HDS8
15	562.5	23.0	568	3	Q8NKG9
16	557.5	22.8	520	10	Q9LEW9

17	548.5	22.4	573	3	Q8NKG8	Q8NKG8 kluyveromyc
18	544	22.2	483	10	Q9LEW0	Q9LEW0 ceratodon p
19	518.5	21.2	459	10	Q944W4	Q944W4 pythium irr
20	512.5	20.9	525	10	Q9ZRW2	Q9ZRW2 physcomitrite
21	502.5	20.5	457	3	Q9UVV3	Q9UVV3 mortierella
22	500.5	20.4	457	3	Q9HEY4	Q9HEY4 mortierella
23	500.5	20.4	467	3	Q9EVC3	Q9EVC3 mucor circi
24	498.5	20.4	457	3	Q8X173	Q8X173 mortierella
25	492.5	20.1	457	3	Q9UVV3	Q9UVV3 mortierella
26	492.5	20.1	457	3	Q9HEY1	Q9HEY1 mortierella
27	492.5	20.1	457	3	Q8X174	Q8X174 mortierella
28	492	20.1	477	10	Q8RXB0	Q8RXB0 phaeodactyl
29	456	18.6	454	13	Q98SW7	Q98SW7 oncorhynch
30	455.5	18.6	444	11	Q9ZOR9	Q9ZOR9 mus musculu
31	453	18.5	452	13	Q8UMW5	Q8UMW5 oncorhynch
32	451.5	18.4	444	11	Q9Z122	Q9Z122 ratius norv
33	450.5	18.4	454	13	Q8QGE2	Q8QGE2 salmo salar
34	447	18.3	419	10	Q9SMQ9	Q9SMQ9 euglena gra
35	445.5	18.2	447	11	Q9ZOR3	Q9ZOR3 ratius norv
36	444.5	18.2	445	13	Q8AY64	Q8AY64 sparus aura
37	441.5	18.0	444	4	Q95864	Q95864 homo sapien
38	441.5	18.0	447	11	Q9EPV4	Q9EPV4 ratius norv
39	439.5	17.9	454	13	Q90Z28	Q90Z28 oncorhynch
40	439	17.9	501	4	Q8NCG0	Q8NCG0 homo sapien
41	436	17.8	445	4	Q9Y5Q0	Q9Y5Q0 homo sapien
42	435	17.8	444	4	Q96139	Q96139 homo sapien
43	435	17.8	444	4	Q96T10	Q96T10 homo sapien
44	435	17.8	444	4	Q60427	Q60427 homo sapien
45	433	17.7	444	4	Q9NRP8	Q9NRP8 homo sapien

ALIGNMENTS

RESULT 1

ID	Q9ZRP7	PRELIMINARY;	PRT;	449 AA.
AC	Q9ZRP7			
DT	01-MAY-1999 (TREMURel. 10, Created)			
DT	01-MAY-1999 (TREMURel. 10, Last sequence update)			
DT	01-MAR-2003 (TREMURel. 23, Last annotation update)			
DE	Delta-8 sphingolipid desaturase (ATG61580/FA19_180).			
GN	SLD1 OR FA19_180 OR ATG61580.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
CC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
CC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
CC	eucosids II; Brassicales; Brassicaceae; Arabidopsids.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia; TISSUE=flower, MAINLY GREEN PARTS, and Root;			
RX	MEDLINE=99003197; PubMed=9786850;			
RA	Sperling P., Zaehring U., Heinz E.;			
RT	"A sphingolipid desaturase from higher plants. Identification of a new			
RT	cytochrome b5 fusion protein."			
RL	J Biol. Chem. 273:28590-28596(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	De Haan M., Maarse A.C., Grievell L.A., Mewes H.W., Lemcke K.,			
RA	Mayer K.F.X., Queller F., Salanoubat M.;			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	EU Arabidopsis sequencing project;			
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Chauk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banj J.,			
RA	Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,			
RA	Ishida J., Jiang P.X., Jones T., Kamita A., Karlin-Neuman G.,			
RA	Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,			
RA	Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,			
RA	Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,			

RA Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
 RA Becker J.R.;
 RT "Arabidopsis cDNA clones";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
 RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
 RA Deng J.M., Hayashizaki Y., Huan V.W., Lee J.M., Ishida J., Kamiya A.,
 RA Seki M., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
 RA Wu H.C., Yamada K., Yu G., Yuan S., Shinzaki K., Ecker J.,
 RA Theologis A., Davis R.W.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AJ224161; CA11858.1; -;
 DR EMBL: AL132962; CAB71088.1; -;
 DR EMBL: AF28420; AAL16189.1; -;
 DR EMBL: BT000442; AAN17419.1; -;
 DR HSSP: P00171; 115U.
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 449 AA; 51675 MW; 145048F9FD1D35964 CRC64;
 Query Match 77.7%; Score 1902; DB 10; Length 449;
 Best Local Similarity 74.7%; Pred. No. 1.6e-167;
 Matches 334; Conservative 54; Mismatches 58; Indels 0; Gaps 0;
 QY 5 EKEKKYITSEBLKGNKEDLWISIQKYYNVDWVKEHFGDVPISNLAGDVTDAFIA 64
 DB 4 ETEKKYITNEDLKGKNSGDLWIAIQKYYNVDWVKEHFGDVTIINLVGDVTDAFIA 63
 QY 65 YHGTAMSHLEKFFTGTHLSDPKVSEVSKDYRKLAEESEKLGFDTKGHTSCTLASVAV 124
 DB 64 FHEGTAMHHDHLEFTGYHNRDPVSEVSRDYRRMAAEFRKLGLEFKKGHTVLTYYTLAFVAA 123
 QY 125 MFLIVYGVLCSTSVANHLGSGMLGLLMMQSAVYVGHDSGHVYVMTNGFNKVAQLISGN 184
 DB 124 MFLGVLYGVLCSTSVFAGHQAALALGLLWIOQAVYIGHDSGHVYVIMSKSNRFAQLISGN 183
 QY 185 CLTGSIAMWKTHNHNHIAACNSLDHDPDLOHMPVFAVSSRFNSITSHFYGRKLEFDP 244
 DB 184 CLTGSIAMWKTHNHNHIAACNSLDYDPDLOHMPVFAVSTKFFSSITSRFYDRKLTFFDPV 243
 QY 245 ARFLICYOHTFTYVWCVARVNLVLOTILLFSRRKVDORALNIMGILVFWTFPFLVSC 304
 DB 244 ARFLVYOHFTYVWCVARVNLVLOTILLFSRRKVDORALNIMGILVFWTFPFLVSC 303
 QY 305 LPMWPERWVFLASFAVCSIOHIOFCLNHFANVYVGPSPGNDWFEKOTSGTLDISCAS 364
 DB 304 LPMWPERWVFLASFAVCSIOHIOFCLNHFADVYVGPSPGNDWFEKOAAGTIDISCRSY 363
 QY 365 MDWFFGGLQFOLEHNLFPRLPRCOLKISPLVSDLCCKGNLPRYSLSFWEANQWTRTLR 424
 DB 364 MDWFFGGLQFOLEHNLFPRLPRCHLRKVSPPVQELCKGNLPRYSMSWFEANVLTINTLK 423
 QY 425 TAAIQARDLTNPAPKQNLWEAVNTHG 450
 DB 424 TAAIQARDVANPVKQNLWEALNTHG 449

RESULT 2
 OBLB96 PRELIMINARY; PRT; 449 AA.
 AC OBLB96;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)

DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Delta-8 sphingolipid desaturase.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Haas B.J., Volovicky N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation";
 RL Genome Biol. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RT "Full-length cDNA from Arabidopsis thaliana";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AY087345; AAM64895.1; -;
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 449 AA; 51744 MW; A1EB57B8CE03E18 CRC64;
 Query Match 77.5%; Score 1899; DB 10; Length 449;
 Best Local Similarity 74.7%; Pred. No. 3e-167;
 Matches 333; Conservative 54; Mismatches 59; Indels 0; Gaps 0;
 QY 5 EKEKKYITSEBLKGNKEDLWISIQKYYNVDWVKEHFGDVPISNLAGDVTDAFIA 64
 DB 4 ETEKKYITNEDLKGKNSGDLWIAIQKYYNVDWVKEHFGDVTIINLVGDVTDAFIA 63
 QY 65 YHGTAMSHLEKFFTGTHLSDPKVSEVSKDYRKLAEESEKLGFDTKGHTSCTLASVAV 124
 DB 64 FHEGTAMHHDHLEFTGYHNRDPVSEVSRDYRRMAAEFRKLGLEFKKGHTVLTYYTLAFVAA 123
 QY 125 MFLIVYGVLCSTSVANHLGSGMLGLLMMQSAVYVGHDSGHVYVMTNGFNKVAQLISGN 184
 DB 124 MFLRVLYGVLCSTSVFAGHQAALALGLLWIOQAVYIGHDSGHVYVIMSKSNRFAQLISGN 183
 QY 185 CLTGSIAMWKTHNHNHIAACNSLDHDPDLOHMPVFAVSSRFNSITSHFYGRKLEFDP 244
 DB 184 CLTGSIAMWKTHNHNHIAACNSLDYDPDLOHMPVFAVSTKFFSSITSRFYDRKLTFFDPV 243
 QY 245 ARFLICYOHTFTYVWCVARVNLVLOTILLFSRRKVDORALNIMGILVFWTFPFLVSC 304
 DB 244 ARFLVYOHFTYVWCVARVNLVLOTILLFSRRKVDORALNIMGILVFWTFPFLVSC 303
 QY 305 LPMWPERWVFLASFAVCSIOHIOFCLNHFANVYVGPSPGNDWFEKOTSGTLDISCAS 364
 DB 304 LPMWPERWVFLASFAVCSIOHIOFCLNHFADVYVGPSPGNDWFEKOAAGTIDISCRSY 363
 QY 365 MDWFFGGLQFOLEHNLFPRLPRCOLKISPLVSDLCCKGNLPRYSLSFWEANQWTRTLR 424
 DB 364 MDWFFGGLQFOLEHNLFPRLPRCHLRKVSPPVQELCKGNLPRYSMSWFEANVLTINTLK 423
 QY 425 TAAIQARDLTNPAPKQNLWEAVNTHG 450
 DB 424 TAAIQARDVANPVKQNLWEALNTHG 449

RESULT 3
 Q9ZRP8 PRELIMINARY; PRT; 449 AA.
 AC Q9ZRP8;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)

DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Delta-8 sphingolipid desaturase.
 GN SLD1.
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Brassica.
 CX NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Drakkar; TISSUE=Ripening embryos;
 RA MEDLINE=99003197; PubMed=9786850;
 RX Sperling P.; Zaehring U.; Heinz B.;
 RT "A sphingolipid desaturase from higher plants: identification of a new
 cytochrome b5 fusion protein".
 RL J. Biol. Chem. 273:28590-28596 (1998).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AJ224160; CAA11857.1; -.
 DR HSSP; P82291; 10XY.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KM Heme.
 SQ SEQUENCE 449 AA; 51490 MW; FEFEE37AF9D390C1 CRC64;
 Query Match 77.1%; Score 1887; DB 10; Length 449;
 Best Local Similarity 74.7%; Pred. No. 3.9e-166;
 Matches 333; Conservative 52; Mismatches 61; Indels 0; Gaps 0;
 QY 5 EKEKKYITSEBELKHNKEDLMISIQGKYNNVSDWYKHPGADVPISNLAGQVDTDAFI 64
 DB 4 QTKKRFITSDLDKKNQPGDLMISIQGKYVDVSHWVSKHPGEAAILNLAGQVDTDAFI 63
 DB 64 YHPTARHLENLHNGYHVDHVSVDVSRDLRAEFSKRGLEPKGHVTLVTLTGVAA 123
 QY 65 YHPTASHLEKFTGYHLSDFKXSEVSKDYRKLAESFKLGFDTRKGVTSCTLASVA 124
 DB 125 MFLLIVLVGLRCTSVVAHLSGMLLGLMMQSAVYVGHDSGHVYVMTTNGFKNVAQIISGN 184
 DB 124 MAAVVYGVACTIMAHILSAVLGLIMISAVYVGHDSGHVYVNTSTKPCKKLVQLISGN 183
 QY 185 CLTGISIAWMTNNAHIAICNSLDHDPDLQHPVFAVSSRFNSITSHFYGRKLEPFI 244
 DB 184 CITGISIAWMTNNAHIAICNSLDHDPDLQHPVFAVSSRFNSITSHFYGRKLEPFI 243
 QY 245 ARFLICQHFPTFYVVCVAVNLVLTLLFSRRKQDRALNIMGLVFTWEPPLVSC 304
 DB 244 ARFLISYQHSFYIMCVGRINLEIOTLLIFSRBYVDRALNIAGLVFTWEPPLVSC 303
 QY 305 LPMNBEVMPFLAFAVCSIOHIOFCINHFANVYVGPBGNDMPFEKOTSGTLDISCAS 364
 DB 304 LPMNBEVMPFLAFAVCSIOHIOFCINHFANVYVGPBGNDMPFEKOTSGTLDISCAS 363
 QY 365 MDWFFGGLQFLEHNLPRPLRCOLRKISPLVSDLCCKKNLPYRSLSEWENQWITIRL 424
 DB 364 MDWFFGGLQFLEHNLPRPLRCOLRKISPLVSDLCCKKNLPYRSLSEWENQWITIRL 423
 QY 425 TAAQARDLTNPAKULMEAVNTHG 450
 DB 424 KAAVQARDVTPVLENLMEALNTHG 449

RESULT 4
 Q9FR82 PRELIMINARY; PRT; 446 AA.
 AC Q9FR82;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta 8-sphingolipid desaturase.
 GN SLD1.
 OS Borago officinalis (Bourrache) (Borage).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Boraginaceae; Borago.
 CX NCBI_TaxID=13363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21092516; PubMed=11368168;
 RA Libisch B.; Michaelson L.V.; Lewis M.J.; Shewry P.R.; Napier J.A.;
 RT "Chimeras of Delta8-fatty acid and Delta8-sphingolipid desaturases";
 RL Biochem. Biophys. Res. Commun. 279:779-785 (2000).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AF133728; AAG43277.1; -.
 DR HSSP; P00171; 11SU.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KM Heme.
 SQ SEQUENCE 446 AA; 50926 MW; EBD579F035A3AF0C CRC64;
 Query Match 73.6%; Score 1801.5; DB 10; Length 446;
 Best Local Similarity 71.8%; Pred. No. 3.2e-158;
 Matches 321; Conservative 58; Mismatches 67; Indels 1; Gaps 1;
 QY 4 VEKCKYITSEBELKHNKEDLMISIQGKYNNVSDWYKHPGADVPISNLAGQVDTDAFI 63
 DB 1 MEKTKYISVGELEKHNQGLDVMISIQGKYNNVSDWYKHPGADVPISNLAGQVDTDAFI 60
 DB 64 AYHPTASHLEKFTGYHLSDFKXSEVSKDYRKLAESFKLGFDTRKGVTSCTLASVA 123
 DB 61 AYHPTASHLEKFTGYHLSDFKXSEVSKDYRKLAESFKLGFDTRKGVTSCTLASVA 120
 QY 124 VMEFLIVLVGLRCTSVVAHLSGMLLGLMMQSAVYVGHDSGHVYVMTTNGFKNVAQIISG 183
 DB 121 LILCGCYVGLCNSLNVHLSGMLCMCRIOAAVYVGHDSGHVYVMTTNGFKNVAQIISG 180
 QY 184 NCLTGISIAWMTNNAHIAICNSLDHDPDLQHPVFAVSSRFNSITSHFYGRKLEPFI 243
 DB 181 NCLTGISIAWMTNNAHIAICNSLDHDPDLQHPVFAVSSRFNSITSHFYGRKLEPFI 240
 QY 244 IARFLICQHFPTFYVVCVAVNLVLTLLFSRRKQDRALNIMGLVFTWEPPLVSC 303
 DB 241 IARFLICQHFPTFYVVCVAVNLVLTLLFSRRKQDRALNIMGLVFTWEPPLVSC 300
 QY 304 CLPMPERWVFLAFAVCSIOHIOFCINHFANVYVGPBGNDMPFEKOTSGTLDISCAS 363
 DB 301 CLPMPERWVFLAFAVCSIOHIOFCINHFANVYVGPBGNDMPFEKOTSGTLDISCAS 360
 QY 364 SMWFFGGLQFLEHNLPRPLRCOLRKISPLVSDLCCKKNLPYRSLSEWENQWITIRL 423
 DB 361 SMWFFGGLQFLEHNLPRPLRCOLRKISPLVSDLCCKKNLPYRSLSEWENQWITIRL 420
 QY 424 RTAALQARDLTNPAKULMEAVNTHG 450
 DB 421 RTAALQARDLTNPAKULMEAVNTHG 446

RESULT 5

Q43469 ID 043469 PRELIMINARY; PRT; 458 AA.
 AC Q43469; 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Delta-8 sphingolipid desaturase.
 GN SLDI.
 OS Helianthus annuus (Common sunflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Campanulids; Asterales; Asteraceae; Asteroideae;
 OC Heliantheae; Helianthus.
 OC NCBI_TaxID=4232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Indred line HA89;
 RC TISSUE=Cotyledons of developing sunflower fruits;
 RX MEDLINE=96028121; PubMed=7586718;
 RA Sperling P., Schmidt H., Heinz E.;
 RT "A cytochrome b5-containing fusion protein similar to plant acyl lipid
 desaturases";
 RT Eur. J. Biochem. 232:798-805(1995).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=cv. Indred line HA89;
 RC TISSUE=Cotyledons of developing sunflower fruits;
 RX MEDLINE=21116801; PubMed=1171153;
 RA Sperling P., Blume A., Zaehneringer U., Heinz E.;
 RT "Further characterization of delta 8-sphingolipid desaturases from
 higher plants";
 RL Biochem. Soc. Trans. 28:638-641(2000).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: X87143; CAA60621.1; -.
 DR HSSP: P00171; 1F03.
 DR InterPro: IPR001199; Cyt. B5.
 DR InterPro: IPR005804; FA_desat. fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme 1; 1.
 DR ProDom: PD000612; Cyt. B5; 1.
 DR ProDom: PD001081; FA_desat. fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 DR Heme.
 SQ SEQUENCE 458 AA; 52231 MW; D182287AB0E99245 CRC64;
 Query Match 73.5%; Score 1801; DB 10; Length 458;
 Best Local Similarity 71.6%; Pred. No. 3.7e-158;
 Matches 317; Conservative 55; Mismatches 71; Indels 0; Gaps 0;

Qy 368 FRGGLQFOLEHHLPRLPRCOLRKISPLVSDLCCKGNLPYSLSEMEANQWITRLRTAA 427
 |||||
 Db 376 FRGGLQFOLEHHLPRLPRCHLRISISPCRELCKKNLPYSLSEFYNATVTLKTLRTAA 435
 |||||
 Qy 428 LQARDLTNPAPKNLMEAVNTG 450
 |||||
 Db 436 LQARDLTNPAPKNLMEAVNTG 458
 |||||
 RESULT 6
 ID 092TY9 PRELIMINARY; PRT; 446 AA.
 AC 092TY9;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Desaturase/cytochrome b5 protein.
 OS Ricinus communis (Castor bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucoside 1; Malpighiales; Euphorbiaceae; Ricinus.
 OC NCBI_TaxID=3988;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Seed endosperm;
 RX MEDLINE=97268723; PubMed=9108131;
 RA Savanova O., Smith M.A., Lapinikas P., Stobart A.K., Dobson G.,
 RA Christie W.W., Shewry P.R., Napier J.A.;
 RT "Expression of a borage desaturase cDNA containing an N-terminal
 cytochrome b5 domain results in the accumulation of high levels of
 delta6-desaturated fatty acids in transgenic tobacco";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AF005096; AAD01240.1; -.
 DR HSSP: P00171; 115U.
 DR InterPro: IPR001199; Cyt. B5.
 DR InterPro: IPR005804; FA_desat. fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme 1; 1.
 DR ProDom: PD000612; Cyt. B5; 1.
 DR ProDom: PD001081; FA_desat. fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 DR Heme.
 SQ SEQUENCE 446 AA; 51418 MW; A1954FDB2DDB600F CRC64;
 Query Match 71.4%; Score 1749.5; DB 10; Length 446;
 Best Local Similarity 69.1%; Pred. No. 2.1e-153;
 Matches 306; Conservative 58; Mismatches 78; Indels 1; Gaps 1;

QY 368 FFGGLQOLEHNLPRPLRCQRLKISPLVSDLCCKHNPYRSLSFWEANQMTITRTAA 427
 DB 364 FHGGLQFQMEHNLPRPLRVLTRKRSFVRELCKCKHNPYDSASFMANELTFTLRRAA 423

QY 428 LQARDLTPAPKXNLMEAVNTHG 450
 DB 424 LQARDLTPAPKXNLMEAVNTHG 446

RESULT 7

Q8BLD7 PRELIMINARY; PRT; 446 AA.
 AC Q8BLD7;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Spingolipid long chain base delta 8 desaturase.
 OS Aquilegia vulgaris.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
 OC Ranunculaceae; Aquilegia.
 OX NCBI_TaxID=3451;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Longman A.J., Michaelson L.V., Napier J.A.;
 RT "Isolation and characterization of a cDNA encoding a delta 8
 RT spingolipid desaturase from Aquilegia vulgaris."
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AF06816; AAN03619.1; -.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; FA desat. fam.
 DR Pfam; PF00487; FA desaturase; 1.
 DR PRINTS; PR00173; heme_1; 1.
 DR PRODOM; PD000612; Cyt B5; 1.
 DR PRODOM; PD001081; FA desat. fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.

SO SEQUENCE 446 AA; 51273 MW; 76366DB0B956D09 CRC64;

Query Match 69.1%; Score 1692.5; DB 10; Length 446;
 Best Local Similarity 66.7%; Pred. No. 4e-148;
 Matches 297; Conservative 63; Mismatches 84; Indels 1; Gaps 1;

QY 6 KEKYYTSEELKGNKKGDLWISIOGKYVNSDWKHEPGGDVPSINLAGODVDAFYAF 65
 DB 3 EKREITSEELKGNKKGDLWISIOGKYVNSDWKHEPGGDVPSINLAGODVDAFYAF 62
 QY 66 HPGTAMSHLEKFTGYHLSDFKVSVDYRKLASEFSGKGLPTKGHTSCTLASVAVM 125
 DB 63 HPGTAMSHLEKFTGYHLSDFKVSVDYRKLASEFSGKGLPTKGHTSCTLASVAVM 121
 QY 126 FLIVLYGVLRCTSVMAHLGSGMLGLLWMOGAYVGHDSGHVYVMTNGFNKVAQILSGNC 185
 DB 122 MAISVMGLGSDKVTMAHLASAAVIGLWMQIGFVGHDSGHVYVMTNGFNKVAQILSGNC 181
 QY 186 LTGISIAMWKTTHNAHIAACNSLDHDPLOHMPVAVSSRPFNSTSTHFYGRKLEFDIA 245
 DB 182 ITGISIGMKWKNNAHIAACNSLDHDPLOHMPVAVSSRPFNSTSTHFYGRKLEFDIA 241
 QY 246 RELCYOHFTFYVWCVAVNLYLQITILLFSRRKVDORAININGILVMTMPLVACL 305
 DB 242 RELCYOHFTFYVWCVAVNLYLQITILLFSRRKVDORAININGILVMTMPLVACL 301
 QY 306 PNWPERVWVFLASFAVCSIOHIOFCLNHPAANVYVGPSPGNDWPEKOTSGTLDISCASMS 365
 DB 302 PNWPERVWVFLASFAVCSIOHIOFCLNHPAANVYVGPSPGNDWPEKOTSGTLDISCASMS 361
 QY 366 DMFEGLOFQLEHNLPRPLRCQRLKISPLVSDLCCKHNPYRSLSFWEANQMTITRTAA 425
 DB 362 DMFEGLOFQLEHNLPRPLRCQRLKISPLVSDLCCKHNPYRSLSFWEANQMTITRTAA 421

QY 426 AALQARDLTPAPKXNLMEAVNTHG 450
 DB 422 AALQARDLTPAPKXNLMEAVNTHG 446

RESULT 8

Q8VZ22 PRELIMINARY; PRT; 448 AA.
 AC Q8VZ22;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Delta-6-desaturase.
 OS Echinium gentianoides.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Lamiales; Boraginaceae; Echinium.
 OX NCBI_TaxID=173991;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maroto F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz J.R.;
 RT "Cloning and Molecular Characterization of the D6-Desaturase from
 RT Echinium: Functional Expression in Yeast and Tobacco."
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AY055117; AAL23580.1; -.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; FA desat. fam.
 DR Pfam; PF00487; FA desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR PRODOM; PD000612; Cyt B5; 1.
 DR PRODOM; PD001081; FA desat. fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.

SO SEQUENCE 448 AA; 51428 MW; C2A937951B87C183 CRC64;

Query Match 68.2%; Score 1670; DB 10; Length 448;
 Best Local Similarity 64.8%; Pred. No. 4.8e-146;
 Matches 287; Conservative 75; Mismatches 81; Indels 0; Gaps 0;

QY 8 KKYITSEELKGNKKGDLWISIOGKYVNSDWKHEPGGDVPSINLAGODVDAFYAF 67
 DB 6 KKYITSEELKGNKKGDLWISIOGKYVNSDWKHEPGGDVPSINLAGODVDAFYAF 65
 QY 66 GTAMSHLEKFTGYHLSDFKVSVDYRKLASEFSGKGLPTKGHTSCTLASVAVMFL 127
 DB 66 GTAMSHLEKFTGYHLSDFKVSVDYRKLASEFSGKGLPTKGHTSCTLASVAVMFL 125
 QY 128 ILYGVLRCTSVMAHLGSGMLGLLWMOGAYVGHDSGHVYVMTNGFNKVAQILSGNCLT 187
 DB 126 MSYGVLFCEGVLVHLAAGLGMGFWWIOSGIGHDAGHYVMPRLNKLMLGIYAGNCLS 185
 QY 188 GISIAMWKTTHNAHIAACNSLDHDPLOHMPVAVSSRPFNSTSTHFYGRKLEFDIARF 247
 DB 186 GISIAMWKTTHNAHIAACNSLDHDPLOHMPVAVSSRPFNSTSTHFYGRKLEFDIARF 245
 QY 248 LICYOHFTFYVWCVAVNLYLQITILLFSRRKVDORAININGILVMTMPLVACL 307
 DB 246 LICYOHFTFYVWCVAVNLYLQITILLFSRRKVDORAININGILVMTMPLVACL 305
 QY 308 WPEVWVFLASFAVCSIOHIOFCLNHPAANVYVGPSPGNDWPEKOTSGTLDISCASMDW 367
 DB 306 WPEVWVFLASFAVCSIOHIOFCLNHPAANVYVGPSPGNDWPEKOTSGTLDISCASMDW 365
 QY 368 FFGGLQOLEHNLPRPLRCQRLKISPLVSDLCCKHNPYRSLSFWEANQMTITRTAA 427
 DB 366 FFGGLQOLEHNLPRPLRCQRLKISPLVSDLCCKHNPYRSLSFWEANQMTITRTAA 425
 QY 428 LQARDLTPAPKXNLMEAVNTHG 450
 DB 426 LQARDLTPAPKXNLMEAVNTHG 446

RESULT 9	
Q9SAU5	Q9SAU5
ID	PRELIMINARY;
AC	Q9SAU5;
DT	01-MAY-2000 (TREMBlrel. 13, Created)
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT	01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE	Delta 6-desaturase.
OS	Borago officinalis (Bourrache).
OC	Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
OC	Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
OC	Asteridae, lamids; Boraginaceae; Borago.
OX	NCBI_TaxID=13363;
OX	[1]
RN	SEQUENCE FROM N.A.
RP	TISSUE=Seed;
RC	Numberg A.N., Beremand P.D., Thomas T.L.;
RT	"Engineering of Plant Seed Oils to Produce Gamma Linolenic Acid
RT	(GIA).";
RL	Submitted (JUN-1997) to the EMBL/genbank/DBJ databases.
CC	-1 SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC	EMBL; AF007561; AAD01410.1; -
DR	InterPro; IPR001199; Cyt_B5.
DR	InterPro; IPR005804; FA_desat_fam.
DR	Pfam; PF00487; FA_desaturase; 1.
DR	Pfam; PF00173; heme_1; 1.
DR	ProDom; PD000612; Cyt_B5; 1.
DR	ProDom; PD001081; FA_desat_fam; 1.
DR	PROSITE; PS50255; CYTOCHROME_B5_2; 1.
DR	Heme.
Q9	SEQUENCE 448 AA; 51626 MW; EAC3F0BF22EBDE00 CRC64;

Query Match	67.6%	Score 1656	DB 10	Length 448
Best Local Similarity	63.4%	Pred. NO. 9.6e-145		
Matches 281	Conservative 78	Mismatches 84	Indels 0	Gaps 0

[illegible]

RESULT 10	
004353	
ID 004353	PRELIMINARY; PRT; 448 AA

DT	01-JUL-1997	(TREMBlrel. 04, Created)
DT	01-JUL-1997	(TREMBlrel. 04, last sequence update)
DT	01-OCT-2002	(TREMBlrel. 22, last annotation update)
DE	Delta 6 desaturase.	
OS	Borago officinalis (Bourrache) (Borago).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
OC	Asteridae; lamiales; Boraginaceae; Borago.	
OX	NCBI_TaxID=13363;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=97268723; Pubmed=9108131;	
RA	Sayanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,	
RA	Christie W.W., Shewry P.R., Napier J.A.;	
RT	"Expression of a borago desaturase cDNA containing an N-terminal	
RT	cytochrome b5 domain results in the accumulation of high levels of	
RT	delta6-desaturated fatty acids in transgenic tobacco."	
RL	Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).	
CC	1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.	
DR	EMBL, U79010; AAC49700.1; -;	
DR	InterPro, IPR001199; Cyt_B5.	
DR	InterPro, IPR005804; FA_desat fam.	
DR	Pfam; PF00487; FA_desaturase; 1.	
DR	Pfam; PF00173; heme_1; 1.	
DR	ProDom; PD000612; Cyt_B5; 1.	
DR	ProDom; PD001081; FA_desat fam; 1.	
DR	PROSITE; PSS0255; CYTOCHROME_B5_2; 1.	
KW	Heme.	
SO	SEQUENCE 448 AA; 51635 MW; B62EEB701680909F CRC64;	
Query Match	67.6%; Score 1655; DB 10; Length 448;	
Best Local Similarity	63.4%; Pred. No. 1,2e-144;	
Matches 281; Conservative 78; Mismatches 84; Indels 0; Gaps 0;		
QY	8 KKYYTSELKGNHNEGDLWISIQKVVNVSDWKVEHGGGVPSINLAGVDVTAFLIAYHP 67	
DB	6 KKYYTSELKGNHNEGDLWISIQKAYVSDWKVDHGGSFPLKSLAGQVTDFAFAFHP 65	
QY	68 GTAWSHLEKFFGYTHLSDFYVSEVSKDYRLKASEFSKGLPTDKGHVTSCTLASVAVMFL 127	
DB	66 ASATWKNLDFKFTGYLKDYSVSEVSKDYRLKAEFSKMGLYDKKHIMFATLTCFIAMLF 125	
QY	128 ILYLVGLRCTSWAHLGSGMLTLGLIMQKAYVGHDSHYVVMVTNGNKAKAQLISGCLT 187	
DB	126 MSYVGLFEGCVLVHIFSGCLMFLWISQGWIGHDAGHYVSDSLRNKFMGIFPAACLS 185	
QY	188 GISIAWKKWTHNAHLACNSLIDHPDLQHNHPVAVSSRPFNSITSHFYGRKLEDFIARF 247	
DB	186 GISIGMKKMHNAHLACNSLELDPDLQYIFPLVSSKFFGSLTSHFYEGRLTFDSLSRF 245	
QY	248 LICYOHEFTFYVNCVAVRNLYLTILLFSSRRKQVDALNIMGILVFTWFPPLVSCLPN 307	
DB	246 FVSYGHTFTFPIPCARLNNVYQSLIMLTKRVNYSRAHLLGLVPSIWIYPLVSCLPN 305	
QY	308 WPERWVFLASFVACSIQHIQFCLNHPAANVYVGPBGNDWPFKQISGTLIDISCASSMDW 367	
DB	306 WGERIMVFLASLTSTGQVOVFSLNHPSSSVYVKGPKGNWPFKQIDGTLDICPPMWD 365	
QY	368 FFGGLQQLLHHLPRLPRCOLKRISPLVSDLCCKKHLPRYSLSFPEANOMTIRTLTA 427	
DB	366 FHGGLQQLLHHLPKMPKRCNLKRISYVLELCCKHLPYNVYASFANEMTLRTLRNTA 425	
QY	428 LQARDLTNPAPKNILMEAVNTHG 450	
DB	426 LQARDITKPLPKULVMEALHTHG 448	
RESULT 11		
ID	08VZ21	
AC	08VZ21	
DT	01-MAR-2002 (TREMBlrel. 20, Created)	
	PRELIMINARY; PRT; 448 AA.	

RESULT	11	
Q8VZ1		
ID	Q8VZ1	PRELIMINARY;
AC	Q8VZ1;	PRT; 448 AA.
DT	01-MAR-2002	(TRENDArel, 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Delta-6-deaturase.
 GN D6DS.
 OS Ectium pitaridi var. pitaridi.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Boraginaceae; Ectium.
 OX NCBI_TaxID=174255;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Marto F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz J.R.;
 RT "Cloning and Molecular Characterization of the D6-Desaturase from
 RT Ectium: Functional Expression in Yeast and Tobacco."
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AY055118; AAL23581.1; -.
 DR InterPro; IPR001199; Cyf_B5.
 DR InterPro; IPR005804; FA_deat_fam.
 DR Pfam; PF00487; FA_deaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyf_B5; 1.
 DR ProDom; PD001081; FA_deat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 448 AA; 51394 MW; 486D6EA905DE263 CRC64;

Query Match 67.5%; Score 1653; DB 10; Length 448;
 Best Local Similarity 64.3%; Pred. No. 1.8e-144;
 Matches 285; Conservative 75; Mismatches 83; Indels 0; Gaps 0;

QY 8 KKYITSEELKGNKNGDLMISIOGKVVNVSDWKEHPCGADVPSISLAGODVDAFIAYHP 67
 DB 6 KKYITAEELKGNKNGDLMISIOGKVVNVSDWKEHPCGADVPSISLAGODVDAFIAYHP 65
 QY 68 GTAWSHLEKFTGYHLSDFKVSSESKDYRKLASSEFSKGLFPTKGHTVSCITLAAVAVMFL 127
 DB 66 GSTWMLDSFPTGYLYLKDYSVSESKDYRKLVFENKMGKLPDKKHIVLVTFEFTAMMFA 125
 QY 128 IYLVGVLRCTSWMAHLSGMLGLIMOSAYVGHDSGHVYVNTTNGFNKVAQILSGNCLT 187
 DB 126 MSVGVLRCEGVLYLHFGCLMGFLVIOGWIHGHPGHYVNVSDSLKFMGIFPANCIS 185
 QY 188 GISIAMKWTNAHNAHIAACNSLDHPDLOHMPFAVSSRFPSITSHPYGRKLEPFIFARF 247
 DB 186 GISIAMKWTNAHNAHIAACNSLDHPDLOHMPFAVSSRFPSITSHPYGRKLEPFIFARF 245
 QY 248 LICVGHFTFYPMCVARVNLVLTILLFSRRKVOADRANIMGLVFTWPEPLVSCLPN 307
 DB 246 FVSHQHTFYPVPCARVNMVQSLIMLTKNVFRSQELGLVFWIMVPLVSCLPN 305
 QY 308 WPERVMTFLASPAVCSIOHIOFCLNHFAANYVGPSPGNDWPEKOTSGTLDISCASSMDW 367
 DB 306 WGERIMFVIALSVTGMQVQFSLNHFPSSVYVGKPKNNMFEOTDGTLDISCPMMMDW 365
 QY 368 FFGGLQFQLEHNLPRRLPCOLRXISPLVSDCKKHNLPYRSLSPWEANOMTIRTLRTAA 427
 DB 366 FHGGLQFQLEHNLPRRLPCOLRXISPLVSDCKKHNLPYRSLSPWEANOMTIRTLRTAA 425
 QY 428 LQARDLTNPAPKNLMEAVNTHG 450
 DB 426 LQARDLTNPAPKNLMEAVNTHG 448

RESULT 12
 ID 08L717 PRELIMINARY; PRT; 448 AA.
 AC 08L717;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Delta-6-deaturase.
 OS Argania spinosa.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Sapotaceae; Argania.
 OX NCBI_TaxID=85884;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA El Filali A., Anderson M., Abbas K.;
 RT "Characterization and cloning of delta-6-deaturase in Argania spinosa
 RT fruit."
 RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AY131238; AAM94345.1; -.
 DR InterPro; IPR001199; Cyf_B5.
 DR InterPro; IPR005804; FA_deat_fam.
 DR Pfam; PF00487; FA_deaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyf_B5; 1.
 DR ProDom; PD001081; FA_deat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 448 AA; 51304 MW; 0B46F81B7DEE29EF CRC64;

Query Match 65.2%; Score 1597; DB 10; Length 448;
 Best Local Similarity 61.6%; Pred. No. 2.8e-139;
 Matches 273; Conservative 78; Mismatches 92; Indels 0; Gaps 0;

QY 8 KKYITSEELKGNKNGDLMISIOGKVVNVSDWKEHPCGADVPSISLAGODVDAFIAYHP 67
 DB 6 KKYITSEELKGNKNGDLMISIOGKVVNVSDWKEHPCGADVPSISLAGODVDAFIAYHP 65
 QY 68 GTAWSHLEKFTGYHLSDFKVSSESKDYRKLASSEFSKGLFPTKGHTVSCITLAAVAVMFL 127
 DB 66 ASTWMLDKFTGYLYLKDYSVSESKDYRKLVFENKMGKLPDKKHIVLVTFEFTAMMFA 125
 QY 128 IYLVGVLRCTSWMAHLSGMLGLIMOSAYVGHDSGHVYVNTTNGFNKVAQILSGNCLT 187
 DB 126 MSVGVLRCEGVLYLHFGCLMGFLVIOGWIHGHPGHYVNVSDSLKFMGIFPANCIS 185
 QY 188 GISIAMKWTNAHNAHIAACNSLDHPDLOHMPFAVSSRFPSITSHPYGRKLEPFIFARF 247
 DB 186 GISIAMKWTNAHNAHIAACNSLDHPDLOHMPFAVSSRFPSITSHPYGRKLEPFIFARF 245
 QY 248 LICVGHFTFYPMCVARVNLVLTILLFSRRKVOADRANIMGLVFTWPEPLVSCLPN 307
 DB 246 FVSHQHTFYPVPCARVNMVQSLIMLTKNVFRSQELGLVFWIMVPLVSCLPN 305
 QY 308 WPERVMTFLASPAVCSIOHIOFCLNHFAANYVGPSPGNDWPEKOTSGTLDISCASSMDW 367
 DB 306 WGERIMFVIALSVTGMQVQFSLNHFPSSVYVGKPKNNMFEOTDGTLDISCPMMMDW 365
 QY 368 FFGGLQFQLEHNLPRRLPCOLRXISPLVSDCKKHNLPYRSLSPWEANOMTIRTLRTAA 427
 DB 366 FHGGLQFQLEHNLPRRLPCOLRXISPLVSDCKKHNLPYRSLSPWEANOMTIRTLRTAA 425
 QY 428 LQARDLTNPAPKNLMEAVNTHG 450
 DB 426 LQARDLTNPAPKNLMEAVNTHG 448

RESULT 13
 ID 09ZTU8 PRELIMINARY; PRT; 469 AA.
 AC 09ZTU8;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE S276.
 GN S276.
 OS Triticum aestivum (wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;

[1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ET3;
RA Delhaize E., Hobb D.M., Gardner R.C., Richards K.D.;
RT "Aluminum tolerance in yeast conferred by over-expression of wheat
RT gene";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL: AF031194; AAD10250.1; -
DR HSSP: P00171; 115U.
DR InterPro: IPR001199; Cyt B5.
DR InterPro: IPR005804; FA_desat_fam.
DR InterPro: IPR001092; HLH_basic.
DR Pfam: PF00487; FA_desaturase; 1.
DR Pfam: PF00173; heme_1; 1.
DR PRINTS: PR00363; CYTOCHROME_B5.
DR ProDom: PD000612; Cyt_B5; 1.
DR ProDom: PD001081; FA_desat_fam; 1.
DR PROSITE: PS00255; CYTOCHROME_B5_2; 1.
DR PROSITE: PS00038; HLH_1; 1.
KW Heme.
SQ SEQUENCE 469 AA; 52617 MW; 16F223CC1F79740D CRC64;

Query Match 59.7%; Score 1463; DB 10; Length 469;
Best Local Similarity 57.6%; Pred. No. 7.6e-127;
Matches 255; Conservative 79; Mismatches 107; Indels 2; Gaps 2;

QY 9 KYTSELKHNKNEGDLWISIQKRVNVSDWKEHPCGDVPIINLACQDYTDAPFIAVHG 68
DB 28 RMISTELQHAADADLMWISISGDVYDVTPMLRHHPCGEVPLITLGAQDADTAFMAVHPP 87
QY 69 TAWSHLEKFTGYHLSDFKVEVKDYKRLASEFSKGLPDTKGHVTSCITLAAVAFLLI 128
DB 88 SVAPLRLRFVVG-RITDYTVTPASADPRRLAQLSSAGLEFERYGHPKFLVAVSLFCI 146
QY 129 VLYGLRCTSVMAHLGSMILGLIMQSAVYVGHDSGHVYVMTTNGFNKVAQIIISGNCITG 188
DB 147 ALYCVLAASSTGAMFAGLIGFTWIGSGWIGHDSGHQITRRPALRLILQVAVSGNCLTG 206
QY 189 ISIAWKKMTNAHHIHCNSLDHPDLOHMPVAVSSSFENSIHFGRLSEDFIARFL 248
DB 207 LGIAWKKFNNTNHHISCSLDHPDLOHLPFANVSTLFPNNLWVSCERTLAADALSKFF 266
QY 249 ICYQHFTEYVMCVARVNLVLTILLFSRRKYODRALINMGLIVETWTFPLVSCLEPN 308
DB 267 VSYQHHTFYVWGFARINLVOSIVELITQKVRQRRLLEAGAAFFWVPLVSCLEPN 326
QY 309 PERVMEVLASFAVCSIQHIOFCLNHPANVYVGPSSGNDWFEKQTSGLTIDISCASSNDWF 368
DB 327 WERVAVFLASFVITGIQHVQFCINHFSSAVYVGPKNDFEERQTAGTLDIKCSPMWDMF 386
QY 369 FGGLOQLNHLPRRLPRCQARKISPIVSDLCCKHNLPRSLSPFWEANQMTITRTAAL 428
DB 387 HGGLOQLNHLPRRLPRCQARKISPIVSDLCCKHNLPRSLSPFWEANQMTITRTAAL 446
QY 429 QARD-LTNPAKKNLWEAVNTHG 450
DB 447 QAREATTGAAPKVLWEALNTHG 469

RESULT 14

Q9HDS8 PRELIMINARY; PRT; 523 AA.
AC Q9HDS8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
DE Delta-6 desaturase.
OS Mucor rouxi.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OC Mucor.
ON NCBI_TaxID=29923;
RX

RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 24905;
RX MEDLINE=20563795; PubMed=1112411;
RA Laoteng K., Mannontarat R., Tanticharoen M., Cheevadhanarak S.;
RT "Delta(6)-desaturase of Mucor rouxi with high similarity to plant
RT delta(6)-desaturase and its heterologous expression in Saccharomyces
RT cerevisiae";
RL Biochem. Biophys. Res. Commun. 279:17-22(2000).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL: AF296076; AAG36960.1; -
DR EMBL: AF290983; AAG36959.1; -
DR HSSP: P00173; 1JEX.
DR InterPro: IPR001525; C5_DNA_meth.
DR InterPro: IPR001199; Cyt B5.
DR InterPro: IPR005804; FA_desat_fam.
DR Pfam: PF00487; FA_desaturase; 1.
DR Pfam: PF00173; heme_1; 1.
DR ProDom: PD000612; Cyt_B5; 1.
DR ProDom: PD001081; FA_desat_fam; 1.
DR PROSITE: PS00095; C5_MTASE_2; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS00255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 523 AA; 60622 MW; A03727AF39EB7857 CRC64;

Query Match 28.1%; Score 688.5; DB 3; Length 523;
Best Local Similarity 28.5%; Pred. No. 4.7e-55;
Matches 147; Conservative 87; Mismatches 199; Indels 83; Gaps 7;

QY 6 KEKKYTSBELKHNKNEGDLWISIQKRVNVSDWKEHPCGDVPIINLACQDYTDAPFIAV 65
DB 17 RSSNITTEBEFQRLIKQGSVFIEQKYRVVNFMAKHGGEAALRSALGRDVTDEIRTW 76
QY 66 HPSTASHLEKFTGYHLSDF----- 86
DB 77 HRPQVY--EKMINLYCIGDMPDVIRPASKQOHTFTPKEDKPYLTATWBSGFTVQAV 133
QY 87 -----KVESEVKD-----YRKLASEFSKGLPDTKGHVTSCITLAS 121
DB 134 DDAIQDLHKNHSHDLKDAVLQKDLNGDQIRNAYRGLAEVLAKGLF-----KCNWYK 186
QY 122 VA-----VMEILVLYGLRCTSVMAHLGSMILGLIMQSAVYVGHDSGHVYVMTTNGF 174
DB 187 YAREGCRYTLIFLSIMFTLKTGETNHYMAGAFAFMAMFNQVLFTAHDAHGHEITKSEI 246
QY 175 NKVAQLSNGCLGISIAWKKMTNAHHIHCNSLDHPDLOHMPVAVSSSFENSIHFGRLSE 234
DB 247 DHVIGVLIANFTGSLGSMKDNHNVHHIVTNHPEHDPDLOHVPFMAITTKFFNNIYSTV 306
QY 235 YGRKLEFDFIARFLCYQHFTEYVMCVARVNLVLTILLFSRRKYODRALINMGLIVF 294
DB 307 YKRVLPFDASRFRVNHQHYLYLLISFGRFNLRHSFAYLLCKNVRRTLELVGITTF 366
QY 295 WTFPPLVSCLEPNRPERVMEVLASFAVCSIQHIOFCLNHPANVYVGPSSGNDWFEKQTS 354
DB 367 FVWFSGILSTLPTNIRIIVIMVYMLTFPLVQILSHFGMSTEDRGPD-BEPFAKMR 425
QY 355 GTLIDISCASSMDWFFGGLOQLNHLPRRLPRCQARKISPIVSDLCCKHNLPRSLSPFWE 414
DB 426 TTMDVDCEPWLDFHGGLOQVAVNHLFPRRLPRINLQCVPLVKKFCDEGLHLYMYNFS 485
QY 415 ANQMTITRTAALQARDLTNPAPKNL-LWEAVNTH 449
DB 486 GNGVVLGTLSVADQVGFNNEVAKSAEINANDKEH 521

RESULT 15

Q8NKG9 PRELIMINARY; PRT; 568 AA.
AC Q8NKG9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
RX

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OM protein - protein search, using SW model

Run on: January 1, 2004, 06:29:49 ; Search time 15.634 Seconds
(without alignments)
1217.848 Million cell updates/sec

Title: US-09-857-524B-8
Perfect score: 2449
Sequence: 1 MEVKEKKYITSEELKGN.....RDLTPAPKLLMEAVNTG 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1712	69.9	452	4	US-08-934-254-27 Sequence 27, Appl
2	1650	67.4	448	1	US-08-366-779-5 Sequence 5, Appl
3	1650	67.4	448	1	US-08-789-936-5 Sequence 5, Appl
4	1650	67.4	448	4	US-08-934-254-5 Sequence 5, Appl
5	1633	66.7	446	2	US-08-833-610-5 Sequence 5, Appl
6	1633	66.7	446	3	US-08-834-033A-15 Sequence 15, Appl
7	1091	44.5	252	2	US-08-834-655-7 Sequence 8, Appl
8	1091	44.5	252	3	US-08-834-033A-8 Sequence 8, Appl
9	1091	44.5	252	3	US-09-363-574-7 Sequence 7, Appl
10	1091	44.5	252	4	US-09-363-526-7 Sequence 7, Appl
11	502.5	20.5	457	2	US-08-834-655-2 Sequence 2, Appl
12	502.5	20.5	457	3	US-08-834-033A-2 Sequence 2, Appl
13	502.5	20.5	457	3	US-09-363-574-2 Sequence 2, Appl
14	502.5	20.5	457	4	US-09-363-526-2 Sequence 2, Appl
15	502.5	20.5	457	4	US-09-330-235-18 Sequence 18, Appl
16	502.5	20.5	458	4	US-09-439-261-10 Sequence 10, Appl
17	502.5	20.5	458	4	US-09-439-261-44 Sequence 11, Appl
18	502.5	20.5	458	4	US-09-227-613-11 Sequence 11, Appl
19	502.5	20.5	458	4	US-09-227-613-41 Sequence 41, Appl
20	500.5	20.4	457	2	US-08-833-610-4 Sequence 4, Appl
21	500.5	20.4	457	3	US-08-834-033A-14 Sequence 14, Appl
22	496	20.3	125	2	US-08-834-655-8 Sequence 8, Appl
23	496	20.3	125	3	US-08-834-033A-9 Sequence 9, Appl
24	496	20.3	125	3	US-09-363-574-8 Sequence 8, Appl
25	496	20.3	125	4	US-09-363-526-8 Sequence 8, Appl
26	436	17.8	445	4	US-09-048-888-1 Sequence 1, Appl
27	429	17.5	444	4	US-09-048-888-3 Sequence 3, Appl

28	425	17.4	444	4	US-09-439-261-11 Sequence 11, Appl
29	425	17.4	444	4	US-09-227-613-12 Sequence 12, Appl
30	425	17.4	445	4	US-09-439-261-39 Sequence 39, Appl
31	425	17.4	445	4	US-09-439-261-45 Sequence 45, Appl
32	422.5	17.3	432	4	US-09-439-261-9 Sequence 9, Appl
33	422.5	17.3	432	4	US-09-227-613-9 Sequence 9, Appl
34	422.5	17.3	465	4	US-09-439-261-40 Sequence 40, Appl
35	422.5	17.3	465	4	US-09-227-613-38 Sequence 38, Appl
36	418.5	17.1	444	4	US-09-439-261-43 Sequence 43, Appl
37	418.5	17.1	444	4	US-09-227-613-42 Sequence 42, Appl
38	385.5	15.7	355	2	US-08-834-655-5 Sequence 5, Appl
39	385.5	15.7	355	3	US-08-834-033A-6 Sequence 6, Appl
40	385.5	15.7	355	3	US-09-363-574-5 Sequence 5, Appl
41	385.5	15.7	355	4	US-09-363-526-5 Sequence 5, Appl
42	370.5	15.1	104	2	US-08-834-655-6 Sequence 6, Appl
43	370.5	15.1	104	3	US-08-834-033A-7 Sequence 7, Appl
44	370.5	15.1	104	3	US-09-363-574-6 Sequence 6, Appl
45	370.5	15.1	104	4	US-09-363-526-6 Sequence 6, Appl

ALIGNMENTS

```
RESULT 1
US-08-934-254-27
; Sequence 27, Application US/08934254
; Patent No. 6355861
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; NUMBER OF INVENTION: DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,254
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-934-254-27
; Query Match 69.9%; Score 1712; DB 4; Length 452;
; Best local Similarity 69.6%; Pred. No. 7,1e-180;
; Matches 311; Conservative 54; Mismatches 78; Indels 4; Gaps 4;
QY 8 KYITSEELKNGKGDLMISIQKYYNVSDVWKEHGGDVPISNLAGDVTDAFYAHP 67
DB 6 KYITAEEDRRNRKSGDLMISIQKYYDCSRWAAEHFGGEVPLLSIAGDVTDAFYAHP 65
QY 68 GRWMSHLEKFFPG-VHLSDFKYBVSXKDYRKLASERSKGLPDTKGVHVSCTLASVAWVF 126
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Db 66 GTAMRHLDPLFTGYIYLKDFEVEISEISDVRRLNEMSRSGIFPKKHIMMTFVGVAVMM 125
Qy 127 LVLVGLRSTYVAHIGSMILGLMVGSAVYGHDSGHVVTNGFNKVAOILSGNCL 186
Db 126 AAVYGLASESVGMHLCALLGLMIQAAVYGHDSGHVQVMPTRGYNRITOLIAGNIL 185
Qy 187 TGISIMMKWTNNAHNAHIAHNSLDHDPDLOHMPVAVSSRFNSITSHFYGRKLEPFIAR 246
Db 186 TGISIMMKWTNNAHNAHIAHNSLDYDPLQHI PVFASTRFNSITSHFYGRVLEKDEVAR 245
Qy 247 FLICYHFTFPYVWCARVNLVYOTILLFSRRKVODRALNMGILVFWTWPFLVSCLP 306
Db 246 FLVSYQHMTYTPMIRERVNLFIOTILLTRDVPDRALNMGIAVFWTWPFLVSCLP 305
Qy 307 WPERVWFVLASFVACSIOHIOFCLNHPAANYVGPSPGNDWEKOTSGTLDISCASMD 366
Db 306 WPERVWFVLASFVACSIOHIOFCLNHPAANYVGPSPGNDWEKOTSGTLDISCASMD 365
Qy 367 WFGGLOFQLEHHLFPLPRCQLRKISPLVSDLCCKNLPYRSLSEFW-EANQMTIRTLRT 425
Db 366 WFGGLOFQLEHHLFPLPRCQLRKIAPLARDLCCKHGMFYSFGFWDANVETIRTLRD 425
Qy 426 AALQARDLTN-PAPKNILM-EAVNTHG 450
Db 426 AAVQARDLNASAPCKKLGVEAVNTHG 452

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RESULT 2
US-08-366-779-5
Sequence 5, Application US/08366779
Patent No. 5614393

```

GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Reddy, Avutu S.
APPLICANT: Nuccio, Michael
APPLICANT: Freysinet, Georges L.
APPLICANT: Nunberg, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,779
FILING DATE: 30-DEC-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83832YXW
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-366-779-5

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Query Match 67.4%; Score 1650; DB 1; Length 448;
Best Local Similarity 63.2%; Pred. No. 4,8e-173;
Matches 280; Conservative 78; Mismatches 85; Indels 0; Gaps 0;

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Qy 8 KKITSEELKGNKEDLMISIQKRYNVSDVKEHGGDVPISNAGDVTDAFIAYHP 67
Db 6 KKITSDLEKNDHKPDDLWISIQKAYDVSDWKHPPGSGFPLKSLAQGBVTDAPVAFHP 65
Qy 68 GTAMSHLEKFPFGYHSLDPKSVESVDYKRLASEPSKGLFPTKGHTSCTLASVAMFL 127
Db 66 ASTWKNLDRFFGYXLYKDVSVESVDYKRLVFEFSKMLYDKKHIMFATLCTFIAMLP 125
Qy 128 IVLVGLRSTYVAHIGSMILGLMVGSAVYGHDSGHVVTNGFNKVAOILSGNCL 187
Db 126 MSYVGLPCEGYVHLFSGCLMGFLMIQSGWIGHDGHVNVSDSLNFMGIFANCL 185
Qy 188 GISIAWKKWTNNAHNAHIAHNSLDHDPDLOHMPVAVSSRFNSITSHFYGRKLEPFIAR 247
Db 186 GISIGWKKWNNAHNAHIAHNSLDYDPLQHI PFLVSSKFEGLTSHFYGRKLEPFIAR 245
Qy 248 LICYHFTFPYVWCARVNLVYOTILLFSRRKVODRALNMGILVFWTWPFLVSCLP 307
Db 246 FLVSYQHMTYTPMIRERVNLFIOTILLTRDVPDRALNMGIAVFWTWPFLVSCLP 305
Qy 308 WPERVWFVLASFVACSIOHIOFCLNHPAANYVGPSPGNDWEKOTSGTLDISCASMD 367
Db 306 WGERIMFVLASLSTYGMQVQFSLNHFSSVYGRKGNWMEKOTDGLTDLISCPMMMD 365
Qy 368 FFGGLOFQLEHHLFPLPRCQLRKISPLVSDLCCKNLPYRSLSEFW-EANQMTIRTLRT 427
Db 366 FFGGLOFQLEHHLFPLPRCQLRKISPLVYELCKKNLPYVASFSGKAMEMTLRTLRN 425
Qy 428 LQARDLTNPAKKNILMEAVNTHG 450
Db 426 LQARDITKPLKXVLWEALHTHG 448

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RESULT 3
US-08-789-936-5

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Sequence 5, Application US/08789936
Patent No. 5789220
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Reddy, Avutu S.
APPLICANT: Nuccio, Michael
APPLICANT: Freysinet, Georges L.
APPLICANT: Nunberg, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,936
FILING DATE: 28-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/366,779
FILING DATE: 30-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83832YXW

```



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;
; ZIP: 94306
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,610
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAB-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.123.000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
;
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-833-610-5

```

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Query Match 66.7%; Score 1633; DB 2; Length 446;
Best Local Similarity 63.0%; Pred. No. 3.5e-171;
Matches 278; Conservative 78; Mismatches 85; Indels 0; Gaps 0;

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QY 8 KKYITSEELGKHNKGGDLWISIGKAYVNSDVKVKEHGGDVPISNLGADVDTDAFIAYHP 67
DB 6 KKYITSEELGKHNKGGDLWISIGKAYVNSDVKVKEHGGDVPISNLGADVDTDAFIAYHP 65
QY 68 GTAMSHLEKFFGTGHLSDFKVSEVSKDYRKLAESFKLGFDTKGHVTSCTLASAVAMFL 127
DB 66 ASTWKMLDKFETGYLKDYSVSESVKYRKLVFEFSKGLYDKKGHIMFATLCFIAMLFA 125
QY 128 IVLYGRLCTSVNAHLGSGMLGLLMMQSAVGHDSGHVYVMTNGNKAQIISGNCIT 187
DB 126 MSYGVLFCEGVVHLFSGCLMGFLWIOSGWIIGHDGHVWVSDSLNKFEMGIFAANCIS 185
QY 188 GISIAMWKTTHNAHHTACNSLDHDPDLOHMPVPAVSSRFNSITSHFYGRKLEFDIARF 247
DB 186 GISIAMWKTTHNAHHTACNSLDHDPDLOHMPVPAVSSRFNSITSHFYGRKLEFDIARF 245
QY 248 LICVGHFTFYVNCVAVNLVLTITLLFSRRKVQDRAINIGILVFWTFPLVSCLPN 307
DB 246 FVSGQWTFEPIMGARLNNVYQSLIMLTRKNNVSYRAQELGLCVFSIWPPLVSCLPN 305
QY 308 WPERWVFVLASFVACSIQHIQFCLNHPAANNVYVGPSPGNDWFEKQISGTLDISCASMDW 367
DB 306 WGERIMFVIASLSTVGMOQVQFSLNHFSSSVYVGKPRGNWFEKQIDGTLDISCPMMDW 365
QY 368 FFGGLQFQLEHHLFPRPLRCQRLKISPLVSDLCCKKNLFPYRSLSPFMANQMTIRTLRTAA 427
DB 366 FFGGLQFQLEHHLFPRPLRCQRLKISPLVSDLCCKKNLFPYRSLSPFMANQMTIRTLRTAA 425
QY 428 LQARDLTNPAPKULLMEAVNT 448
DB 426 LQARDLTNPAPKULLMEALHT 446

```

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RESULT 6
US-08-834-033A-15
; Sequence 15, Application US/08834033A
; Patent No. 6075183
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MUKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER

```

```

;
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
;
; ZIP: 94111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,033A
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-300.USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
;
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-834-033A-15

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```

Query Match 66.7%; Score 1633; DB 3; Length 446;
Best Local Similarity 63.0%; Pred. No. 3.5e-171;
Matches 278; Conservative 78; Mismatches 85; Indels 0; Gaps 0;

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QY 8 KKYITSEELGKHNKGGDLWISIGKAYVNSDVKVKEHGGDVPISNLGADVDTDAFIAYHP 67
DB 6 KKYITSEELGKHNKGGDLWISIGKAYVNSDVKVKEHGGDVPISNLGADVDTDAFIAYHP 65
QY 68 GTAMSHLEKFFGTGHLSDFKVSEVSKDYRKLAESFKLGFDTKGHVTSCTLASAVAMFL 127
DB 66 ASTWKMLDKFETGYLKDYSVSESVKYRKLVFEFSKGLYDKKGHIMFATLCFIAMLFA 125
QY 128 IVLYGRLCTSVNAHLGSGMLGLLMMQSAVGHDSGHVYVMTNGNKAQIISGNCIT 187
DB 126 MSYGVLFCEGVVHLFSGCLMGFLWIOSGWIIGHDGHVWVSDSLNKFEMGIFAANCIS 185
QY 188 GISIAMWKTTHNAHHTACNSLDHDPDLOHMPVPAVSSRFNSITSHFYGRKLEFDIARF 247
DB 186 GISIAMWKTTHNAHHTACNSLDHDPDLOHMPVPAVSSRFNSITSHFYGRKLEFDIARF 245
QY 248 LICVGHFTFYVNCVAVNLVLTITLLFSRRKVQDRAINIGILVFWTFPLVSCLPN 307
DB 246 FVSGQWTFEPIMGARLNNVYQSLIMLTRKNNVSYRAQELGLCVFSIWPPLVSCLPN 305
QY 308 WPERWVFVLASFVACSIQHIQFCLNHPAANNVYVGPSPGNDWFEKQISGTLDISCASMDW 367
DB 306 WGERIMFVIASLSTVGMOQVQFSLNHFSSSVYVGKPRGNWFEKQIDGTLDISCPMMDW 365
QY 368 FFGGLQFQLEHHLFPRPLRCQRLKISPLVSDLCCKKNLFPYRSLSPFMANQMTIRTLRTAA 427
DB 366 FFGGLQFQLEHHLFPRPLRCQRLKISPLVSDLCCKKNLFPYRSLSPFMANQMTIRTLRTAA 425
QY 428 LQARDLTNPAPKULLMEAVNT 448
DB 426 LQARDLTNPAPKULLMEALHT 446

```

RESULT 7

US-08-834-655-7

; Sequence 7, Application US/08834655

; Patent No. 5968809

; GENERAL INFORMATION:

; APPLICANT: KNOTZON, DEBORAH

; APPLICANT: MURKERT, PRADIP

; APPLICANT: HUANG, YUNG-SHENG

; APPLICANT: THURMOND, JENNIFER

; APPLICANT: CHAUDHARY, SUNITA

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.

; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039

; CITY: PALO ALTO

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/834,655

; FILING DATE: 11-APR-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: RAE-VENTER, BARBARA

; REGISTRATION NUMBER: 32,750

; REFERENCE/DOCKET NUMBER: CGNE.124.000S

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 328-4400

; TELEFAX: (650) 328-4477

; TELEX: N/A

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 252 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-834-655-7

Query Match 44.5%; Score 1091; DB 2; Length 252;

Best Local Similarity 74.9%; Pred. No. 8e-112;

Matches 188; Conservative 31; Mismatches 32; Indels 0; Gaps 0;

QY 129 VLVGVRCTSVMAHLSSGMLLGLIMQSAVYGHDSGHVYVMTTNGFNKVAQILLSGNCLTG 188

DB 2 VLVGVLACTSVFHAQIAALLGLIMQSAVYIGHDSGHVYVMTTNGFNKVAQILLSGNCLTG 61

QY 189 ISIAAMKMTNNAHIAICNSLDHPDLOHMPVFAVSSRFNSITSHFYGRLEDFIARFL 248

DB 62 ISIAAMKMTNNAHIAICNSLDHPDLOHMPVFAVSTKFSLSLTSRFDKLTGCPVARFL 121

QY 249 ICYQHFTFFVPMCVARNVLYQTILLFSRRKQVDRALNMGILVFWTWFPPLVSCLPNW 308

DB 122 VSVQHFTFFVPMCVARNVLYQTILLFSRRKQVDRALNMGILVFWTWFPPLVSCLPNW 181

QY 309 PERVMVVLASFAVCSIQHIOFCLNHPAANYVGPBGNDWFEEKQSGTLDISCASSMDWF 368

DB 182 PERFFVFTSFTVTAQHIOFTLNHPADVYVGPBGNDWFEEKQAGTIDISCRSYMDWF 241

QY 369 FGGLOPQLEHH 379

DB 242 FGGLOPQLEHH 252

RESULT 8

US-08-834-033A-8

; Sequence 8, Application US/08834033A

; Patent No. 6075183

; GENERAL INFORMATION:

; APPLICANT: KNOTZON, DEBORAH

; APPLICANT: MURKERT, PRADIP

; APPLICANT: HUANG, YUNG-SHENG

; APPLICANT: THURMOND, JENNIFER

; APPLICANT: CHAUDHARY, SUNITA

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.

; STREET: 2001 FERRY BUILDING

; CITY: SAN FRANCISCO

; STATE: CA

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/834,033A

; FILING DATE: 11-APR-1997

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: WARD, MICHAEL R.

; REGISTRATION NUMBER: 38,651

; REFERENCE/DOCKET NUMBER: CGAB-300.USA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 433-4150

; TELEFAX: (415) 433-8716

; TELEX: N/A

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 252 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-834-033A-8

Query Match 44.5%; Score 1091; DB 3; Length 252;

Best Local Similarity 74.9%; Pred. No. 8e-112;

Matches 188; Conservative 31; Mismatches 32; Indels 0; Gaps 0;

QY 129 VLVGVRCTSVMAHLSSGMLLGLIMQSAVYGHDSGHVYVMTTNGFNKVAQILLSGNCLTG 188

DB 2 VLVGVLACTSVFHAQIAALLGLIMQSAVYIGHDSGHVYVMTTNGFNKVAQILLSGNCLTG 61

QY 189 ISIAAMKMTNNAHIAICNSLDHPDLOHMPVFAVSSRFNSITSHFYGRLEDFIARFL 248

DB 62 ISIAAMKMTNNAHIAICNSLDHPDLOHMPVFAVSTKFSLSLTSRFDKLTGCPVARFL 121

QY 249 ICYQHFTFFVPMCVARNVLYQTILLFSRRKQVDRALNMGILVFWTWFPPLVSCLPNW 308

DB 122 VSVQHFTFFVPMCVARNVLYQTILLFSRRKQVDRALNMGILVFWTWFPPLVSCLPNW 181

QY 309 PERVMVVLASFAVCSIQHIOFCLNHPAANYVGPBGNDWFEEKQSGTLDISCASSMDWF 368

DB 182 PERFFVFTSFTVTAQHIOFTLNHPADVYVGPBGNDWFEEKQAGTIDISCRSYMDWF 241

QY 369 FGGLOPQLEHH 379

DB 242 FGGLOPQLEHH 252

RESULT 9

US-09-363-574-7

; Sequence 7, Application US/09363574

Patent No. 6136574
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-574-7

Query Match 44.5%; Score 1091; DB 3; Length 252;
Best Local Similarity 74.9%; Pred. No. 8e-112;
Matches 188; Conservative 31; Mismatches 32; Indels 0; Gaps 0;

QY 129 VLVGVLRCTSVMAHLSGMLLGLIMQSAVYVGHDSGHVYVMTTNGPKVAQILSGNCLTG 188
DB 2 VLVGVLACTSVFAHQIAALLGLIMIQSAVYIGHDSGHVYVMTSNGSYNRFAGQLLSGNCLTG 61
QY 189 ISIAMWKTNNAHNHAICNSLDHDPDLOHMPVAVSSRFNSITSHFYGRKLEFDFIARFL 248
DB 62 ISIAMWKTNNAHNHAICNSLDYDPDLOHMPVAVSTKFPSSLSRPFDRKLTGCPVARFL 121
QY 249 ICYOHFTFYVMCVAVNLVLOTLLLSFRKQVODRALNIMGLIVFTWTFPLVSCIPNW 308
DB 122 VSYOHFTFYVNCGRINLFIQTLLLSFKREVDRLNPAAGILVFTWTFPLVSCIPNW 181
QY 309 PERVMFLAFVAVCSIOHIOFCLNHPAANYVGPSPGNDWFEKOTSGTLDISCASSNDWF 368
DB 182 PERFFVFTSFTYALOHIOFTLNHPADVYVGPPTSDFWEKQAGTIDISCSYNDWF 241
QY 369 FGGILOFOLLEHH 379
DB 242 FGGILOFOLLEHH 252

RESULT 10
US-09-363-526-7
Sequence 7, Application US/09363526
Patent No. 6410288
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP

APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,526
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-201 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-363-526-7

Query Match 44.5%; Score 1091; DB 4; Length 252;
Best Local Similarity 74.9%; Pred. No. 8e-112;
Matches 188; Conservative 31; Mismatches 32; Indels 0; Gaps 0;

QY 129 VLVGVLRCTSVMAHLSGMLLGLIMQSAVYVGHDSGHVYVMTTNGPKVAQILSGNCLTG 188
DB 2 VLVGVLACTSVFAHQIAALLGLIMIQSAVYIGHDSGHVYVMTSNGSYNRFAGQLLSGNCLTG 61
QY 189 ISIAMWKTNNAHNHAICNSLDHDPDLOHMPVAVSSRFNSITSHFYGRKLEFDFIARFL 248
DB 62 ISIAMWKTNNAHNHAICNSLDYDPDLOHMPVAVSTKFPSSLSRPFDRKLTGCPVARFL 121
QY 249 ICYOHFTFYVMCVAVNLVLOTLLLSFRKQVODRALNIMGLIVFTWTFPLVSCIPNW 308
DB 122 VSYOHFTFYVNCGRINLFIQTLLLSFKREVDRLNPAAGILVFTWTFPLVSCIPNW 181
QY 309 PERVMFLAFVAVCSIOHIOFCLNHPAANYVGPSPGNDWFEKOTSGTLDISCASSNDWF 368
DB 182 PERFFVFTSFTYALOHIOFTLNHPADVYVGPPTSDFWEKQAGTIDISCSYNDWF 241
QY 369 FGGILOFOLLEHH 379
DB 242 FGGILOFOLLEHH 252

RESULT 11
US-08-834-655-2
Sequence 2, Application US/08834655
Patent No. 5968809
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP

APPLICANT: HUANG, YUNG-SHENG
 APPLICANT: THURMOND, JENNIFER
 APPLICANT: CHAUDHARY, SUNITA
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
 STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
 CITY: PALO ALTO
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/834,655
 FILING DATE: 11-APR-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: RAE-VENTER, BARBARA
 REGISTRATION NUMBER: 32,750
 REFERENCE/DOCKET NUMBER: CGNE.124.00US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 328-4400
 TELEFAX: (650) 328-4477
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 457 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-834-655-2

Query Match 20.5%; Score 502.5; DB 2; Length 457;

Best Local Similarity 30.2%; Pred. No. 1.5e-46;
 Matches 130; Conservative 72; Mismatches 191; Indels 37; Gaps 11;

11 ITSEELKGNHK--EGDLWISIGKVVNVSDWKEHFGDVPISNLGQVTDFAFIAYHPG 68
 16 LNAEALNECKKDAEAPFLMIDNKYIDVAREFVDPHFGSVILTHV-GKQSTVDFDTFHP 74
 69 TAWSHLEKEFTG--YHLSDFKVSVDKRYKLASEFSKLGFDTKGHVTSCTLASVAVM 125
 75 AAMETLANFYVGDIDESDRIDKNDPFAAEVRKRLTIFQSLGYVD-----SSKAYVAFKVS 129
 126 FLIVLYGVLR-----TSVAHLGSGMLGLIMQSAVYVGHDSGHVYVMTTNGRNKVA 178
 130 FNLCTWGLSTVIVAKKQSTLANVLSAALLGLFWQCCGMLADFLHGVFQDRFGDLF 189
 179 QILSGNCLGSIAMWKMTNNAHILACNSLDHDPDLQHPVFAVSS---RFGSITSHPY 235
 190 GAFLGVCVCGFSSWMKDKNTHTAHPVNGEDPDIDTHTPLTWSHALEMFSVDVDEEL 249
 236 GRKLEDFIARPLICYQHTFYVPMCVARNLYLTILLF-----SRKRVDRALN 287
 250 TR-----MMSRFVNLQNTWTFYFPLISFARLSWCLQSLFVLPRNGQAHKSGARVPISLVE 304
 288 IMKILVFTWTFPLVVSCLPNWP-ERVMFVLASFAVC-SIOHIOFCINHPAANYVGPSPG 345
 305 QSLAHMWTWYLAITMPLFIKDPVNMMLVYFLVSGAVCNLAIVFSINHMGMPIVSKEAV 364
 346 N-DWPKQTSGLDISCASSMDWPFGLQROLSEHILFRLPRCOLKISPLVSDLCCKN 404
 365 DWDFPKQIITGADVHGLFANMFVGGANVQIEHHLFSPMPHNFSTKIQPAVETLCKCN 424
 405 LPYRSLSPWE 414

DB 425 VRYHTTGME 434

RESULT 12

US-08-834-033A-2
 Sequence 2, Application US/08834033A

Patent No. 6075183

GENERAL INFORMATION:

APPLICANT: KNOTZON, DEBORAH

APPLICANT: MUKERJI, PRADIP

APPLICANT: HUANG, YUNG-SHENG

APPLICANT: THURMOND, JENNIFER

APPLICANT: CHAUDHARY, SUNITA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.

STREET: 2001 FERRY BUILDING

CITY: SAN FRANCISCO

STATE: CA

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/834,033A

FILING DATE: 11-APR-1997

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: WARD, MICHAEL R.

REGISTRATION NUMBER: 38,651

REFERENCE/DOCKET NUMBER: CGAB-300.USA

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 433-4150

TELEFAX: (415) 433-8716

TELEX: N/A

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 457 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

Query Match 20.5%; Score 502.5; DB 3; Length 457;

Best Local Similarity 30.2%; Pred. No. 1.5e-46;
 Matches 130; Conservative 72; Mismatches 191; Indels 37; Gaps 11;

11 ITSEELKGNHK--EGDLWISIGKVVNVSDWKEHFGDVPISNLGQVTDFAFIAYHPG 68
 16 LNAEALNECKKDAEAPFLMIDNKYIDVAREFVDPHFGSVILTHV-GKQSTVDFDTFHP 74
 69 TAWSHLEKEFTG--YHLSDFKVSVDKRYKLASEFSKLGFDTKGHVTSCTLASVAVM 125
 75 AAMETLANFYVGDIDESDRIDKNDPFAAEVRKRLTIFQSLGYVD-----SSKAYVAFKVS 129
 126 FLIVLYGVLR-----TSVAHLGSGMLGLIMQSAVYVGHDSGHVYVMTTNGRNKVA 178
 130 FNLCTWGLSTVIVAKKQSTLANVLSAALLGLFWQCCGMLADFLHGVFQDRFGDLF 189
 179 QILSGNCLGSIAMWKMTNNAHILACNSLDHDPDLQHPVFAVSS---RFGSITSHPY 235
 190 GAFLGVCVCGFSSWMKDKNTHTAHPVNGEDPDIDTHTPLTWSHALEMFSVDVDEEL 249
 236 GRKLEDFIARPLICYQHTFYVPMCVARNLYLTILLF-----SRKRVDRALN 287
 250 TR-----MMSRFVNLQNTWTFYFPLISFARLSWCLQSLFVLPRNGQAHKSGARVPISLVE 304

Query Match:	20.5%;	Score 502.5;	DB 4;	Length 457;
Best Local Similarity	30.2%;	Pred. No. 1.5e-46;		
Matches 130; Conservative	72;	Mismatches 191;	Indels 37;	Gaps 11;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:37:05 ; Search time 85.7267 Seconds
(without alignments)
1053.214 Million cell updates/sec

Title: US-09-857-524B-8

Perfect score: 2449
Sequence: 1 MEVVEKEKKYITSEELKGNH.....RDLTPAPKLLWEAVNTHG 450

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 733937 seqs, 200641211 residues

Total number of hits satisfying chosen parameters: 733937

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*
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2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1801	73.5	458	US-10-340-779A-11	Sequence 11, Appl1
2	1712	69.9	452	US-10-029-756-27	Sequence 27, Appl1
3	1655	67.6	448	US-10-340-779A-13	Sequence 13, Appl1
4	1650	67.4	448	US-10-029-756-5	Sequence 5, Appl1
5	560.5	22.9	366	US-10-369-493-4137	Sequence 4137, Ap
6	518.5	21.2	459	US-09-967-477B-8	Sequence 8, Appl1
7	516	21.1	453	US-09-769-863-14	Sequence 14, Appl1
8	516	21.1	453	US-10-054-534B-14	Sequence 14, Appl1
9	516	21.1	453	US-10-431-952-14	Sequence 14, Appl1
10	502.5	20.5	457	US-10-278-391-4	Sequence 4, Appl1
11	502.5	20.5	458	US-10-191-513A-11	Sequence 11, Appl1
12	502.5	20.5	458	US-10-191-513A-41	Sequence 41, Appl1
13	436	17.8	445	US-10-262-617-1	Sequence 1, Appl1
14	429	17.5	444	US-10-262-617-3	Sequence 3, Appl1
15	425	17.4	444	US-10-191-513A-12	Sequence 12, Appl1

16	422.5	17.3	432	US-10-191-513A-9	Sequence 9, Appl1
17	422.5	17.3	465	US-10-191-513A-38	Sequence 38, Appl1
18	419	17.1	443	US-10-340-779A-20	Sequence 20, Appl1
19	418.5	17.1	444	US-10-191-513A-42	Sequence 42, Appl1
20	401	16.4	473	US-10-369-493-6108	Sequence 6108, Ap
21	364	14.9	448	US-10-340-779A-4	Sequence 4, Appl1
22	363.5	14.8	323	US-10-191-513A-17	Sequence 17, Appl1
23	361	14.7	454	US-10-369-493-6107	Sequence 6107, Ap
24	345	14.1	439	US-09-967-477B-4	Sequence 4, Appl1
25	343.5	14.0	470	US-09-769-863-20	Sequence 20, Appl1
26	343.5	14.0	470	US-10-054-534B-20	Sequence 20, Appl1
27	343.5	14.0	470	US-10-431-952-20	Sequence 20, Appl1
28	312	12.7	456	US-09-967-477B-6	Sequence 6, Appl1
29	303.5	12.4	365	US-10-156-761-9835	Sequence 9835, Ap
30	297	12.1	456	US-10-054-534B-33	Sequence 33, Appl1
31	293.5	12.0	430	US-10-120-637A-69	Sequence 69, Appl1
32	293.5	12.0	443	US-10-120-637A-55	Sequence 55, Appl1
33	293	12.0	442	US-10-054-534B-35	Sequence 35, Appl1
34	287.5	11.7	439	US-10-054-534B-31	Sequence 31, Appl1
35	286.5	11.7	353	US-10-156-761-9130	Sequence 9130, Ap
36	285.5	11.7	439	US-09-769-863-29	Sequence 29, Appl1
37	285.5	11.7	439	US-10-054-534B-29	Sequence 29, Appl1
38	285.5	11.7	439	US-10-431-952-29	Sequence 29, Appl1
39	284.5	11.6	287	US-10-191-513A-14	Sequence 14, Appl1
40	284.5	11.6	288	US-10-191-513A-15	Sequence 15, Appl1
41	282.5	11.5	446	US-10-340-779A-3	Sequence 3, Appl1
42	282.5	11.5	446	US-10-340-779A-14	Sequence 14, Appl1
43	282	11.5	360	US-10-191-513A-39	Sequence 39, Appl1
44	273.5	11.2	446	US-09-903-456-30	Sequence 30, Appl1
45	273.5	11.2	446	US-10-278-391-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-10-340-779A-11
; Sequence 11, Application US/10340779A
; Publication No. US20030152983A1
; GENERAL INFORMATION:
; APPLICANT: Napier, Johnathan A.
; APPLICANT: Stobart, Keith
; TITLE OF INVENTION: Desaturase
; FILE REFERENCE: 005407.00004
; CURRENT APPLICATION NUMBER: US/10/340.779A
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/582,034
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/GB96/03895
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: UK 9814034.6
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: UK 9727256.1
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Helianthus annuus

US-10-340-779A-11

Query Match 73.5%; Score 1801; DB 12; Length 458;
Best Local Similarity 71.6%; Pred. No. 1.5e-174;
Matches 317; Conservative 55; Mismatches 71; Indels 0; Gaps 0;

QY 8 KKYTSELKHKKEGDIWISIOGKYVNVSDWKYKHEKGVPTSNLAGOVTAFIYHP 67
DB 16 KKYTSELKHKHNPDLWISIGKYVNVTEMAHEKGVAPLNLGGOVTDFAIYHP 75
QY 68 GTAWSHLEKFTGYHLSDFVSEVSKDYRLKASEFSLGLPDTKGHTSCTLASAVAVFL 127

Db 76 GTAMKHLDKLFTGYHLKDYOVSISRDKLASEFAKAGFEKKHGVYSLCFVSLLS 135
 QY 128 ILYGVLRCTSVMAHLGSGMLGLIMQSAVYGHDSGHVYVMTTNGFNKVAQILSGNCLT 187
 Db 136 ACYGVGLYSSFFIMHLSGAILGLAMQALYLGHDAGHYQMMATRGKNAAGIFIGNCIT 195
 QY 188 GISIAWMKWTNAHHAACNSLDHDPDLQHPMPVAVSSRPFSITSFHYGRKLEPFIARF 247
 Db 196 GISIAWMKWTNAHHAACNSLDYDPLQHPMLAVSSKLFNSITSVFYGRQLFDFPLARF 255
 QY 248 LITGYFTFPVNCVAVNLYLQTLILFSSRKVODRALNMGILVFWTFPLVSCLPN 307
 Db 256 FASYQHYLYPIMCVARVNLVYQTLILLSKRKIPDRGINLIGTLIFWTFPLVSLRPN 315
 QY 308 WPERVAVLASFAVCSIOHIOFCLNHPAANYVYGPSPGNDWPEKOTSGTLDISCASSMD 367
 Db 316 WPERVAVLASFAVCSIOHIOFCLNHPAANYVYGPSPGNDWPEKOTSGTLDISCASSMD 375
 QY 368 FFGGLQFQLEHHLFPRILPRCOLRKISPLVSDLCCKHNLPRYSLSFWEANOMTIRTLRTAA 427
 Db 376 FFGGLQFQLEHHLFPRILPRCHLSISPIICHELCKKYNLPVLSFYDANVTITKILRTAA 435
 QY 428 LQARDLTNPAPKULMEAVNTHG 450
 Db 436 LQARDLTNPAPKULMEAVNTHG 458

RESULT 2

US-10-029-756-27
 ; Sequence 27, Application US/10029756
 ; Publication No. US20020108147A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/029, 756
 ; FILING DATE: 21-Dec-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/934,254
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Presser, Leopold
 ; REGISTRATION NUMBER: 19,827
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 27:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 452 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
 US-10-029-756-27

Query Match

69.9%; Score 1712; DB 14; Length 452;

Best Local Similarity 69.6%; Pred. No. 1.7e-165;
 Matches 311; Conservative 54; Mismatches 78; Indels 4; Gaps 4;

QY 8 KKYITSEELKGNKSGDLWISIOGKYVYSDWVKEHGGDVPISNLAGODVDAFIAYHP 67
 Db 6 KKYITSEELKGNKSGDLWISIOGKYVYSDWVKEHGGDVPISNLAGODVDAFIAYHP 65
 QY 68 GTAMSHLEKFTG-YHLSDPKVSEVSKDYRKLASSEFSKGLPDTKGHTVSCITLASVAVNF 126
 Db 66 GTAMRHLDPLFTGYLYLKDFEVSSEISKDYRRLNEMSRGIEBKGHIMMTFVGAVM 125
 QY 127 LILVGVLRCTSVMAHLGSGMLGLIMQSAVYGHDSGHVYVMTTNGFNKVAQILSGNCL 186
 Db 126 AALVGVLASSEVGYMLGALLGLIMQAAVYGHDSGHVYVMTTNGFNKVAQILSGNCL 185
 QY 187 TGISTAMKWTNAHHAACNSLDHDPDLQHPMPVAVSSRPFSITSFHYGRKLEPFIARF 246
 Db 186 TGISTAMKWTNAHHAACNSLDYDPLQHPMPVAVSSRPFSITSFHYGRKLEPFIARF 245
 QY 247 FLICYGHFTFPVNCVAVNLYLQTLILFSSRKVODRALNMGILVFWTFPLVSCLPN 306
 Db 246 FLVSYGHFTFPVNCVAVNLYLQTLILFSSRKVODRALNMGILVFWTFPLVSCLPN 305
 QY 307 WPERVAVLASFAVCSIOHIOFCLNHPAANYVYGPSPGNDWPEKOTSGTLDISCASSMD 366
 Db 306 WPERVAVLASFAVCSIOHIOFCLNHPAANYVYGPSPGNDWPEKOTSGTLDISCASSMD 365
 QY 367 WFGGLQFQLEHHLFPRILPRCOLRKISPLVSDLCCKHNLPRYSLSFWEANOMTIRTLRT 425
 Db 366 WFGGLQFQLEHHLFPRILPRCOLRKISPLVSDLCCKHNLPRYSLSFWEANOMTIRTLRT 425
 QY 426 AALQARDLTNPAPKULMEAVNTHG 450
 Db 426 AALQARDLTNPAPKULMEAVNTHG 452

RESULT 3

US-10-340-779A-13
 ; Sequence 13, Application US/10340779A
 ; Publication No. US20030152963A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Napier, Johnathan A.
 ; APPLICANT: Michaelson, Louise
 ; APPLICANT: Stobart, Keith
 ; TITLE OF INVENTION: Desaturase
 ; FILE REFERENCE: 005407, 00004
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/340, 779A
 ; CURRENT FILING DATE: 2003-03-24
 ; PRIOR APPLICATION NUMBER: US 09/582, 034
 ; PRIOR FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: PCT/GB98/03895
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: UK 9814034.6
 ; PRIOR FILING DATE: 1998-06-29
 ; PRIOR APPLICATION NUMBER: UK 9727256.1
 ; PRIOR FILING DATE: 1997-12-23
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PaasSEQ for windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 448
 ; TYPE: PRT
 ; ORGANISM: Borago officinalis
 US-10-340-779A-13

Query Match 67.6%; Score 1655; DB 12; Length 448;
 Best Local Similarity 63.4%; Pred. No. 1.1e-159;
 Matches 281; Conservative 78; Mismatches 84; Indels 0; Gaps 0;

QY 8 KKYITSEELKGNKSGDLWISIOGKYVYSDWVKEHGGDVPISNLAGODVDAFIAYHP 67
 Db 6 KKYITSEELKGNKSGDLWISIOGKYVYSDWVKEHGGDVPISNLAGODVDAFIAYHP 65
 QY 68 GTAMSHLEKFTG-YHLSDPKVSEVSKDYRKLASSEFSKGLPDTKGHTVSCITLASVAVNF 127


```

1  APPLICANT: Dae, Tapas
2  APPLICANT: Thurmond, Jennifer M.
3  APPLICANT: Pereira, Suzette L.
4  TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
5  FILE REFERENCE: 6763_US_P1
6  CURRENT APPLICATION NUMBER: US/10/054,534B
7  CURRENT FILING DATE: 2002-01-22
8  PRIOR APPLICATION NUMBER: US 09/769,863
9  PRIOR FILING DATE: 2001-01-25
10 NUMBER OF SEQ ID NOS: 55
11 SOFTWARE: PastedSeq for Windows Version 4.0
12 SEQ ID NO 14
13 LENGTH: 453
14 TYPE: PR1
15 ORGANISM: Saprolegnia diclina
16 US-10-054-534B-14

```

Quest Match	21.1%	Score 516;	DB 12;	Length 453;
Best Local Similarity	29.0%	Pred. No. 1.2e-43;		
Matches 128; Conservative	89;	Mismatches 174;	Indels 50;	Gaps 13;

Qy	5	EKEKKYITSEBKGNKKGDDMIISIOGKYVYNDWKCHPGGDVPIISNAGODVDAFLA	64
Db	5	QKAK-ISMATIREHNRODNAMIVHHKYDLSAF-EDHPGSVMFTQ-AGEDATDAV	61
Qy	65	YHPTAMSHLEKFTTG-----YHSDPKYSEVSK-----DYRKLASEPSKGL	107
Db	62	FHPSSALKLEIQQYYGVGDQSTAAVDITSID-----EVKKSQSDFIASYKRLLEVKRGL	117
Qy	108	FDTGHTYTSCTLASAYAMFLIVLVGVLCTSVMAHLGSGMLLGLLMGSAVYGHDSGYV	167
Db	118	YDSKRLYYLYQCASTLSTALVSAAICLHPDSTAMTMAVAIVLIGLFYQQCGMLADHFLHQ	177
Qy	168	VMTNGFNKVAQILSGNCLTGISIAWMKXTNHHIACN-----SLDHPDLOHMEVF	220
Db	178	VFEHMLFDOLGVWVGNLMGFSYQWGNKGNTHAIINLHATPEIAFHAGDPDITWIL	237
Qy	221	AVSRFRFNSTISHFYGRKLEDFLAFELICQHFHYVMCYARNLYQITILLF----	276
Db	238	AWSLK---MAQHAVDSP-----VGLFPMRYOAYLYFELLFARISWYIQSAMAIFYNVG	288
Qy	277	---SRKQVODALNIMGILVFWTW-FPLVSVCLPMPRVMFVLASFVCSI-CHIQCL	331
Db	289	PGCFPDKQYVLLBRAGILLYYGNMLGLVYANNSLLQAAFLFVFSQASCGLFLAMVSV	348
Qy	332	NHPAANYVGPSPGNDWFEKOTSGTLDISCASSNDWFFGGLQFOLEHLLPRLPRCOLRK	391
Db	349	GHNGMEVF-DSDSKPDFWKLOVLSTRYNTSSIMIDWFMGGLNTYQIDHLLFPVPRHNLPA	407
Qy	392	ISPLVSDLCCKHNLPYRSLSF	412
Db	408	LNVLVKSLCKQYDIPYHETGF	428

```

RESULT 9
US-10-431-952-14
: Sequence 14. Application US/10431952
: Publication NO. US20030190733A1
: GENERAL INFORMATION:
: APPLICANT: Abbott Laboratories
: APPLICANT: Mukerji, Pradip
: APPLICANT: Huang, Yung-sheng
: APPLICANT: Das, Tapas
: APPLICANT: Thurmond, Jennifer
: APPLICANT: Pereira, Suzette L.
: TITLE OF INVENTION: DESSATURASE GENES AND USES THEREOF
: FILE REFERENCE: 6'63. US '01
: CURRENT APPLICATION NUMBER: US/10/431,952
: CURRENT FILING DATE: 2003-05-08
: PRIOR APPLICATION NUMBER: US/09/769,863
: PRIOR FILING DATE: 2001-01-25
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: FASTSEQ for Windows Version 4.0

```

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; SEQ ID NO 14
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Saprolegnia diclina
US-10-431-952-14

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Query Match	21.1%;	Score 516;	DB 12;	Length 453;
Best Local Similarity	29.0%;	Pred. NO. 1.2e-43;		
Matches 128;	Conservative 89;	Mismatches 174;	Indels 50;	Gaps 13

QY	5	EKEKYTTSSEELKHNKEGDLMIISIOGKVYVSMVKEHPCGADVISYLAGODVDATFIA	64
Db	5	QKAEK-ISMATIRRHNQDNAMIVIHKKVYDISAF-EDHPGCVMTFG-AGEDATDAFAV	61
QY	65	YHPTASWLSHEKFTG-----YHLSDFKVEYSK-----DYKLASEFSKGL	107
Db	62	FHPSSALKLEQQYVGVGDVDDOSTAANDTISD-----EYKQSODEIASYKRLLEVXRGGL	117
QY	108	FDPTGHTTSCITLAAVAAWPLILVLYGVLCRSVMAHLSGMLLGLLMMOASAVVGHDSGNY	167
Db	118	YDSKSLYYLYKCASTLSIALVSAALCLHPDSTAMVMAAVITGLPYQQCGLAHDFLEHQ	177
QY	168	VMTINGENKVAQILSGNCITGISIAWKKWTINAHIACN-----SLDHPDLOHMEVF	220
Db	178	VFEHNLGLDVGWAVGVLMOGFSYQWKKKKNKNTHAIPLNLTATBEIAHAGSPDIDTWEIL	237
QY	221	AVSRRFPNNSITSHFYGKLEBFDIARPLICYQHFTFYPMCVARVNLVLTOTLLLF----	276
Db	238	AMSLK-----NAOHAVDSP-----VGLFFMRQVALYLPILLFARISWIOSAMVAFYVVG	288
QY	277	---SRKRVORALINMILIVFWTW--PFLVASCLEPNRPVRVFLVASFVCSI-QHIOFCL	331
Db	289	PGGTFDKQVPLERAGLLLYGNNLGLVYAANNSLDAAAFLVYSQASCGFLAMVSV	348
QY	332	NHPAANYVSPSGNDWFEKQTSCTLIDISCASSNDWEPFGIQLFOLENHLPRLPRCOLRK	391
Db	349	GHNMGEVAF-EKDSKPDPMKQLVLESTRVTSGLWIDWFGGLNLYQIDHLLPVPVPRHNLEPA	407
QY	392	ISPLVSDLCCKHNPYRSLSF	412
Db	408	LNVLVSKLCQYDIPYHETGF	428

RESULT 10
 US-10-278-391-4
 : Sequence 4, Application US/10278391
 : Publication No. US20030159164A1
 : GENERAL INFORMATION:
 APPLICANT: KOPCHIK, JOHN J.
 KELDER, BRUCE
 HUANG, YUNG-SHENG
 KIRCHNER, STEPHEN J.
 MUKERJI, PRADIP
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM
 PRODUCTS
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MEDLEN & CARROLL, LLP
 STREET: 220 MONTGOMERY STREET, SUITE 2200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/278,391
 FILING DATE: 23-Oct-2002
 CLASSIFICATION: 800

NUMBER OF SEQ ID NOS: 54
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 41
 LENGTH: 458
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (458)...(458)
 OTHER INFORMATION: Xaa = Unknown or other at position 458
 US-10-191-513A-41

Query Match 20.5%; Score 502.5; DB 15; Length 458;
 Best Local Similarity 30.2%; Pred. No. 2.9e-42;
 Matches 130; Conservative 72; Mismatches 191; Indels 37; Gaps 11;

QY 11 ITSELKHNK--BEDLMISIQKYYNSDWKKEHFGDVPISNLAGDVTDAFIAYHPG 68
 DB 16 LNAELNKGKDAEAPFLMIIDNKYVDREVPDHPGGSVILITHV-GDGDVDVPTFPAHE 74
 QY 69 TAWSHLEKFTG---YHLSDFVSEVSQDYRKLAESFSLGLPDTKGVTSCTLASVAVM 125
 DB 75 AAWETLANFYGGDDIDESDRDIKNDDFAAEVRKRLTLFQSLGYD---SKAYYAFKVS 129
 QY 126 FLIVLYGLRC-----TSVAHLGSGMLGLMMQSAVYGHDSGHVYVVTNGFNKVA 178
 DB 130 FNLCTWGLSTVYAKWGQSTLANVLSAALGLFWQCGWLAHDLHHQVQDRFWGDLF 189
 QY 179 QILGNCITGISIMWKTHNAHHIACNSLDHDPLOHMPVPAVSS--RFPNSTSHFY 235
 DB 190 GATLGVCQGGSSSWMKDKNTHAARVNHGSDPDIDHPLLTWSEHALEMFSDVPDEEL 249
 QY 236 GRKLEPFIARFLICYQHFTFYVVCVARVNLVLOTILLF-----SRKYOQDRALN 287
 DB 250 TR-----MWSFMYLANQTFYFPILISFARLSKCLQSLFVLPNGCAHPSGARVPISIVE 304
 QY 288 IMGILVFTWPEPLVSCLPNP-ERVMEVLASFAVC-SIOHIOFLNHPAANVYVGPSPG 345
 DB 305 QLSLHMTWYLAITWFLFIKDPVNNLVYELVSAVCGMLAIVSLNNGMPVLSKEAV 364
 QY 346 N-DWFEKTSGLTDISCASSMDWFFGGLQFQLEHHLFRLRCQRLKISPLVSLCKKH 404
 DB 365 DMDFETKQITGRDVHPGLFANWFTGSLNYQIEHHLFSPMRHNFPSKIQPAVETLCKKYN 424
 QY 405 LPYRSLSEFME 414
 DB 425 VRYHTGMIE 434

RESULT 13
 US-10-262-617-1
 Sequence 1, Application US/10262617
 Publication No. US2003007747A1
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Guegler, Karl J.
 APPLICANT: Corley, Neil C.
 APPLICANT: Shah, Purvi
 TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS
 FILE REFERENCE: PP-0494-1 DIV
 CURRENT APPLICATION NUMBER: US/10/262,617
 PRIOR FILING DATE: 2002-09-30
 PRIOR APPLICATION NUMBER: 09/048,888
 PRIOR FILING DATE: 1998-03-26
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PERL Program
 SEQ ID NO 1
 LENGTH: 445
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. US2003007747A1 2451043CD1

US-10-262-617-1
 Query Match 17.8%; Score 436; DB 15; Length 445;
 Best Local Similarity 28.4%; Pred. No. 1.7e-35;
 Matches 127; Conservative 65; Mismatches 179; Indels 76; Gaps 15;

QY 14 BELGHNKREGDLMISIQKYYNSDWKKEHFGDVPISNLAGDVTDAFIAYHPGTAWSH 73
 DB 26 EQIAHQDPGDKMLVIRRAYDISRMAQRHGGSRLLGHGAEDATDAFRAHQDL--NF 83
 QY 74 LEKFTGHLSDFFVSEVS-----KDYRKLAESFSLGLPDTK-----GHVT 115
 DB 84 VRKFLQPLIGELAPBEPSSQDGPLNAQLVEDFRALHOAEDMKLFDSPTFEFLGHIL 143
 QY 116 SCLTASVAVWFLVLYGLVLAQCTSVMAHLGSGMLGLMMQSAVYGHDSGHVYVVTNGFN 175
 DB 144 A--MEVLAHLVLYLQPGVPSALA---AFITAIQAOQSWCQHDHGHASIFRKSWN 196
 QY 176 KVAQILGNCITGISIMWKTHNAHHIACNSLDHDPLOHMPVPAVSSRFPNSTSHFY 235
 DB 197 HVAQKFMQGLKGFSAHMANFRHQHAKNFIHKPDVTVAPVFLGE-----SSVEY 250
 QY 236 GRKLEPFIARFL-ICYQHFTFY---PVMCAVAVNLVLOTILLFRRKXQDRALNMG 290
 DB 251 GKRR-----RYLPYNOQHLYFFLIGPPLTL--VNEFEV-----MLAY 287
 QY 291 ILVFTWPEPL-----VSCLPNM--PERVMEVLASFAVCSIQHIOC-LNHFAAN 337
 DB 288 MLVCMQADLLMAASFAARFPLSTLPYGVGVLFVAVARVLSHFWITQNHLPKE 347
 QY 338 VYVGPSPGNDWFEKTSGLTDISCASSMDWFFGGLQFQLEHHLFRLRCQRLKISPLVS 397
 DB 348 --IGHEHGRDWSQLATCNVBSLFTNMFSGHLNQHIEHHLFRRPRHNYSRVAVLVK 405
 QY 398 DLCKGNLPYRSLSEFMEANQTTITLR 424
 DB 406 SLCAKHGLSYEVKPFALTALVDIVASLK 432

RESULT 14
 US-10-262-617-3
 Sequence 3, Application US/10262617
 Publication No. US2003007747A1
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Guegler, Karl J.
 APPLICANT: Corley, Neil C.
 APPLICANT: Shah, Purvi
 TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS
 FILE REFERENCE: PP-0494-1 DIV
 CURRENT APPLICATION NUMBER: US/10/262,617
 PRIOR FILING DATE: 2002-09-30
 PRIOR APPLICATION NUMBER: 09/048,888
 PRIOR FILING DATE: 1998-03-26
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PERL Program
 SEQ ID NO 3
 LENGTH: 444
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. US2003007747A1 2056310CD1
 US-10-262-617-3
 Query Match 17.5%; Score 429; DB 15; Length 444;
 Best Local Similarity 28.3%; Pred. No. 8.7e-35;
 Matches 128; Conservative 66; Mismatches 181; Indels 76; Gaps 15;
 QY 9 KITSELKHNKREGDLMISIQKYYNSDWKKEHFGDVPISNLAGDVTDAFIAYH-- 66
 DB 18 RYFTWDEVAORSQGEERMLVIDRKVNISETTRHHPGGSVISHYACQDATDPEVAFHIN 77

QY 169 MTNNGNKYAOALISNGCTGTSIAWKKTNHAAHIAACSLDHDLDQMEVFAVSSRFN 228
 Db 187 FSTSKNHLHHFVGLHKGAPASMMNMHQHAKRCPFKDIDIMHFFFAKGLIS 246
 QY 229 SITSHPYGRKEEDFIARPLICYQHFTFYPMVCARVNLTYQTLLF--SRKVDRL 286
 Db 247 VEBKQKKKKMYM-----HOKHYFLLGPRLALPLYQWYIFVYLQKKWDLAW 298
 QY 287 NI-MGILVFWTFPRL-----VSCF--PMPBRVMEVLASFAVCSIOHIOFLAH 333
 Db 299 MTFYRFRFLTYRPLLGKALGLGFYIRPLESN-----FVW-----VTQNMHPIHIDH 349
 QY 334 PAANVTGPPSNDMEPEKQTSGLDIDISCASSDMFPGLOFQLEHNLPRPLRCOLAKIS 393
 Db 350 -----DRMDMVSQTQLATCIVHNSAANDMFSGHLNFOIEHNLPTMPRPNHYKVA 400
 QY 394 PLYSDLCCKGNLPIYRSLSPMEANQWITITLR 424
 Db 401 PLVQSLCAKRGIEYQSKPLSHFADITHSLK 431

Job time : 86.7267 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:39:42 ; Search time 2065.16 Seconds
(without alignments)
16303.117 Million cell updates/sec

Title: US-09-857-524B-16
Perfect score: 823
Sequence: 1 cccccaacaacaccgcgtt.....cgtnaagacttgtagcat 823

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GeneBml:*

1: gb_ba:*

2: gb_hcg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_ses:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_ov:*

22: em_or:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_ses:*

28: em_un:*

29: em_vl:*

30: em_hcg_hum:*

31: em_hcg_inv:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pin:*

35: em_hcg_rtd:*

36: em_hcg_mam:*

37: em_hcg_vrt:*

38: em_sy:*

39: em_hcg_hum:*

40: em_hcg_mus:*

41: em_hcg_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	531.6	64.6	1788	AF031194	AF031194 Triticum
2	272.4	33.1	96312	AF005554	AF005554 Oryza sat
3	120.4	14.6	1681	AY234124	AY234124 Primula f
4	113.8	13.8	1385	AY234126	AY234126 Primula f
5	107	13.0	1618	AY234127	AY234127 Primula v
6	106.8	13.0	1702	AR200409	AR200409 Sequence
7	98.8	12.0	1410	AY234125	AY234125 Primula f
8	95.4	11.6	11000	RN52A06_00	BN52A06_00
9	94.8	11.5	1594	AX007239	AX007239 Sequence
10	94.8	11.5	1610	BN4J4160	BN4J4160 Brassaica
11	94.8	11.5	303091	AC084799	AC084799 Mus muscu
12	93.6	11.4	840	CNS01BNS	AL114464 Botrytis
13	93	11.3	144979	AC016280	AC016280 Homo sapi
14	92.6	11.3	108409	AF083424	AF083424 Aceline h
15	92.6	11.3	220469	AC074307	AC074307 Oryza sativ
16	92.2	11.2	2000	OSNIA134	OSNIA134
17	92.2	11.2	2817	AX660410	AX660410 Sequence
18	92.2	11.2	2877	AX654602	AX654602 Sequence
19	92.2	11.2	2877	AX660148	AX660148 Sequence
20	92.2	11.2	149879	AP005381	AP005381 Oryza sat
21	92.2	11.2	163285	AP004585	AP004585 Oryza sat
22	92.2	11.2	252689	AC079433	AC079433 Mus muscu
23	91.8	11.2	205691	AC087227	AC087227 Mus muscu
24	91.4	11.1	77884	AC139551	AC139551 Homo sapi
25	91.4	11.1	164751	BX293567	BX293567 Danio rer
26	90.6	11.0	300695	AC079431	AC079431 Mus muscu
27	90.4	11.0	265537	AC087228	AC087228 Mus muscu
28	90	10.9	150695	AC023576	AC023576 Homo sapi
29	89.8	10.9	8043	AF153448	AF153448 Zea mays
30	89.8	10.9	202083	AC023833	AC023833 Mus muscu
31	88.8	10.8	222707	AC079425	AC079425 Mus muscu
32	88.6	10.8	81417	AC023265	AC023265 Homo sapi
33	88.6	10.8	141892	AC023197	AC023197 Mus muscu
34	88.4	10.7	78320	AC023212	AC023212 Homo sapi
35	88.2	10.7	75628	AC021793	AC021793 Homo sapi
36	88	10.7	110000	BX119993_0	BX119993 Mus muscu
37	87.6	10.6	235310	AC094274	AC094274 Rattus no
38	87.2	10.6	266935	AC144767	AC144767 Mus muscu
39	87	10.6	1080	CNS019XP	AL112229 Botrytis
40	86.8	10.5	3163	AX647321	AX647321 Sequence
41	86.8	10.5	74138	AC021272	AC021272 Homo sapi
42	86.6	10.5	69515	AC099971	AC099971 Mus muscu
43	86.6	10.5	76052	AC023262	AC023262 Homo sapi
44	86.4	10.5	33058	AC100211	AC100211 Mus muscu
45	86.4	10.5	134940	AC018939	AC018939 Homo sapi

ALIGNMENTS

RESULT 1

LOCUS AF031194 1788 bp mRNA linear PLN 29-JAN-1999

DEFINITION Triticum aestivum S276 (S276) mRNA, complete cde.

ACCESSION AF031194

VERSION AF031194.1 GI:4104055

KEYWORDS

SOURCE

ORGANISM

Triticum aestivum (bread wheat)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticaceae; Triticum.

REFERENCE

1 (bases 1 to 1788)
Delhaize, E., Hebb, D.M., Gardner, R.C. and Richards, K.D.
Aluminum tolerance in yeast conferred by over-expression of wheat

Pred. No. is the number of results predicted by chance to have a

Db	88146	GCCG-----GCTCTCCCCCAAGAGGCGCAGAAAGCCGCGCGCGCGCGCTCCGCAATGAT	88199
Qy	206	CTTCACCAAGAGAGCTGAGGCGCAACGCCCGCCGCGAGACATCTTGATCTTCATCTCCGG	265
Db	88200	CTCCTCGAGAGAGCTCCGCGCGACACGCGCTGAGAGGAGACATCTGTGATCTTCATCTCCGG	88255
Qy	266	GGAGCTTAAAGAGTCAACGCCCTTGCTGCTGCGCCACACACCCGGCGGGGAGAGTCCCGCTCAT	325
Db	88260	GGAGGTGTAAAGAGTCAACGCCCGTGGGGTCCCAACACCCGGCGGGGAGACATCTCCGCTCTCT	88319
Qy	326	CACCTTGCGCGGCGAGGACGCACCGACGCTTCATGAGCTTACACCCCGCCCTCGGTGGG	385
Db	88320	GAGCTTGCGGGGAGGAGACGCACCGACGCTTGCGCGCTTACACCCCGCCGTCGGCGGG	88379
Qy	386	CCGCGTCTCTCCGCGGCTTCTTCTGTCGGGCGCGCTCACCGAATCACTGTCCGCCGCCCTCTC	445
Db	88380	CCCGCTCTCGGGAGAGTCTCTCTGTGGGCGCGGCTTCAGAGATCAACGGTCTCTCGCGGCGCTC	88439
Qy	446	CGCGGACTTCCGCGCGCTCTCTCGCGGACGCTCTCTTCGCGGGGCTCTTGAGAGCGGT-CG	504
Db	88440	CGCGGACTTCCGCGCGCTCTCTCGCGGAGCTCTCTCCGCGGGGCTGTGAGAGGGTGGG	88499
Qy	505	GCACACCCCAAGTCTCTGCTGTGCGAAGTCMGTGCTTCTTGCAATGAGCTCTTACTG	564
Db	88500	GCCCAACCCCAAGGTGAGGTTCGCGGGAGTGTGCTCTCTCTGCGCGCGCTTACTG	88555
Qy	565	C-TCTCGCTGCTCAACACCGGGGACCAATGTTCCGCGGGG	605
Db	88560	CGTCTCTGCTTCGCGGAGCGCGTGTGGGCGCACCTTCTTGCCCGG	88601

RESULT 3

LOCUS	AV234124	1681 bp	mRNA	linear	PLAN 04-MAY-2003
DEFINITION	Primula farinosa sphingolipid delta-8 desaturase mRNA, complete cde.				
ACCESSION	AY234124				
VERSION	AY234124.1	GI:30350274			
SOURCE	.				
ORGANISM	Primula farinosa Primula farinosa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asterales; Ericales; Primulaceae; Primula. 1 (bases 1 to 1681) Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and Napier,J.A. Identification of Primula fatty acid Delta(6)-desaturases with n-3 substrate preferences (1) FEBS Lett. 542 (1-3), 100-104 (2003) 22615586 12729906 2 (bases 1 to 1681) Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and Napier,J.A. Direct Submission Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton Research Station, Long Ashton, Bristol BS41 9AF, UK Location/Qualifiers 1..1681				
TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS
FEATURES					
SOURCE					

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CDS
53..1411
/note="cytochrome b5 fusion desaturase"
/codon_start=1
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/protein_id="Amp2032_1"
/db_xref="GI:30350273"
/translation="MADPEPNPKTYGITSDDIKAHNKAGDLMISIHGOVYVSSWMAI
HGGAFALMALAGDVDAFLAYHPSPFARLLPGLASLLLEHYSVSPSSDYRKLRL
NHNKLDLCCTSHKTCCTFVAMVAVLFTSLILGFCSDSTWHLALSGWVGWVAIOGNG

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BASE COUNT	353	a	445	c	404	g	479	t
ORIGIN	<p> LGDSGCHGYOIMSRKTNRPQVSLSGNGLAITSIAMKMNNAHHLACNSLDYDPDIL MPFVVSXKREFNSLTSFYPRKANPDGVSFPLVSYQMSFYPMCLARITULFAOSFHL LFSSRKVPDRVQELFGIGVFWVYPLVLSCLPMWGEKINFVASFSVTGIVQVFCILN HFSAEVLVLCRPGNDMEFKQTAGTILNISMSNDWFFGGIQFOI EHHLPRLPSQLR KVSFPPVLDLCKKNLPPYNTVSFTMANVLTJLKTLRNAIQARDLSNPPKVLVWEAVNT HG" </p>							

Query Match	14.6%;	Score 120.4;	DB 8;	Length 1681;
Best Local Similarity	62.1%;	Pred. No. 2.5e-05;		
Matches 223;	Conservative 0;	Mismatches 132;	Indels 4;	Gaps 2;
QY	204	ATCTCCACCAAGAGCTGCAGGCGCAGCGCCGCGGAGCAGCCTCTGATCTCCATCTCC	263	
Db	89	ATAACCAAGCTCAGACCTGAAAGCCCAACACAAAGGACAGGTAGCATTGATATCAATCAT	148	
QY	264	GGGGAAGCTCTACGACGCTCAACGCGCCCTGGCTGGCCACCAACCCGGGCGGGAGGTTCGCGCTC	323	
Db	149	GGCCCAATCTACGACGCTCTCTCGTGGGCGCGCCCTTCATCCGGGGGGACACGCGCCCTCTC	208	
QY	324	ATCAACCTCGCGCGGACGAGACGCGACGCGCCTTACATGGCGCTACACACCGCGCCCTCCGCTG	383	
Db	209	ATGGCCCTTCGGAGGACACGACGTAACCGACGCTTTCCTTGTTACATATCCCCCTTCACAC	268	
QY	384	CGCCCGCTCTCTCGCGCGCTTCTTGTCGTGGCGCGCTCAACG---ACTACACTGTATCCCGCC	440	
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QY	441	GCTTCGCGCGACTTTCGCGCGGCTCTCTGCGGAGCTCTCTTCGCGGCGCTCTTTCGAG-CG	499	
Db	329	ACCTCTCTCGACATCACCGCAAACTCTCTCCACAACTTCATTAACCTGCACCTTTTCCAAACC	388	
QY	500	CGTGGGACACCCCGAAGTTCTGCTGCTGCGCAAAAGTCNGTGCCTCTTGATCGAGGCT	558	
Db	389	AAATTCACACACACTCTCTTACGTTGTGTGCGCAATGATAGTCTTGTCTCTACGCTT	447	

RESULT 4

LOCUS	AY2341426	1385 bp	mRNA	linear	PLN 04-MAY-2003
DEFINITION	Primula vialii sphingolipid delta-8 desaturase mRNA, complete cds.				
ACCESSION	AY2341426				
VERSION	AY2341426.1	GI:30350278			
KEYWORDS					
ORGANISM	Primula vialii				
SOURCE	Primula vialii				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Primulaceae; Primula.				
AUTHORS	1 (bases 1 to 1385) Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and Napier,J.A.				
TITLE	Identification of Primula fatty acid Delta(6)-desaturases with n-3 substrate preferences (1)				
JOURNAL	FEBS Lett. 542 (1-3), 100-104 (2003)				
MEDLINE	22615586				
PUBMED	12729906				
REFERENCE	2 (bases 1 to 1385)				
AUTHORS	Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and Napier,J.A.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton Research Station, Long Ashton, Bristol BS41 9AF, UK				
FEATURES	Location/Qualifiers				
SOURCE	1..1385				

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CDS      27..1385
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        /codon_start=1
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Best Local Similarity	60.3%	Fred. No. 0.00015;		
Matches 223;	Conservative 0;	Mismatches 143;	Indels 4;	Gaps 2;
Qy	204	ATCTCCACCAAGAGCTCAGAGCGCAGCGCGCGGAGCAGCCTCTGATCTCCATCTCC	263	
Db	63	ATAACGAGCTCAGACCTTAAGGCGACAAAGGAGGAAACCTTAGATTCATCTAC	122	
Qy	264	GGGAGCGTCTACGACGTCACGCCCTGTGCGGCACCAACCGGCGGCGAGTCCCGCTC	323	
Db	123	GGGAGGATACGACGTCGTCTCGGCGCGCGCTTCAACCGGGGGGAGTGGCCCTTC	182	
Qy	324	ATCACCTCTCGCGCGCGCAGAGCGCCACGACGCTTACATGAGCTTACACCGCCCTC	380	
Db	183	ATGAGCCCTCGGAGGACAGGACGAGTAAACGACCTTTCTAGGCTATCTCTCTTAC	242	
Qy	381	GTGCGCGCGCTCTCTCGCGCGCTCTCTGTCGAGCGCCTCACGCTACATCTGCTCC	440	
Db	243	GCGCGCT	302	
Qy	441	GCTCTCGCGCGCGCT	499	
Db	303	ACCT	362	
Qy	500	CGTGGGACACCCCGCAAGTCTCTGCTGTCGCAAGTGTGCTCTTGTGATGGCTC	559	
Db	363	AAATCCCACTTACATGCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	422	
Qy	560	TACGTCT	569	
Db	423	TACGGGCT	432	
RESULT 5				
LOCUS	AY234127	1618 bp	DNA	linear
DEFINITION	Primula vialii fatty acid delta-6 desaturase gene, complete cds.			PLN 04-MAY-2003
ACCESSION	AY234127			
VERSION	AY234127.1	GI:30350280		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
MEDLINE				
PubMed				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				

FEATURES	source	Location/Qualifiers
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		/db_xref="taxon:175103"
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cds		/join(36..522,744..1618)
		/note="cytochrome b5 fusion desaturase; has a preference for n-3 fatty acid substrates"
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		523..743
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ORIGIN		
Query Match	13.0%; Score 107; DB 8; Length 1618;	
Best Local Similarity	65.2%; Pred. No. 0.00091;	
Matches 174; Conservative 0; Mismatches 90; Indels 3; Gaps 1;		
OY	204 ATCTCCACCAAGAGCTGCGAGGCGCGCCGCGGAGCACTCTTGATTCGATCTCC	263
Db	75 ATTACCGAGCTCAGACCTGAAAGGCGACAAAGACAGAGACCTATGAGATCAATCCAC	134
OY	264 GGGGAGCTACAGACGTCACGCGCTGCGTGGCGACACCGGGGGCGAGGTCCGCTC	323
Db	135 GGGAGGATACGACGATGCTCTGTGGCGCGGCTTACCCGGGGGCAAGTCCCTTC	194
OY	324 ATCACTCTCGCGCGCCAGACGCGACCGACGCTTCATGCGCTACCAACCGCGCTC	380
Db	195 ATGACCTCTCGAGGACACGAGTAAACGAGGCTTTCTAGAGTATCATCTCTTACAC	254
OY	381 GTGCGCCGCTCTCTCGCGCGCTTCTTGTCGGCGGCTCACCGACTACATGTCCTCC	440
Db	255 GCCGCGCTCTCTCTCTCTCTCTCTCCACCAACCTCTCTTCAAAACCATCTGCTCC	314
OY	441 GCCTCGCGGCACTTCGCGCGGCTCTC 467	
Db	315 ACCTCTCTGACTACGCAATCTCTC 341	
RESULT 6		
LOCUS	AR200409	1702 bp DNA linear PAT 20-APR-2002
DEFINITION	Sequence 26 from patent US 6355861.	
ACCESSION	AR200409	
VERSION	AR200409.1	GI:20250483
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 1702)	
TITLE	Thomas, T. L.	
JOURNAL	Production of gamma linolenic acid by a DELTA-6-desaturase	
FEATURES	Patent: US 6355861-A 26 12-MAR-2002;	
source	Location/Qualifiers	
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	/organism="unknown"	
BASE COUNT	358 a 471 c 446 g 427 t	
ORIGIN		

RESULT	7
LOCUS	AY234125
DEFINITION	AY234125 1410 bp mRNA linear
VERSION	AY234125 Primula farinosa fatty acid delta-6 desaturase mRNA, complete cds.
KEYWORDS	AY234125.1 GI:30350276
SOURCE	Primula farinosa

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49_1410
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for n-3 fatty acid substrates"
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YIPLLVSPKFEFNTLSRFYDKLINTDSCFSLVLCQWMTYPMVCARLIMLACSF
TLFSREYCHRAOEVEGLAVFWNMFPLLSCLPMWEGEIMFLASYSYLOHVSF
NHFSVDYVGPDPGVNDMKOTAGTLINSCAMNDPMWEGGLQFOVEHTLPRMGQSG
RKISIPVARDLCKGNLPLNINASFKNAYFTLKITLRNTATEARDSLNPFLKMMVDEAL
TLG"

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RESULT 8	
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WPCOMMENT	
Sequence split into 10 fragments	LOCUS RMS2A06 Acc666810 BX511200

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LOCUS          1002253 bp   DNA   linear   HTG 23-MAY-2003
DEFINITION    Rattus norvegicus chromosome 1 clone R332-52A6, *** SEQUENCING IN
PROGRESS ***, 721 unordered pieces.
ACCESSION     BX511200
VERSION       BX511200.1 GI:31074747
KEYWORDS      HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE        Rattus norvegicus (Norway rat)
ORGANISM      Rattus norvegicus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
               Rattus.
REFERENCE     1 (bases 1 to 1002253)
AUTHORS      Schoen,O., Conrad,A., Hornischer,K., Loehner,T.H., Thies,S.,
               Scharte,M. and Bloecker,H.
TITLE        Direct Submission
JOURNAL      Submitted (23-MAY-2003) GBF, Dept. of Genome Analysis, Mascheroder
               Weg 1, D-38124 Braunschweig, Germany, E-mail: info.genome@gbf.de
COMMENT      All annotations in this database entry are developed by
               computational tools. It is therefore not explicitly noted in the
               feature lines that evidence is not experimental.
               ----- Genome Center
Center: GBF, Braunschweig
Center code: GBF
Web site: http://genome.gbf.de/
Contact: info.genome@gbf.de
               ----- Project Information
Center project name: R332-52A06
               ----- Summary Statistics
Sequencing vector: ###:
Chemistry: Dye-terminator-amersham: ##% of reads

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Chemistry: Dye-primer-amersham: ## of reads
Assembly program: #
Consensus quality: 276318 bases at least Q40
Consensus quality: 315218 bases at least Q30
Consensus quality: 355218 bases at least Q20
Estimated insert size: ##; agarose-fp estimation
Estimated insert size: 930153; sum-of-ctdigs estimation

PROGRAMS AND PARAMETERS USED FOR ANNOTATION:
+ + + + +
+ Analysis and annotation were performed with the automatic +
+ 'first-pass' annotation and submission tool +
+ 'AnnotMitter' (Hornischer & Bloeker). +
+ Programs used by 'AnnotMitter': +
+ + + + +
* NOTE: This is a 'working draft' sequence. It currently
* consists of 721 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 101 1688: contig of 1588 bp in length
* 1689 1788: gap of 100 bp
* 1789 3060: contig of 1272 bp in length
* 3061 3164: gap of 104 bp
* 3165 4800: contig of 1636 bp in length
* 4801 4900: gap of 100 bp
* 4901 6139: contig of 1239 bp in length
* 6140 6239: gap of 100 bp
* 6240 7377: contig of 1138 bp in length
* 7378 7477: gap of 100 bp
* 7478 8502: contig of 1025 bp in length
* 8503 8602: gap of 100 bp
* 8603 9759: contig of 1157 bp in length
* 9760 9859: gap of 100 bp
* 9860 10886: contig of 1027 bp in length
* 10887 10986: gap of 100 bp
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* 12236 12335: gap of 100 bp
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* 16615 16715: gap of 101 bp
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* 19422 20474: contig of 1053 bp in length
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* 32582 33856: contig of 1275 bp in length

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* 35385 35485: gap of 101 bp
* 35486 36552: contig of 1067 bp in length
* 36553 36657: gap of 105 bp
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* 37801 37900: gap of 100 bp
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* 39334 40818: contig of 1465 bp in length
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* 44159 45250: contig of 1092 bp in length
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* 45351 46733: contig of 1383 bp in length
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* 53392 54443: contig of 1052 bp in length
* 54444 54543: gap of 100 bp
* 54544 55878: contig of 1335 bp in length
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* 71060 71161: gap of 102 bp
* 71162 72185: contig of 1024 bp in length
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* 81238 81327: gap of 100 bp
* 81328 82704: contig of 1377 bp in length
* 82705 82804: gap of 100 bp
* 82805 83839: contig of 1035 bp in length
* 83840 83941: gap of 102 bp

PUBMED 9786850
 REFERENCE 2 (bases 1 to 1610)
 AUTHORS Sperling P.
 TITLE Direct Submission
 JOURNAL Submitted (13-FEB-1998) Sperling P., Physiologie, Institut fuer
 Allgemeine Botanik der Universitaet Hamburg, Ohnhorststrasse 18,
 D-22609 Hamburg, GERMANY
 COMMENT Related sequence: X87143.
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 DB 136 AAGGCAAGCTACGACGCTCCACGCGGTCAATCCATCCCGGAGGGAAGACCGA 195
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 QY 379 CCGTGGCGCGCTCTCCGCGCTTCTTGTGCGCGCGCTTACCGACTACGACTGTCGCC 438
 DB 256 CATGGCGCACTCTGAAACCTTCACACGCGCTACCACTGAAAGACCAACGATGTCCG 315
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 DB 316 ACGTGCGGTGACTACCGCTGTTAGCCGCGGAGTTTCAAAACGCGACGACTCTTGA 373

RESULT 11
 AC084799/c
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 DEFINITION Mus musculus chromosome 16 clone RP23-197M9, WORKING DRAFT
 SEQUENCE 101 unordered pieces.
 AC084799

VERSION AC084799.1 GI:11922127
 KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS 1 (bases 1 to 303091)
 TITLE DOE Joint Genome Institute.
 JOURNAL Sequencing of Human Chromosome 16
 REFERENCE 2 (bases 1 to 303091)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (17-NOV-2000) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 COMMENT
 Center: Joint Genome Institute
 Center Code: JGI
 Web site: <http://www.jgi.doe.gov>

 Project Information
 Center Project Name: 0
 Center Clone Name: RP23-197M9

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 Consensus quality: 152568 bases at least Q40
 Consensus quality: 175579 bases at least Q30
 Consensus quality: 186949 bases at least Q20
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 Estimated insert size: 293091; sum-of-coverage estimation
 Quality coverage: 4.85 in Q20 bases; agarose-1p estimation
 Quality coverage: 3.28 in Q20 bases; sum-of-coverage estimation.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 101 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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 4157 4157: gap of unknown length
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 6561 6561: gap of unknown length
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 7726 7726: gap of unknown length
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 19453 19452: gap of unknown length
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 21112 21112: gap of unknown length
 22169 22169: contig of 1057 bp in length

[illegible]

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Db	316	GCC	375
OY	274	ACGACGTGACGCGCTGGCGCCACAACCGGGGGGAGGTCGCGTCATCAACCTCG	333
Db	376	CC	435
OY	334	CCGGCAGAGACGCCACGAGCGCTTCATGCGCTTACACCGCGCTTCGTCGCGCGCTCC	393
Db	436	CCCGG	495
OY	394	TCCGCGGCTTCCTGTCGCGCGGCTCAACGACTACATGTCGCCGCCCGGCTCCGCGACT	453
Db	496	CCCGCC	555
OY	454	TCCGCGCGCTTCGCGAGGCTTCTCTCGCGGAGCGCTTCGAGCGCGTCGACACCCC	513
Db	556	CCCCCCCCCCCCCCCCCCCCCCCCCGGCCCCCCCCCCCCCCCCCCCCCGGCCCC	615
OY	514	CAAGTTCCTGCTCGTCGCAAGTCAGTCCTTCTTGCAATCGGCGCTTACTGCTCCTCGCC	573
Db	616	CCCCGCCCCCCCCCCCCCCCCCGCGGCCCCCCCCCCCCCCCCCCCCCCCCCCCC	675
OY	574	TGCTCAACCC	584
Db	676	CGCCCCCCCC	686

RESULT 13	LOCUS	AC016280	144979 bp	DNA	linear	HTG 13-JUL-2000
AC016280	DEFINITION	Homo sapiens clone RP11-20N19, LOW-PASS SEQUENCE SAMPLING.				
	ACCESSION	AC016280				
	VERSION	AC016280.3	GI:9123976			
	KEYWORDS	HTG; HTGS PHASE0.				
	SOURCE	Homo sapiens (human)				
	ORGANISM	Homo sapiens				
	REFERENCE	Eukaryote, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
	AUTHORS	1 (bases 1 to 144979)				
	TITLE	Bliren,B., Linton,L., Nusbaum,C. and Lander,E.				
	JOURNAL	Homo sapiens, clone RP11-20N19				
	REFERENCE	Unpublished				
	AUTHORS	2 (bases 1 to 144979)				
		Bliren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukagalter,B., Brown,A., Castle,A., Colangelo,W., Collins,S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Domingo,M., Donelan,L., Doyle,M., Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kamm,L., Karatas,A., Klein,J., Lowickoy,J., Lieu,C., Locke,K., MacDonald,P., Marguis,N., McEwen,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J., Metrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Seifage,Thomas,N., Stojanovic,N., Subramanian,A., Talamas,J., Tsifane,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.				
	TITLE	Direct Submission				
	JOURNAL	Submitted (24-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 300 Charles Street, Cambridge, MA 02141, USA				
	COMMENT	On Jul 13, 2000 this sequence version replaced gi:6730879. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html				
		----- Genome Center				
		Center: Whitehead Institute/ MIT Center for Genome Research				

Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: L3944
Center clone name: 20_N_19

* NOTE: This record contains 138 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1
872 871: contig of 871 bp in length
972 971: gap of 100 bp
1882 1881: contig of 910 bp in length
1882 1881: gap of 100 bp
2870 2869: contig of 888 bp in length
2970 2969: gap of 100 bp
3880 3880: contig of 911 bp in length
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4853 4853: contig of 873 bp in length
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19789 19788: gap of 100 bp
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20799 20799: contig of 911 bp in length
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21830 21829: gap of 100 bp
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49618 49617: gap of 100 bp
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51543 51543: contig of 932 bp in length
51544 51543: gap of 100 bp
51644 51643: gap of 100 bp
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58600 58600: gap of 100 bp
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Db 102287 CTCCTGCTCCCCATGCGCCCCCGCTCTTCCCGCTCCCGCTCTCCCGCTCTCCCGCT 102346
Qy 497 GCGCGTGGACACCCCAAGTCTGCTGTCGCAAGTGNCTCTTCTGATCGGC 556
Db 102347 CTCCTGCTCCCCCGCTCTCTCCCGCTCTCCCGCTCTCCCGCTCTCTCCCGCTCTC 102406
Qy 557 C 557
Db 102407 C 102407

RESULT 15
AC074307/c
LOCUS
DEFINITION
AC074307 220469 bp DNA linear HTG 26-JUL-2000
Mus musculus chromosome 16 clone RP23-6K21, WORKING DRAFT SEQUENCE,
42 unordered pieces.
AC074307
AC074307.1 GI:9454523
VERSION
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 220469)
DOE Joint Genome Institute.
TITLE
Sequencing of Mouse
2 (bases 1 to 220469)
DOE Joint Genome Institute.
DIRECT SUBMISSION
Submitted (26-JUL-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 0
Center clone name: RP23-6K21

Summary Statistics
Consensus quality: 156592 bases at least Q40
Consensus quality: 179034 bases at least Q30
Consensus quality: 187032 bases at least Q20
Estimated insert size: 236300; agarose-fp estimation
Estimated insert size: 216369; sum-of-contigs estimation
Quality coverage: 3.09 in Q20 bases; agarose-fp estimation
Quality coverage: 3.37 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 42 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1485 1484: gap of unknown length
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2688 2687: gap of unknown length
4000 4000: contig of 1313 bp in length
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4101 5461: contig of 1361 bp in length
5462 5561: gap of unknown length
5562 6699: contig of 1138 bp in length
6700 6799: gap of unknown length
7973 7972: contig of 1173 bp in length
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9196 9195: contig of 1123 bp in length
9296 9295: gap of unknown length
10796 10795: contig of 1500 bp in length
10895: gap of unknown length

FEATURES
source

10896 12066: contig of 1171 bp in length
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20521 22007: contig of 1487 bp in length
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22108 23564: contig of 1457 bp in length
23565 23664: gap of unknown length
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29186 29285: gap of unknown length
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37361 37460: gap of unknown length
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52363 57511: contig of 5150 bp in length
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57612 61854: contig of 4243 bp in length
61855 61954: gap of unknown length
61955 66982: contig of 5028 bp in length
66983 67082: gap of unknown length
67083 70791: contig of 3709 bp in length
70792 70891: gap of unknown length
70892 76429: contig of 5538 bp in length
76429 76529: gap of unknown length
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Location/Qualifiers
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/organism="Mus musculus"
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/chromosome="16"

BASE COUNT 63413 a 42075 c 48606 g 53951 t 6420 others
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 /clone lib="RP21 mouse BAC library 23"

Query Match 11.3%; Score 92.6; DB 2; Length 220469;
 Best Local Similarity 43.0%; Pred. No. 0.0099;
 Matches 237; Conservative 0; Mismatches 314; Indels 0; Gaps 0;

QY 34 CCGATCTCCCTTCNCCCTCCCTCCCTTCCTCTGAGTCTGACACCCCTCTCCG 93
 Db 7613 CC 7554
 QY 94 CTCACGTAATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 153
 Db 7553 CC 7494
 QY 154 AAGCCGACGCAATGCGGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 213
 Db 7493 CC 7434
 QY 214 AGGAGCTGACAGGCGACGCGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAG 273
 Db 7433 CCNCCNNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 7374
 QY 274 ACAGAGTCAAGCCTGAGTCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 333
 Db 7373 CCCCCNNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 7314
 QY 334 CCGGCGAGAGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 393
 Db 7313 CC 7254
 QY 394 TCGCGCGCTTCTTCTGCGCGCGCTCAAGCAGTACTGCTCCCGCGCTCGG 453
 Db 7253 CC 7194
 QY 454 TCGCGCGCTTCTTCTGCGCGCGCTCTCTCTGAGGCGGTGCGCAGACCC 513
 Db 7193 CC 7134
 QY 514 CAAGTCTGCTGCTGCGCAAGTCTGCTCTTCTGATGCGCCTTACTGCTCTG 573
 Db 7133 CC 7074
 QY 574 TGCTCAACACC 584
 Db 7073 CCCCCCCCCC 7063

Search completed: December 31, 2003, 21:04:36
 Job time : 2070.16 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:38:37 ; Search time 156.169 Seconds
(without alignments)
14225.873 Million cell updates/sec

Title: US-09-857-524B-16

Perfect score: 823
Sequence: 1 ccccttaacaacaccctccgtt.....cgtnaagacttgtagcat 823

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	809	98.3	823	21	AAD01354
2	552	67.1	1972	21	AAD01353
3	314.8	38.3	1764	21	AAD01350
4	106.8	13.0	1702	24	ABK49503
5	106.8	13.0	1702	25	ABK15367
6	94.8	11.5	1594	21	AA244832
7	85.6	10.4	12733	24	ABK98631
8	85.6	10.4	12739	24	ABK98592

9	82.2	10.0	1337	20	AA217263
10	81.6	9.9	1934	21	AAD01352
11	79.6	9.7	1000	21	AAA02484
12	77.2	9.4	1064	24	ABT09678
13	75.2	9.1	4411529	22	AA199682
14	74.4	9.0	1465	21	AA042244
15	72.4	8.8	1065	24	ABT09682
16	72	8.7	65140	22	AAD17184
17	72	8.7	125401	22	AAD17186
18	71.4	8.7	1606	21	AA244851
19	71.2	8.7	600	24	AB052496
20	71.2	8.7	600	24	AB052497
21	70.8	8.6	77536	21	AAA14651
22	69.4	8.4	1687	25	ABT23249
23	68.6	8.3	1881	24	AA18436
24	68.4	8.3	4403765	22	AA199683
25	67.6	8.2	4403765	22	AA199683
26	67.6	8.2	4411529	22	AA199682
27	67.4	8.2	1380	24	AAD35090
28	67.2	8.2	1350	24	AB213753
29	67.2	8.2	1650	21	AA033846
30	67.2	8.2	1650	21	AA033846
31	67.2	8.2	1678	21	AA244833
32	66.8	8.1	5802	24	ABT78696
33	66.4	8.1	3453	21	AAA79709
34	66.2	8.0	3849	22	AA068452
35	65.8	8.0	1327	24	AB068452
36	65	7.9	4488	17	AAT35520
37	64.8	7.9	1218	21	AAA02488
38	63.8	7.8	1471	21	AAD01349
39	63.4	7.7	58857	21	AAA58471
40	63.2	7.7	320	21	AAA3185
41	63.2	7.7	88421	24	AA140781
42	63	7.7	1362	25	AAD49064
43	63	7.7	24379	18	AAT93095
44	63	7.7	24379	19	AAV25925
45	63	7.7	44377	18	AAT78508

ALIGNMENTS

RESULT 1	
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ID	AAD01354 standard; cDNA; 823 BP.
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AC	AAD01354;
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DT	12-OCT-2000 (first entry)
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DE	Wheat sphingolipid desaturase cDNA #2.
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KW	Wheat; sphingolipid desaturase; membrane-bound desaturase;
KW	transgenic plant; fatty acid; ss.
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OS	Triticum aestivum.
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FT	/note= "Does not include stop codon"
FT	/partial
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PD	08-JUN-2000.
XX	
PF	02-DEC-1999; 99WO-US26589.
XX	
PR	03-DEC-1998; 98US-0110784.
XX	
PA	(DUPO) DU PONT DE NEMOURS & CO E I.

Human gene express
Soybean sphingolip
Human colon cancer
Human PAL-18 polyn
Mycobacterium tube
Mycobacterium tube
Human PAL-18 polyn
Streptomyces nours
Streptomyces nours
Sphingolipid desat
Oligonucleotide fo
Oligonucleotide fo
Nucleotide sequenc
Seed development e
Contig 109 DNA enc
Mycobacterium tube
Mycobacterium tube
Mycobacterium tube
Pythium irregulare
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
A. thaliana sidi D
S. karthausensis D
Eucahyptus grandis
S. chrysomallus ac
Listeria monocytog
Human thrombopoiet
Human colon cancer
Florida bitterbush
Nucleotide sequenc
Primer used in the
86422nt genomic DN
Saprolengna dictin
Streptomyces fireo
Streptomyces roseo
Platenolide syntha

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XX Caohon BB, Cahoon RE, Hitz WD, Kinney AJ;
PI WPI: 2000-412336/35.
DR P-PSDB; AA71556.
XX
PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
PT transgenic plants and for producing antibodies specific to which is
PT useful for screening cDNA expression libraries
XX
PS Claim 2; Page 56-57; 57pp; English.
XX
CC The present sequence is a cDNA encoding sphingolipid desaturase
CC from clone wrel.pk0004.c7 isolated from wheat etiolated
CC seedling root cDNA library; wrel.
CC
CC The present sequence is useful for producing
CC transgenic plants having altered levels of sphingolipid desaturase which
CC in turn would alter the fatty acid composition. The enzyme is useful
CC for producing polyclonal or monoclonal antibodies. The polynucleotide
CC is also useful as primer or probe for screening cDNA libraries to
CC isolate desired full-length cDNA clones.
XX
SQ Sequence 823 BP; 133 A; 329 C; 194 G; 153 T; 14 other;

Query Match      98.3%; Score 809; DB 21; Length 823;
Best Local Similarity 100.0%; Pred. No. 3.4e-133;
Matches 823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTTAACAACTCCGTTGCTGTTTAAAGATCCGATCTCCCTTCCCTCCCTCC 60
DB 1 CTCCTTAACAACTCCGTTGCTGTTTAAAGATCCGATCTCCCTTCCCTCCCTCC 60
QY 61 CTTCTCTAGTCTGACCAACCCCTCTGCGGCTCAGCTAAATCAACGCAACGATG 120
DB 61 CTTCTCTAGTCTGACCAACCCCTCTCTGCGCTCAAGCTAAATCAACGCAATGG 120
QY 121 CCGGCAAGGGCTTGCAGGAGCAAGCGCGGAGAGCGCAATGCGCGCGCGCA 180
DB 121 CCGGCAAGGGCTTGCAGGAGCAAGCGCGGAGAGCGCAATGCGCGCGCGCA 180
QY 121 CCGGCAAGGGCTTGCAGGAGCAAGCGCGGAGAGCGCAATGCGCGCGCGCA 180
DB 121 CCGGCAAGGGCTTGCAGGAGCAAGCGCGGAGAGCGCAATGCGCGCGCGCA 180
QY 181 AGAAGCGCGCGAGTCTCGCATGATCTTCCACAAAGAGCTGACAGGCGCGCGG 240
DB 181 AGAAGCGCGCGAGTCTCGCATGATCTTCCACAAAGAGCTGACAGGCGCGCGG 240
QY 181 AGAAGCGCGCGAGTCTCGCATGATCTTCCACAAAGAGCTGACAGGCGCGCGG 240
DB 181 AGAAGCGCGCGAGTCTCGCATGATCTTCCACAAAGAGCTGACAGGCGCGCGG 240
QY 241 AGCACTCTGATCTCCATCTCGGGGAGCTTACGAGCTGAGCTGCGTCCAC 300
DB 241 AGCACTCTGATCTCCATCTCGGGGAGCTTACGAGCTGAGCTGCGTCCAC 300
QY 301 ACCCGGCGGAGTCCCGCTCATCACTCGCGCGGAGAGCGCAACGCAACGCTTCA 360
DB 301 ACCCGGCGGAGTCCCGCTCATCACTCGCGCGGAGAGCGCAACGCAACGCTTCA 360
QY 301 ACCCGGCGGAGTCCCGCTCATCACTCGCGCGGAGAGCGCAACGCAACGCTTCA 360
DB 301 ACCCGGCGGAGTCCCGCTCATCACTCGCGCGGAGAGCGCAACGCAACGCTTCA 360
QY 361 TGGCTTACACCCGCTCGTGGCGCGCTCTCGCGCGCTTCTTGTGGCGCGCTCA 420
DB 361 TGGCTTACACCCGCTCGTGGCGCGCTCTCTCGCGCGCTTCTTGTGGCGCGCTCA 420
QY 421 CGCACTACATGTCCTCCCGCGCGCTCGCACTTCCCGCGCGCTCTGCGAGCTTCT 480
DB 421 CGCACTACATGTCCTCCCGCGCGCTCGCACTTCCCGCGCGCTCTGCGAGCTTCT 480
QY 421 CGCACTACATGTCCTCCCGCGCGCTCGCACTTCCCGCGCGCTCTGCGAGCTTCT 480
DB 421 CGCACTACATGTCCTCCCGCGCGCTCGCACTTCCCGCGCGCTCTGCGAGCTTCT 480
QY 481 CCGCGGCGCTCTTGAAGCGGCTCGGACACCCCAAGTTCTGTCGTCCAAAGTNGT 540
DB 481 CCGCGGCGCTCTTGAAGCGGCTCGGACACCCCAAGTTCTGTCGTCCAAAGTNGT 540
QY 481 CCGCGGCGCTCTTGAAGCGGCTCGGACACCCCAAGTTCTGTCGTCCAAAGTNGT 540
DB 481 CCGCGGCGCTCTTGAAGCGGCTCGGACACCCCAAGTTCTGTCGTCCAAAGTNGT 540
QY 541 GCTCTTGTGATGGGCTCTACTGCTCTGCTGCTCAACACCGGAGGCAATGTCG 600
DB 541 GCTCTTGTGATGGGCTCTACTGCTCTGCTGCTCAACACCGGAGGCAATGTCG 600
QY 541 GCTCTTGTGATGGGCTCTACTGCTCTGCTGCTCAACACCGGAGGCAATGTCG 600
DB 541 GCTCTTGTGATGGGCTCTACTGCTCTGCTGCTCAACACCGGAGGCAATGTCG 600
QY 601 CCGGCGGCTCATTTGGCTTATCTGTGCAATCGGAGTGGGATTTGGCAATCTCGGCA 660
DB 601 CCGGCGGCTCATTTGGCTTATCTGTGCAATCGGAGTGGGATTTGGCAATCTCGGCA 660
QY 601 CCGGCGGCTCATTTGGCTTATCTGTGCAATCGGAGTGGGATTTGGCAATCTCGGCA 660
DB 601 CCGGCGGCTCATTTGGCTTATCTGTGCAATCGGAGTGGGATTTGGCAATCTCGGCA 660
QY 661 CACAGGCACTGCTCAACGCTCGNAGTGGCTCGGAAATGCTTAAAGGCTCGATGCTG 720
DB 661 CACAGGCACTGCTCAACGCTCGNAGTGGCTCGGAAATGCTTAAAGGCTCGATGCTG 720

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DB 661 CACAGGCACTGCTCAACGCTCGNAGTGGCTCGGAAATGCTTAAAGGCTCGATGCTG 720
QY 721 GGGAGTANACACCAANACANATTTGAAANNGCACATACCTACATCAATTCGNTTCG 780
DB 721 GGGAGTANACACCAANACANATTTGAAANNGCACATACCTACATCAATTCGNTTCG 780
QY 781 GGTCAAGTCTAAACTTGCATGCTTAAAGTGAAGTCTGTTAGCAT 823
DB 781 GGTCAAGTCTAAACTTGCATGCTTAAAGTGAAGTCTGTTAGCAT 823

RESULT 2
AAD01353
ID AAD01353 standard; cDNA; 1972 BP.
XX
XX AAD01353;
AC
AC AAD01353;
XX
XX 12-OCT-2000 (first entry)
DT
XX
XX Wheat sphingolipid desaturase cDNA #1.
DE
XX
XX Wheat; sphingolipid desaturase; membrane-bound desaturase;
KW transgenic plant; fatty acid; ss.
XX
XX Triticum aestivum.
OS
XX
XX Key Location/Qualifiers
FH CDS 124..1533
FT /*tag= a
FT /product= "Sphingolipid desaturase"
XX
XX W0200032790-A2.
XX
XX 08-JUN-2000.
XX
XX 02-DEC-1999; 99MO-US28589.
XX
XX 03-DEC-1998; 98US-0110784.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Caohon BB, Cahoon RE, Hitz WD, Kinney AJ;
XX P-PSDB; AA71555.
XX
XX WPI: 2000-412336/35.
XX
XX Polynucleotide encoding delta-6 desaturase enzyme useful for producing
XX transgenic plants and for producing antibodies specific to which is
XX useful for screening cDNA expression libraries
XX
XX Disclosure; Page 48-49; 57pp; English.
XX
XX The present sequence is a cDNA encoding sphingolipid desaturase
XX from clone wrel.pk0004.c7:file isolated from wheat etiolated
XX seedling root cDNA library; wrel.
XX
XX The present sequence is useful for producing
XX transgenic plants having altered levels of sphingolipid desaturase which
XX in turn would alter the fatty acid composition. The enzyme is useful
XX for producing polyclonal or monoclonal antibodies. The polynucleotide
XX is also useful as primer or probe for screening cDNA libraries to
XX isolate desired full-length cDNA clones.
XX
XX Sequence 1972 BP; 382 A; 616 C; 490 G; 484 T; 0 other;

Query Match      67.1%; Score 552; DB 21; Length 1972;
Best Local Similarity 94.6%; Pred. No. 3.5e-88;
Matches 615; Conservative 0; Mismatches 27; Indels 8; Gaps 4;

QY 1 CTCCTTAACAACTCCGTTGCTGTTTAAAGATCCGATCTCCCTTCCCTCCCTCC 60
DB 8 CTCCTTAACAACTCCGTTGCTGTTTAAAGATCCGATCTCCCTTCCCTCCCTCC 67

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OY 61 CTTCCTCTGAGTCTCTGACACCCCTCTCGGCTCTCACTAAATCAAGCCACCGATAG 120
DB 68 CTTCCTCTGAGTCTCTGACACCCCTCTCGGCTCTCACTAAATCAAGCCACCGATAG 127
OY 121 CCGGCAAGGGCTTCCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
DB 128 CCGGCAAGGGCTTCCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 187
OY 181 AGGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
DB 188 AGGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 247
OY 241 AGGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
DB 248 AGGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 307
OY 301 ACCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
DB 308 ACCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 367
OY 361 TGGGCTTACACACCGGCTCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
DB 368 TGGGCTTACACACCGGCTCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 427
OY 421 CCGACTACACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
DB 428 CCGACTACACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 487
OY 481 CCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 539
DB 488 CCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 547
OY 540 TGGCTTCTGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 596
DB 548 TGGCTTCTGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 607
OY 597 TGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 642
DB 608 TGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 657

```

RESULT 3
AAD01350
ID AAD01350 standard; cDNA; 1764 BP.
AC AAD01350;
XX
XX
XX 12-OCT-2000 (first entry)
DE Corn sphingolipid desaturase cDNA.
XX
XX Corn; sphingolipid desaturase; membrane-bound desaturase;
KW transgenic plant; fatty acid; ss.
XX
XX Zea mays.
OS
FH Key Location/Qualifiers
FT CDS 89..1477
FT /tag= a
FT /product= "Sphingolipid desaturase"
XX
XX PN MO200032790-A2.
XX PD 08-JUN-2000.
XX PF 02-DEC-1999; 99WO-US28589.
XX PR 03-DEC-1998; 98US-0110784.
XX (DUP0) DU PONT DE NEMOURS & CO E I.
XX PA Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;
XX

```

DR WPI: 2000-412336/35.
DR P-PSDB; AAY71552.
XX
PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
PT transgenic plants and for producing antibodies specific to which is
PT useful for screening cDNA expression libraries
XX
PS Claim 2; Page 41-42; 57pp; English.
XX
CC The present sequence is a cDNA encoding sphingolipid desaturase
CC from clone cdeic.p001.08.115 isolated from corn developing
CC embryo cDNA library, cdeic. The present sequence is useful for producing
CC transgenic plants having altered levels of sphingolipid desaturase which
CC in turn would alter the fatty acid composition. The enzyme is useful
CC for producing polyclonal or monoclonal antibodies. The polynucleotide
CC is also useful as primer or probe for screening cDNA libraries to
CC isolate desired full-length cDNA clones.
XX
SQ Sequence 1764 BP; 310 A; 602 C; 456 G; 396 T; 0 other;

```

Query Match 38.3%; Score 314.8; DB 21; Length 1764;
Best Local Similarity 78.2%; Pred. No. 1.3e-46;
Matches 417; Conservative 0; Mismatches 108; Indels 8; Gaps 3;

```

OY 82 CCCCTCTCGGCTCTCACTAAATCAAGCCACCGATAGGAGGAGGAGGAGGAGGAGGAGGAG 141
DB 27 CCTCCCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 86
OY 142 CAAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 195
DB 87 CAATGCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 146
OY 136 TCCGATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 255
DB 147 TCCGATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 206
OY 256 CCATCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 315
DB 207 CCATCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 266
OY 316 TCCGCTCATCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 375
DB 267 TCCGCTCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 326
OY 376 CCTCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 435
DB 327 CCTCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 386
OY 436 CCGGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 495
DB 387 CCGGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 446
OY 496 AGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 554
DB 447 AACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 506
OY 555 GCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 606
DB 507 GCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 559

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RESULT 4
ABK49503
ID ABK49503 standard; DNA; 1702 BP.
AC ABK49503;
XX
XX
XX 15-JUL-2002 (first entry)
DE DNA encoding Evening primrose delta6-desaturase.
XX
XX delta6-desaturase; sunflower; soybean; maize; tobacco;
KW peanut; carrot; oil seed rape; gamma linolenic acid; GLA;
XX

KM chilling tolerance; gene; ds; evening primrose.
 XX Oenothera biennis.
 OS
 XX
 XX
 PH Key Location/Qualifiers
 FT CDS 48..1406
 FT /*tag= a
 FT /product= "delta6-desaturase"
 XX
 XX US6355861-B1.
 XX
 PD 12-MAR-2002.
 XX
 PF 19-SEP-1997; 97US-0934254.
 XX
 PR 13-OCT-1992; 92US-0959952.
 PR 10-OCT-1991; 91US-0774475.
 PR 08-JAN-1992; 92US-0817919.
 PR 14-SEP-1994; 94US-0307382.
 PR 28-JAN-1997; 97US-0789936.
 XX
 XX (RHON) RHONE-FOULENC AGROCHIMIE.
 XX
 PI Thomas TL;
 XX
 DR MPI; 2002-380944/41.
 DR P-PSDB; AAU79851.
 XX
 PT Novel nucleic acid encoding evening primrose delta6-desaturase which
 PT converts linoleic acid to gamma linolenic acid useful for producing
 PT gamma linolenic acid in transgenic plant or bacteria
 XX
 PS Claim 2; Column 41-46; 53pp; English.
 XX
 CC The invention describes an isolated nucleic acid encoding an evening
 CC primrose Delta6-desaturase. The nucleic acid and a vector expressing the
 CC nucleic acid are useful for producing a plant such as sunflower, soybean,
 CC maize, tobacco, peanut, carrot or oil seed rape plant, with increased
 CC gamma linolenic acid (GLA) content, and also for inducing or increasing
 CC production of GLA in a bacteria or plant deficient, lacking in or
 CC producing low levels of GLA. The nucleic acid is also useful for inducing
 CC chilling tolerance in plants. This sequence encodes the evening primrose
 CC delta6 desaturase involved in the production of gamma linolenic acid.
 CC
 SQ Sequence 1702 BP; 358 A; 471 C; 446 G; 427 T; 0 other;
 XX
 Query Match 13.0%; Score 106.8; DB 24; Length 1702;
 Best Local Similarity 62.3%; Pred. No. 3.4e-10;
 Matches 187; Conservative 0; Mismatches 107; Indels 6; Gaps 1;
 QY 204 ATCTCCACCAAGAGCTGCAAGCGCGCGCGCGAGAGCTTGATCTTCATCTCC 263
 DB 72 ATACGCGCGAGGACCTCGCGCGCGCACAACTCCGCGATCTTGATCTTCATCCAG 131
 QY 264 GGGAGCGTCTACGACGTCAAGCCCTGAGTGGCCACCAACCGGCGCGAGTCCGCTC 323
 DB 132 GGGAAAGTCTACGACGTCTCTCGTGGGCGGAGACCCCGGCGAGGTCTCCGCTC 191
 QY 324 ATCACTCTGCGCGCGAGAGCGGCGGAGCGCTTATGCTTCAACCGCGCCCTCCGTG 383
 DB 192 CTCAGTCTGGCGCGGCGGAGGAGCTGACGAGCGCTTATGCGTACCAACCGGCGAGG 251
 QY 384 CGCGCGCTCTCGCGCGCTTCTTCGTCG-----CGGCTTACCGAGTCACTGTCGCC 437
 DB 252 TGGCGGCTATGATCGGCTCTTACCGGCTACTTACTCTCAAGACTTGAAGTGTG 311
 QY 438 CCGGCTCGCGCGAGCTTCCGCGCGCTCTGCGGAGCTCTCCCGGCGGCGCTTCGAG 497
 DB 312 GAGATCTCCAGAGCTACCGGAGGCTTTTGAACGAGATGTGCGGTCCGGAATCTTCAG 371
 RESULT 5
 ABX15367

ID ABX15367 standard; cDNA; 1702 BP.
 XX
 XX
 AC ABX15367;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Evening primrose delta-6-desaturase #1 cDNA.
 XX
 XX
 KM Delta-6-desaturase; gene; ss; delta-12-desaturase; sunflower; soybean;
 KM maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
 KM octadecatetraenoic acid; alpha-linolenic acid; delta-15-desaturase;
 KM evening primrose.
 XX
 OS Oenothera biennis.
 XX
 PH Key Location/Qualifiers
 FT CDS 48..1406
 FT /*tag= a
 FT /product= "Evening primrose delta-6-desaturase #1"
 XX
 XX US2002108147-A1.
 XX
 PD 08-AUG-2002.
 XX
 PF 21-DEC-2001; 2001US-0029756.
 XX
 PR 13-OCT-1992; 92US-0959952.
 PR 19-SEP-1997; 97US-0934254.
 PR 10-OCT-1991; 91US-0774475.
 PR 08-JAN-1992; 92US-0817919.
 PR 14-SEP-1994; 94US-0307382.
 PR 28-JAN-1997; 97US-0789936.
 XX
 XX (THOM) THOMAS T L.
 XX
 PI Thomas TL;
 XX
 DR MPI; 2003-066559/06.
 DR P-PSDB; ABG73416.
 XX
 PT Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
 PT for producing plant with increased gamma linolenic acid content, and
 PT for inducing octadecatetraenoic acid production in plant
 XX
 PS Claim 2; Fig 10; 55pp; English.
 XX
 CC The invention relates to a nucleic acid encoding an evening primrose
 CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
 CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
 CC for producing a plant (such as sunflower, soybean, maize, tobacco,
 CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
 CC acid (GLA) content by transforming a plant cell with the nucleic acid or
 CC vector and regenerating a plant with increased GLA content from the plant
 CC cell, for inducing or increasing production of GLA in an organism lacking
 CC in or producing low levels of GLA and for inducing production of
 CC octadecatetraenoic acid in at least one of a plant deficient or lacking
 CC in or producing low levels of octadecatetraenoic acid, a bacterium which
 CC produces alpha-linolenic acid or a bacterium which exhibits a
 CC delta-15-desaturase activity on a GLA substrate. This sequence represents
 CC cDNA encoding an evening primrose delta-6-desaturase polypeptide.
 CC
 SQ Sequence 1702 BP; 358 A; 471 C; 446 G; 427 T; 0 other;
 XX
 Query Match 13.0%; Score 106.8; DB 25; Length 1702;
 Best Local Similarity 62.3%; Pred. No. 3.4e-10;
 Matches 187; Conservative 0; Mismatches 107; Indels 6; Gaps 1;
 QY 204 ATCTCCACCAAGAGCTGAGGCGGCGCGGAGAGAGCTTGTGATCTTCATCTCC 263
 DB 72 ATACGCGCGAGGACCTCGCGCGCGCACAAAGTCCGCGGATCTTGATCTTCATCCAG 131
 QY 264 GGGAGCGTCTACGACGTCAAGCCCTGAGTGGCCACCAACCGGCGCGAGTCCGCTC 323

DB 132 GCGAAGTCTACAGTCTCTCGGTGGGCGGAGACCCCGGCGGAGTCCGCTC 191
 QY 324 ATCACCCTGCGCGGCGGAGGACCGACCGCTTCATGGCTACACCGCGCTTCGCG 383
 DB 192 CTCAGTCTGGCGCGGAGGACGTCACCGCTTCATGGCTACACCGCGGAGTCCG 251
 QY 384 CGCGCGCTCTCGCGGCTTCCTTCGTCG-----CGGCTCAACGACTACACTGTC 437
 DB 252 TGGCGGCTATGGATCGGCTTCACCGGCTACTACTCAAGGACTTCGAAGTGTG 311
 QY 438 CCGGCTCGCGGAGTCTCGCGGCTTCCTTCGCGGAGTCTTCCTCGCGGCTTCGAG 497
 DB 312 GAGATCTCCAGGACTACCGGAGGCTTTTGAACGAGATGTGCGGCTTCGAGTCTTCGAG 371

RESULT 6
 ID AAZ44832 standard; DNA; 1594 BP.
 XX AAZ44832;
 AC AAZ44832;
 XX
 DT 27-APR-2000 (first entry)
 XX
 DE B. napus sld1 DNA.
 XX
 KW sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
 KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
 KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KW pharmaceutical; food; chemical raw material; ds.
 XX
 OS Brassica napus.
 XX
 FH Key Location/Qualifiers
 FT 51..1400
 FT CDS /*tag= a
 FT /product= "sld1"
 XX
 PN DE19828850-A1.
 XX
 PD 30-DEC-1999.
 XX
 PF 27-JUN-1998; 98DE-1028850.
 XX
 PR 27-JUN-1998; 98DE-1028850.
 XX
 PA (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
 XX
 PI Heinz E, Zaehrlinger U, Schmidt H, Sperling P;
 XX
 DR WPI; 2000-127549/12.
 XX
 PS P-PSDB; AAY51333.
 XX
 PT New sphingolipid desaturase that selectively introduces double bond
 PT into sphingolipids and capnoids -
 XX
 PS Claim 11; Fig 1; 62pp; German.
 XX
 CC This invention describes a novel sphingolipid desaturase that selectively
 CC introduces a double bond into the sphingobase of the ceramide residue of
 CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to
 CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered
 CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
 CC compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw

CC materials. This sequence encodes the Brassica napus sphingolipid
 CC desaturase sld1 protein described in the method of the invention.
 XX
 SO Sequence 1594 BP; 382 A; 369 C; 375 G; 468 T; 0 other;

Query Match 11.5%; Score 94.8; DB 21; Length 1594;
 Best Local Similarity 59.7%; Pred. No. 4,4e-08;
 Matches 178; Conservative 0; Mismatches 117; Indels 3; Gaps 1;

QY 202 TGATCTCCACGAAGAGTGCAGGCGGACGCGCGGAGGAGGAGTTCGATTCGATCT 261
 DB 76 TCAATTAACAGCATGATCTGAAAAAACAACACCAACCGGAAATTTATGATCTCAATCC 135
 QY 262 CCGGAGAGCTTACGACGATGACGCGCTGCTGCGGACCAACCGGCGGAGGAGTCCGCG 321
 DB 136 AAGGCAAGTCTACGACGCTCTCCCACTGGGTGAAATCCCATCCGGAAGGAGGAGCGGA 195
 QY 322 TCATCAACCTCGCGCGGCGGAGGAGCGGACGCGGCTTACATGGCTTACCAACC---GCCCT 378
 DB 196 TCTTAACCTCGCGCGGCTCAAGAGCTCACCGGCGGCTTACATCCCGGAACCG 255
 QY 379 CCGTGGCGCGGCTCTCCGCGGCTTCTGTGCGCGGCTCAACGACTACATGTCGCC 438
 DB 256 CATGGGCGGACCTCGAAAACTTCACAAAGGCTTACGATGAAAGACACAGTGTCCG 315
 QY 439 CCGGCTCGCGGAGTCTCGCGGCTTCCTGCGGAGCTCTCCGCGGCTTCCTTGA 496
 DB 316 AGCTGTGCGTACATCCGCTTTAGCCGCGGAGTTTCCAAACCGGAGCTTTCGA 373

RESULT 7
 ID ABR98631/C
 XX ABR98631 standard; DNA; 12733 BP.
 XX
 AC ABR98631;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Vector pPERF14 containing L. lactis derived promoter sequence.
 XX
 KW ds; promoter; gram positive bacteria; fusion promoter; T5; CP25; P32;
 KW P59; P1P2; PL; xy10; telo; trpD; malO; lambdacl; cellular proliferation;
 KW antibiotic; vector.
 XX
 OS Lactococcus lactis.
 OS Synthetic.
 OS Staphylococcus aureus.
 OS Leuconostoc mesenteroides.
 XX
 PN WO200251982-A2.
 XX
 PD 04-JUL-2002.
 XX
 PF 21-DEC-2001; 2001WO-US50250.
 XX
 PR 27-DEC-2000; 2000US-259434P.
 XX
 PR 06-SEP-2001; 2001US-0948993.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Wall D, Gross M;
 XX
 DR WPI; 2002-575374/61.
 XX
 PT Isolated nucleic acid comprises bacterial promoters modified to have
 PT altered activity in at least one gram-positive organism, e.g. Bacillus
 PT anthracis or Clostridium botulinum, useful for regulating gene
 PT expression in bacteria -
 XX
 PS Example 3; Page 224-227; 246pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising a fusion
 CC promoter comprising at least one promoter that is modified to have

CC altered activity in at least one gram-positive organism, or comprising
 CC 15, CP25, P32, P59, p1p2 or pL linked to at least one operator consisting
 CC of xy10, tcrO, trpO, malO or lambdaclO, where at least one operator is
 CC positioned so binding of a repressor to an operator represses
 CC transcription from the fusion promoter. Also included are vectors and
 CC host cells comprising the fusion promoter. A method of identifying genes
 CC involved in cellular proliferation or required for proliferation of a
 CC prokaryotic cell using the vector, a method of identifying compounds that
 CC inhibit the proliferation of a prokaryotic cell using the vector, a
 CC method of identifying a compound that reduces the activity or level of a
 CC gene product required for proliferation of a cell using the vector, a
 CC compound identified by the methods, a method of inhibiting the activity
 CC or expression of a gene in an operon required for proliferation using the
 CC vector, manufacturing an antibiotic comprising using the vector or cell
 CC and identifying a nucleic acid with promoter activity in *Enterococcus*
 CC faecalis. The fusion promoters are useful for regulating nucleic acid or
 CC polypeptide expression, particularly for regulating gene expression in
 CC bacteria and for identifying proliferation-regulated genes or molecules
 CC useful for replacing endogenous promoters to create cells with specific
 CC regulatable genes. The present sequence is vector (or fragment)
 CC incorporating a fusion promoter sequence of the invention.
 CC XX
 SQ Sequence 12733 BP, 3549 A; 2567 C; 3207 G; 3409 T; 1 other;

Query Match 10.4%; Score 85.6; DB 24; Length 12733;
 Best Local Similarity 47.0%; Pred. No. 1.7e-06;
 Matches 262; Conservative 0; Mismatches 296; Indels 0; Gaps 0;

QY 35 CGATCTCCCTTCCCTCCCTCCCTCTCTCTCTGAGTCTGACCAACCCCTCTGCGC 94
 DB 5351 CGACCC 5292
 QY 95 TCCAGCTAAATCCAGCGCACGATGGCGCGACGAGGCTTGGAGAGCGACGCGCGA 154
 DB 5291 CCC 5232
 QY 155 AGCGGACGACATGCGCGCGCGCGACGAGAGCGCGCGACGATCGATCTGACCAA 214
 DB 5231 CCC 5172
 QY 215 GGAAGTCTGACGCGCGCGCGCGCGAGACGCTGTGATCTGCGGAGAGCTTGA 274
 DB 5171 CCC 5112
 QY 275 CGACGTCAGCGCTGAGTGGCGACCAACCGCGGCGGAGAGTCCGCTATACCTCGC 334
 DB 5111 CCC 5052
 QY 335 CGGCGGAGAGCGCGACGCGCTTTCATGAGCTACACCGCGCTCGAGCGCTGCT 394
 DB 5051 CCC 4992
 QY 395 CGGCGCTTCTTGTGTGGCGGCTTACGACGATACGTCGCGCGCTCGCGACTT 454
 DB 4991 CCC 4932
 QY 455 CGCGCGCTCTGTCGCGAGCTCTCTCGGCGGCTTTCGACGCGGTGGCGACACGCC 514
 DB 4931 CCC 4872
 QY 515 AAGTTCTGCTGTCGCAAGTGTGCTTCTGTGATGCGGCTCTACTGCTCTGCGCT 574
 DB 4871 CCC 4812
 QY 575 GCTCAACACCGGGGCGAC 592
 DB 4811 CCCCCCCCCCCCCCCCCCCC 4794

RESULT 8
 ABR98592/c
 ID ABR98592 standard; DNA; 12739 BP.

XX AC ABR98592;
 XX XX
 DT 21-OCT-2002 (first entry)
 XX XX
 DE Vector pPEP1 containing XylR/xy10/CP25 sequences.
 XX XX
 KW ds; promoter; gram positive bacteria; fusion promoter; T5; CP25; P32;
 KM P59; p1p2; pL; xy10; tcrO; trpO; malO; lambdaclO; cellular proliferation;
 KM antibiotic; vector.
 XX XX
 OS *Bacillus*.
 OS Bacteriophage lambda.
 OS *Escherichia coli*.
 OS Synthetic.
 XX XX
 PN WO200251982-A2.
 XX XX
 PD 04-JUL-2002.
 XX XX
 PF 21-DEC-2001; 2001WO-US50250.
 XX XX
 PR 27-DEC-2000; 2000US-259434P.
 PR 06-SEP-2001; 2001US-0948993.
 XX XX
 PA (ELIR-) ELIRRA PHARM INC.
 PI Haselbeck R, Wall D, Gross M;
 XX XX
 DR WPI; 2002-575374/61.
 XX XX
 PT Isolated nucleic acid comprises bacterial promoters modified to have
 PT altered activity in at least one gram-positive organism, e.g. *Bacillus*
 PT *anthracis* or *Clostridium botulinum*, useful for regulating gene
 PT expression in bacteria
 XX XX
 PS Example 1; Page 206-209; 246bp; English.

CC The invention relates to an isolated nucleic acid comprising a fusion
 CC promoter comprising at least one promoter that is modified to have
 CC altered activity in at least one gram-positive organism, or comprising
 CC 15, CP25, P32, P59, p1p2 or pL linked to at least one operator consisting
 CC of xy10, tcrO, trpO, malO or lambdaclO, where at least one operator is
 CC positioned so binding of a repressor to an operator represses
 CC transcription from the fusion promoter. Also included are vectors and
 CC host cells comprising the fusion promoters, a method of identifying genes
 CC involved in cellular proliferation or required for proliferation of a
 CC prokaryotic cell using the vector, a method of identifying compounds that
 CC inhibit the proliferation of a prokaryotic cell using the vector, a
 CC method of identifying a compound that reduces the activity or level of a
 CC gene product required for proliferation of a cell using the vector, a
 CC compound identified by the methods, a method of inhibiting the activity
 CC or expression of a gene in an operon required for proliferation using the
 CC vector, manufacturing an antibiotic comprising using the vector or cell
 CC and identifying a nucleic acid with promoter activity in *Enterococcus*
 CC faecalis. The fusion promoters are useful for regulating nucleic acid or
 CC polypeptide expression, particularly for regulating gene expression in
 CC bacteria and for identifying proliferation-regulated genes or molecules
 CC useful for replacing endogenous promoters to create cells with specific
 CC regulatable genes. The present sequence is vector (or fragment)
 CC incorporating a fusion promoter sequence of the invention.
 CC XX

SQ Sequence 12739 BP, 3543 A; 2572 C; 3211 G; 3413 T; 0 other;

Query Match 10.4%; Score 85.6; DB 24; Length 12739;
 Best Local Similarity 47.0%; Pred. No. 1.7e-06;
 Matches 262; Conservative 0; Mismatches 296; Indels 0; Gaps 0;

QY 35 CGATCTCCCTTCCCTCCCTCCCTCTCTCTCTGAGTCTGACCAACCCCTCTGCGC 94
 DB 5357 CGACCC 5298


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QY 95 TCCAGCTAAATGACGCGACCGATGCGCGAGCGGCTTCGCGAGCAACGCGCGCGA 154
Db 5297 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 5238
QY 155 AGCCGACGCAATGCGCGCGCGCGAGGAGAGCGCGCGAGCTCGCATGATTCACCA 214
Db 5237 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 5178
QY 215 GGAGCTGACGAGCGACGCGCGCGCGAGACGCTGAGATTCGATCCGCGGAGCTTA 274
Db 5177 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 5118
QY 275 CGAGCTGACGCGCGCGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 334
Db 5117 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 5058
QY 335 CGGCGAGGAGCGCGAGCGCGCTTATGAGCTACACCGCGCGCTCGTGCGCGCTCT 394
Db 5057 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 4998
QY 395 CGGCGCGCTTCTTGCGCGCGCGCTGACGAGCTACGATGCGCGCGCGCGAGCTT 454
Db 4997 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 4938
QY 455 CGGCGCGCTCTGCGCGAGCTCTCTCGCGGAGCTTTCGAGCGCGCTCGGACACCGCC 514
Db 4937 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 4878
QY 515 AAGTTCTGCTGCTGCGCAAGTNGTGTCTTTCGATGCGGCTTACTGCTCTGCTCT 574
Db 4877 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 4818
QY 575 GGTCAACACCGGCGCGAC 592
Db 4817 CCCCCCCCCCCCCCCCCC 4800

RESULT 9
AA217263
ID AA217263 standard; cDNA; 1337 BP.
XX
XX AA217263;
XX
DT 12-OCT-1999 (first entry)
XX
XX Human gene expression product cDNA sequence SEQ ID NO:4735.
XX
XX Human; gene; gene expression product; diagnosis; therapy; probe;
XX
XX detection; mapping; tissue typing; profiling; forensic; cancer;
XX
XX genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
XX
XX Homo sapiens.
XX
XX WO9318972-A2.
XX
XX 05-AUG-1999.
XX
XX 28-JAN-1999; 99WO-US01619.
XX
XX
XX 03-APR-1998; 98US-0080666.
XX
XX 28-JAN-1998; 98US-0072910.
XX
XX 24-FEB-1998; 98US-0075954.
XX
XX 31-MAR-1998; 98US-0080114.
XX
XX 03-APR-1998; 98US-0080515.
XX
XX
XX (CHIR) CHIRON CORP.
XX
XX (HYSE-) HYSEQ INC.
XX
XX
XX Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
XX
XX Escobedo J, Garcia PD, Garcia V, Glese K, Imis MA;
XX
XX Jones WJ, Kassam A, Kennedy GC, Kita D, Labat I;
XX
XX Lamsen G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
XX
XX Stache-Crain B, Sudduth-Klinger J, Williams LT;

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XX
XX WPI; 1999-494092/41.
DR
XX
XX Novel human genes and their expression products which are
PT differentially expressed in different cell types
XX
XX Claim 1; Page 2250-2251; 2479p; English.
XX
XX
XX The present invention describes a library of human polynucleotides
CC comprising the sequences given in AA212532 to AA21779. Also described is
CC a method of detecting differentially expressed genes correlated with the
CC cancerous state of a mammalian cell, comprising detecting at least one
CC differentially expressed gene product in a test sample from a cell
CC suspected of being cancerous, where the gene product is encoded by one
CC of the 5248 polynucleotide sequences given in AA212532 to AA21779. The
CC polynucleotides can be used as a source of primers and probes, which can
CC be used for a variety of purposes, e.g. detection of expression levels,
CC mapping, tissue typing or profiling, forensics, genetic analysis and
CC detection of polymorphisms. Polypeptides encoded by the polynucleotides
CC can be used for raising antibodies for experimental, diagnostic and
CC therapeutic purposes. The polynucleotides may also be used to construct
CC arrays for diagnostics (which may be used to determine function of an
CC encoded protein); and to detect differences in expression levels between
CC two cells (e.g. to identify abnormal or diseased tissue in a human, to
CC identify a genetic predisposition or susceptibility to a disease such as
CC cancer). The polynucleotides of the invention are especially used in the
CC diagnosis, prognosis and management of colorectal cancer, breast cancer,
CC and lung cancer. The polynucleotides can also be used to screen for
CC peptide analogues and antagonists.
XX
XX
XX Sequence 1337 BP; 42 A; 577 C; 27 G; 22 T; 669 other;
SQ
Query Match 10.0%; Score 82.2; DB 20; Length 1337;
Best Local Similarity 31.2%; Pred. No. 7.1e-06;
Matches 181; Conservative 0; Mismatches 400; Indels 0; Gaps 0;
QY 1 CTCCTTACAAACCTCCGTTGCTGTTTAAATCGATCCCTCCCTCCCTCC 60
Db 378 CCCCCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 437
QY 61 CTTCTCTGAGTCTGACCACTCTCTCTGCGCTTCAGCTAAATTCAGCGCAGATG 120
Db 438 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 497
QY 121 CCGCGACGAGGCTTCCGCGAGCGAGCGCGCGGAGCGCATGCGCGCGCAGCA 180
Db 498 CCGCGACGAGGCTTCCGCGAGCGAGCGCGCGGAGCGCATGCGCGCGCAGCA 557
QY 181 AGAGCGCGCGAGCGATGCGATGCTCCAGCAAGAGGTGAGGCGAGCGCGCGG 240
Db 558 CCCCCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 617
QY 241 ACGACTTGTGATCTCATCTCCGAGGAGCTGACGCTGACGCGCTGCTGCGCAC 300
Db 618 CCCCCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 677
QY 301 ACCCGAGCGGAGGCTCCGCTCATCATCTGCGCGCGGAGCGCAGCGCCTTCA 360
Db 678 CCGCGAGCGGAGGCTCCGCTCATCATCTGCGCGCGGAGCGCAGCGCCTTCA 737
QY 361 TGGCTTACACCGCGCGCTCGTGCGCGCGCTCTCGCGCGCTTCTTCTTCTTCT 420
Db 738 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 797
QY 421 CCGACTTACATCTGCTCCCGCGCTCGCGAGCTTCTCGCGCGAGCTTCTCT 480
Db 798 CCGACTTACATCTGCTCCCGCGCTCGCGAGCTTCTCGCGCGAGCTTCTCTCT 857
QY 481 CCGCGGCGCTTCTTTCAGAGCGCTGCGACACCGCGCAAGTTCTGCTGCGCAAGTCNT 540
Db 858 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 917
QY 541 GCTCTTTCGATGCGGCTTACTGCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 581

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Db	918	NNNCNNNCNNCNCNNNNNNCNCNNCNCNNCNCNNCNCNC	958
		RESULT 10	
		AAD01352	
		ID AAD01352 standard; cDNA, 1934 BP.	
		XX AC	
		XX AAD01352;	
		XX	
		DT 12-OCT-2000 (first entry)	
		DE Soybean sphingolipid desaturase cDNA #2.	
		XX	
		KW Soybean; sphingolipid desaturase; membrane-bound desaturase;	
		XX transgenic plant; fatty acid; ss.	
		OS Glycine max.	
		XX	
		Key Location/Qualifiers	
		FT CDS 305..1657	
		FT /*tag= a	
		FT /product= "Sphingolipid desaturase"	
		XX MO200032790-A2.	
		XX	
		PD 08-JUN-2000.	
		XX	
		PF 02-DEC-1999; 99WO-US28589.	
		XX	
		FR 03-DEC-1998; 98US-0110784.	
		XX	
		PA (DUPO) DU PONT DE NEMOURS & CO E I.	
		XX	
		PI Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;	
		DR WPI; 2000-412336/35.	
		DR P-PSDB; M4V71554.	
		XX	
		PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing	
		PT transgenic plants and for producing antibodies specific to which is	
		PT useful for screening cDNA expression libraries	
		XX	
		PS Claim 2; Page 46; 57pp; English.	
		XX	
		XX	
		CC The present sequence is a cDNA encoding sphingolipid desaturase	
		CC from clone sbl.pB0017.b4:fls isolated from soybean seedling cDNA	
		CC library, sbl. The present sequence is useful for producing	
		CC transgenic plants having altered levels of sphingolipid desaturase which	
		CC in turn would alter the fatty acid composition. The enzyme is useful	
		CC for producing polyclonal or monoclonal antibodies. The polynucleotide	
		CC is also useful as primer or probe for screening cDNA libraries to	
		CC isolate desired full-length cDNA clones.	
		XX	
		XX	
		Sequence 1934 BP, 505 A, 367 C; 448 G; 614 T; 0 other;	
		QO	
		Query Match 9.9%; Score 81.6; DB 21; Length 1934;	
		Best Local Similarity 57.1%; Pred. No. 8.9e-06;	
		Matches 169; Conservative 0; Mismatches 124; Indels 3; Gaps 1	
		QY	
		204 ATCTCCACCAAGAGAGCTGACGCGCAGCCGCCGCGAGACCTTGATCTCCATCTCC 263	
		Db ATTAACCTCAGAGGAGCTGAAGGGTCACAAACAGGAGGAGATTATGATCTCAATTCAA 394	
		QY	
		264 GGGGACGCTCTACAGCTGACGCGCTGGCGGCGCCACCCGGGGGGGAGAGGTCCCGCTC 323	
		Db GGTAAAGGTGTCATATGCTTCAGATTGGGTCAAGAGACACCCGTGGGTGATCTTCAATC 454	
		QY	
		324 ATCAACCTTCGCGCGGCGGACGAGCCACGACGCTTCATGAGCTACACCCGCGCTCGTG 383	
		Db TCAAACTTCGTCGGCGGACGAGATGTACTGATGATTCATAGCATACCATCTCGGACACGA 514	
		QY	
		384 CGCCGCTCTCTCCGCCGCTTCTTC--GTGGCGGCTTCACCGACTCACTGTCCCCCCC 440	

Db 515 TGCTCACACCTTTGAAAAATTTCTTCACTGGCTTACCACTCAGTCACTTCAAGCTCTTGAG 574

Oy 441 GCGTTCGGCGCACTTCCGCGCCTCTCCGCGCAGCTCTCTCCGCGGCGCTTTGCA 486

Db 575 GTGTCCAAAGACTACAGAAAGCTGCATCTGATGTTCTCAAAATTTGGTCTTTTGA 630

RESULT 11

AAA02484/c

ID AAA02484 standard; cDNA, 1000 BP.

XX AC AAA02484;

XX DT 19-MAY-2000 (first entry)

XX DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2475.

XX KW Human; colon cancer; tumour; diagnosis; gene expression product;

XX KW probe; detection; cancerous state; metastasis; identification;

XX KW breast cancer; oestrogen receptor-positive breast cancer; therapy;

XX KW oestrogen receptor-negative breast cancer; lung cancer; ss.

XX OS Homo sapiens.

XX PN WO9958675-A2.

XX PD 18-NOV-1999.

XX PF 13-MAY-1999; 99WO-US10602.

XX PR 14-MAY-1998; 98US-0085426.

XX PR 15-MAY-1998; 98US-0085537.

XX PR 15-MAY-1998; 98US-0085696.

XX PR 21-OCT-1998; 98US-0105234.

XX PR 27-OCT-1998; 98US-0105877.

XX PA (CHIR) CHIRON CORP.

XX PA (HYSE-) HYSEQ INC.

XX PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;

XX PI Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;

XX PI Lammson G, Drmanac R, Kravjenjakov R, Dickson M, Drmanac S, Labat I;

XX PI Leshkowitz D, Kita D, Garcia V, Jones LW, Stache-Crain B;

XX DR WPI; 2000-126369/11.

XX PT Polynucleotide library used to determine cancerous states of mammalian

XX PT cells -

XX PS Claim 1; Page 994; 1097P; English.

XX PS AAA00010 to AAA02716 represent polynucleotides isolated from cDNA

XX CC libraries constructed from human colon cancer cell lines. The present

XX CC invention also describes a method of detecting differentially expressed

XX CC genes correlated with a cancerous state of a mammalian cell, comprising

XX CC detecting at least one differentially expressed gene product in a test

XX CC sample derived from a cell suspected of being cancerous, where detection

XX CC of the differentially expressed gene product is correlated with a

XX CC cancerous state of the cell from which the test sample was derived.

XX CC The polynucleotides sequences can be used in a method for detecting

XX CC differentially expressed genes correlated with a cancerous state of a

XX CC mammalian cell. The polynucleotides can also be used as probes for

XX CC detecting and mapping related genes. They can be used in diagnosis and

XX CC prognosis of diseases and disorders (e.g. identification of

XX CC pre-metastatic or metastatic cancerous states, stages of cancer, or

XX CC responsiveness of cancer to therapy). This is particularly for breast

XX CC cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-

XX CC negative breast cancer, lung cancer, and colon cancer.

XX CC

XX CC Sequence 1000 BP; 21 A; 53 C; 574 G; 22 T; 330 other;

Query Match 9.7%; Score 79.6; DB 21; Length 1000;

PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 24-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 30-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145218.
PR 26-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.

PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0148368.
PR 16-AUG-1999; 99US-0149175.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155486.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0158293.
PR 13-OCT-1999; 99US-0158294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159337.
PR 14-OCT-1999; 99US-0159637.
PR 18-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 9.0%; Score 74.4; DB 21; Length 1465;
Best Local Similarity 55.8%; Pred. No. 0.00016;
Matches 163; Conservative 0; Mismatches 126; Indels 3; Gaps 1;
QY 208 CCACCAAGAGCTGCAGGCGCAGCGCGCGGACCTTGATCTTCATCTCCGGGG 267

Db 147 CAAGCGAGATTGAAAAACACAAACCTGAGATTGATTGATTCAAGTA 206
 Qy 268 ACCTCTACGAGTCAGCGCCCTGCTGCGCCACCAACCGGGGAGAGTCCCGTATCA 327
 Db 207 AAGTTTACGACGTTTCCGATTGGTTAAATCTATCTCCGAGAGGAGACGAGATTCTCA 266
 Qy 328 CCGTCGCGGCGCAGAGACGACGACGCTTCATAGGCTTACCAACCGCCCTCGTGGCC 387
 Db 267 ATCTCGCGGCGCAGAGACGACGACGCTTCATAGGCTTACCAACCGCCGATGGC 326
 Qy 388 CGCTCTCGCGGCGCTTCTTGTGGC---CGCTCACCGACTACACTGTCCCCCGGCT 444
 Db 327 ACCACTTAGAAAAGCTTACCAATGGCTATACAGTGAAGACCAACAGTGTCAAGACTCT 386
 Qy 445 CCGCGGACTTCGCGCGGCTCTCTCGCGGAGCTCTCTCGCGGCGCTTCTGA 496
 Db 387 CAGCTGACTACCTGCTTGTAGCGCGAGTCTTCAACGCGGCTCTTGA 438

RESULT 15

ABT09682
 ID ABT09682 standard; DNA; 1065 BP.

AC ABT09682;

DT 02-DEC-2002 (first entry)

DE Human PAL-18 polynucleotide SEQ ID NO: 33.

KW Human; PAL-18; cancer; chromosome 1q41; prostate cancer; colon cancer;

KW breast cancer; cytosolic; gene; ds.

OS Homo sapiens.

PN US2002106765-A1.

PD 08-AUG-2002.

PF 12-MAR-2001; 2001US-0804682.

PR 10-MAR-2000; 2000US-188586P.

PA (KIND/) KINDERS R J.

PA (CORE/) COREY M J.

PI Kinders RJ, Corey MJ;

DR WPI; 2002-697869/75.

PT New isolated PAL-18 polypeptide, useful for diagnosing, characterizing,

PT and treating disease and in determining disease susceptibility -

PS Claim 1; Page 50-51; 150pp; English.

CC The present invention relates to human PAL-18 polypeptides and

CC polynucleotides. The PAL-18 gene is found on chromosome 1q41. The

CC sequences can be used to diagnose, monitor and treat cancers,

CC particularly breast, colon and prostate cancers. The present sequence is

CC a PAL-18 polynucleotide shown in the invention.

SQ Sequence 1065 BP; 98 A; 606 C; 36 G; 210 T; 115 other;

Query Match 8.8%; Score 72.4; DB 24; Length 1065;

Best Local Similarity 43.8%; Pred. No. 0.00037;

Matches 218; Conservative 0; Mismatches 274; Indels 6; Gaps 1;

Qy 3 CCCTAACAACTCCGCTGCTTGAATCGATCTCCGCTTCNCCCTCCCTCCCT 62
 Db 472 CCNCTCNCACCCCTTCCCNCTCCGCTTCNCTCNCNCCCTCCCTCCCTCCCT 531
 Qy 63 TCCTCTGAGTCTGACCACTCTCTCGGCTTCAGTAAATCAAGCAAGCATGGCC 122
 Db 532 CTCCTCTNNCTCCCTCCCTCCCTCTCTCTCCCTCCCTCCCTCCCTCCCT 591

Qy 123 CGCAGCGGCTTCGCGGAGCCCAACGCGCGGAGAGCCGACATGCGGCGCCAGCAAG 182
 Db 592 CTCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 651
 Qy 183 GACGCGCGGAGCTCCGATGATCTTCACCAAGAGCTGAGGCGGACGCGCGGAG 242
 Db 652 TNNCNCNCCCTCNCNCCNCCCTTCCNCCNCCCTCTCTCTCTCTCTCTCTCT 711
 Qy 243 GACCTTGATCTGCATCTCCGCGGAGGCTTACAGTACAGGCTTGGCTGCGCAC 302
 Db 712 CNAATCCNCCNCTTCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 771
 Qy 303 CCGGCGGCGGAGGTCGCTCATCACTTCGCGGCGGAGAGCGACCGA-----CGCC 356
 Db 772 CCCCNCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 831
 Qy 357 TTGATGAGCTTACCAACCGGCTCTCGTGGCGGCTCTCTCGGCTTCTTCTGCGCGC 416
 Db 832 CTCACCTNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 891
 Qy 417 CTACCGACTACACTGTCCCGGCTTCGCGGCTTCGCGGCTTCGCGGCTTCGCGG 476
 Db 892 CCCCCCTNCTCCCTCNCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 951
 Qy 477 TCCTCCGCGGCTCTTTC 494
 Db 952 TCCCCCCCANCCCTTC 969

Search completed: December 31, 2003, 16:16:56
 Job time : 167.169 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:48:07 ; Search time 1254.26 Seconds
(without alignments)
15947.709 Million cell updates/sec

Title: US-09-857-524B-16

Perfect score: 823
Sequence: 1 ccccccaaacaccctccgtc.....cgtnaagacttgtagcat 823

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_esthum:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vtc:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_png:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	629	76.4	642	14	CA633913 wleln.pk0
2	484.4	58.9	679	13	BQ788546 WHE4151 B
3	466.6	56.7	563	13	BQ606843 BRY 271B
4	448	54.4	665	14	CA502522 WHE4048_E

5	438.6	53.3	674	10	BE414354 SCU008.G0
6	426.2	51.8	500	14	CA030713 HX07011r
7	412	50.1	493	14	CA637422 wrel.pk0
8	394.2	47.9	453	13	BQ238994 TAF05038F
9	342.2	41.6	453	13	BQ605802 BRY_1370
10	314.8	38.3	1764	11	AY103762 Zee mays
11	308.4	37.5	634	12	BI075898 IP1_22.F1
12	306.8	37.3	744	14	CD463185 ETH1_42.C
13	289.8	35.2	576	29	CC344270 OGMBO60TV
14	285.4	34.7	478	14	CA710447 wdk2c.pk0
15	283.6	34.5	400	10	BG158998 RH12_41
16	253	30.7	436	13	BQ239011 TAE05038D
17	195.2	23.7	558	14	CD230432 SS1_43.D0
18	178.6	21.7	257	10	BG158990 RH12_41
19	172	20.9	222	13	BQ998888 H12H15r
20	141.2	17.2	186	14	CB883321 HQ01N24w
21	135.4	16.5	452	29	CC011349 FUEAUS3TD
22	128.8	15.7	413	9	AM099929 gdl8e05.Y
23	121.4	14.8	468	9	A1736850 BD34d09.Y
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25	104.4	12.7	807	13	BX464554 BX464554
26	98.6	12.0	1177	29	CC193928 CH261-95J
27	97.8	11.9	670	29	AG126228 Pan trog1
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29	96	11.7	1424	13	BQ720687 AGENCOURT
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31	95	11.5	1695	29	CC290874 CH261-172
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34	94.6	11.5	1292	29	CC208790 CH261-26P
35	94.6	11.5	1767	29	CC294031 CH261-82A
36	94.4	11.5	918	28	AO895329 HS 4832.A
37	94.4	11.5	1068	9	AL570062 AL570062
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39	94.2	11.4	933	29	AG063086 Pan trog1
40	94.2	11.4	1100	29	CC262597 CH261-167
41	94.2	11.4	1153	29	CC294165 CH261-130
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43	93.8	11.4	588	29	DR102N24T
44	93.8	11.4	1116	10	BF256617 HVSMBF001
45	93.8	11.4	1156	29	CC319460 TAM32-17H

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
wleln.pk0080.d7 wleln Triticum aestivum CDNA clone wleln.pk0080.d7
5' end, mRNA sequence.
ACCESSION
CA633913
VERSION
CA633913.1
KEYWORDS
GI:25212209
SOURCE
EST.
ORGANISM
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticaceae; Triticum.
1 (bases 1 to 642)
REFERENCE
Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
Miao, G., Caraher, N. and Hanafey, M.K.
TITLE
Dupont Wheat cDNA Sequence
JOURNAL
Unpublished
COMMENT
Contact: Scott V. Tingey
Crop Genetics
E. I. Dupont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@usa.dupont.com
Seq primer: M13.
Location/Qualifiers

FEATURES

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/notes="Vector: Bluescript SK+; Site 1: EcoRI; Site 2:
XhoI; Wheat (Triticum aestivum L.) leaf 7 day old
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Best Local Similarity 100.0%; Pred. No. 5.8e-115;
Matches 642; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GAGACGCCGCGACGCTCCGATGATCTCCACCAAGAGCTGAGCGACGCCGCGCGA 60
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Db 361 CTCTTGTGATCGGCTCTAAGTCTCTGCTCGCTGCTCAACACCGGCGCATGTTGCC 420
QY 602 GGGGGCTCATTTGGCTTATCTGCTGAGTGGGCTGGATTGGCATTAATCCGACACAATC 661
Db 421 GGGGGCTCATTTGGCTTATCTGCTGAGTGGGCTGGATTGGCATTAATCCGACACAATC 480
QY 662 ACAGGACCTGCGCTCAACGCTCGNAGTGGCTCGGGAATGCTTNAAGGCTCGATCCTGG 721
Db 481 ACAGGACCTGCGCTCAACGCTCGNAGTGGCTCGGGAATGCTTNAAGGCTCGATCCTGG 540
QY 722 GAGATNANCAACAANACANATTTGTAANNGTCAATACCTGAATCTCAATTCGGTTCGG 781
Db 541 GAGATNANCAACAANACANATTTGTAANNGTCAATACCTGAATCTCAATTCGGTTCGG 600
QY 782 GTACAAAGTCTAAAGCTTGATGCTTNAAGACTTGTTAGCAT 823
Db 601 GTACAAAGTCTAAAGCTTGATGCTTNAAGACTTGTTAGCAT 642
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LOCUS BO788546
DEFINITION WHE4151 B02 C032S Wheat CS whole plant cDNA library Triticum
aestivum cDNA clone WHE4151_B02_C03, mRNA sequence.
ACCESSION BO788546.1 GI:21997018
VERSION BO788546.1
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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REFERENCE
1 (bases 1 to 679)
AUTHORS Anderson,O.D., Akhunov,E., Chao,S., Crossman,C., Deal,K., Dvorak,J.,
Lazo,G.R., Rauscher,C.J., Wilson,C. and Woo,J.
TITLE The structure and function of the expressed portion of the wheat
genomes - Chinese Spring whole plant cDNA library
JOURNAL Unpublished
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.ueda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer.
FEATURES
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1. .679
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tissues from wheat cv. CS grown to full tillering stage in
greenhouse were collected at University of California,
Davis (Jan Dvorak's lab, K. Deal and E. Akhunov). Total
RNA was prepared from leaves (young leaf and third leaf),
whole roots, crown, stem and sheath tissues, and then
equal quantities of RNA were pooled from the these
samples. PolyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo excised
to give bluescript SK(-) phagemids in J. Dvorak's lab (E.
Akhunov, J. Dvorak) at the University of California,
Davis. Colony plating, plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
other authors)."
BASE COUNT      95 a      300 c      176 g      107 t      1 others
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Query Match      58.9%; Score 484.4; DB 13; Length 679;
Best Local Similarity 94.6%; Pred. No. 2.7e-86;
Matches 545; Conservative 0; Mismatches 23; Indels 8; Gaps 4;
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Db 13 CTGACCAACCCCTCTCTGCGCTCCAGCTAAATCAAGCCACCGATGCGCGACGAGCTTC 72
QY 135 GCGGAGCAACGCGCGCGGAGAGCGGACGATGCGCGCGCGCGCAAGAGAGCGCGCGAG 194
Db 73 GCGGAGCAACGCGCGCGGAGAGCGGACGATGCGCGCGCGCGCAAGAGAGCGCGCGAG 132
QY 195 GTCCGATGATCTCCACCAAGAGCTGAGGCGACAGCGCGCGCGAGCAAGCTTGATTC 254
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QY 255 TCCATCTCCGCGGAGCTTAAGAGCTGACGAGCTGCTGCGGACCAAGCTGCGCGGAG 314
Db 193 TCCATCTCCGCGGAGCTTAAGAGCTGACGAGCTGCTGCGGACCAAGCTGCGCGGAG 252
QY 315 GTCCGCTCATACCTCGCGCGGCGGAGCGGACCGAGCGCTTAATGCTTAAGACCGG 374
Db 253 GTCCGCTCATACCTCGCGCGGCGGAGCGGACCGAGCGCTTAATGCTTAAGACCGG 312
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Oy		495	GAGGCGGTGCGG-CACAACCCCAAAGTCTCGTCCGCGGAAGAATGATGATCTCTTCGATC	553
Db		433	GAGGCGGTGCGGCACACCCCAAGTCTCTGCTCGTCCGAAATGCGATCTCTTCGATC	492
Oy		554	GAGCTTAAGTGC-TCCTCGCCTGTCTCA--CACCGGCGCAATTTCCGCGGCGCTCA	610
Db		493	GCCCTTAAGTGCCTCTCGCCTGTCTCCAGCAACCGGCGCCACATTTCCGCGGCGCTC	552
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Db		553	ATTGCTTCATCTGTGATCCAGTCCGGCTGATGCG	588
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DEFINITION	BQ606843	563 bp	mRNA	linear EST 25-JUN-2002
ACCESSION	BRY 2718	wheat EST endosperm library	Triticum aestivum cDNA 5'	
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SOURCE	BQ606843.1	GI:21556172		
ORGANISM	EST.			
REFERENCE	Triticum aestivum (bread wheat)			
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
TITLE	Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae			
JOURNAL	; Triticaceae; Triticum.			
MEDLINE	1 (bases 1 to 563)			
PUBMED	Clarke,B., Lambrecht,M. and Rhee,S.Y.			
COMMENT	Arabidopsis genomic information for interpreting wheat EST sequences			
FEATURES	Funct. Integr. Genomics 3 (1-2), 33-38 (2003)			
SOURCE	22478026			
	Contact: Lambrecht M			
	The Arabidopsis Information Resource			
	Carnegie Institution of Washington, Dept. of Plant Biology			
	260 Panama Street, Stanford, CA 94305, USA			
	Tel.: 1 650 325 1521 x 251			
	Fax: 1 650 325 3748			
	Email: rhee@coma.stanford.edu.			
	Location/Qualifiers			
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	/dev_stage="developing endosperm tissue 8, 10 and 12 DPA			
	(days post anthesis)"			
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Oy		144	ACGGCGCGGAAGCGCGCAATGCGCGCTCGCGCAAGAGCGCGCGCATGTCGCATG	203
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Oy		204	ATTTCCACCAAGAGCTCAGCGGACCGCGCGCGGAGACCTTGAATCTTCATCTCC	263

Db		121	ATCTCCACCAAGGAGCTGAGGGGACAAGCTTGCGCGGAGACAGACTCTTGGATTCATCTC	180
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Db		421	GGCACAACCCCCAAGTTCCTGCTGCTGTGGCAAATGCTGCTTCTTGCAATGGGCTTAC	480
Oy		563	TGC-TCTCGCTGCTCTCAA--CACCGGGGCGCACATGTTCCCGGGGGCG 607	
Db		481	TGCCTCTCTCCGCTCTCTCCAGCACCGGGGCCAACATGTTCCCGGGGGCG 528	
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DEFINITION			aestivum cDNA clone WHB4048_E08_J16, mRNA sequence.	
ACCESSION			CAS02522	
VERSION			CAS02522.1 GI:24993482	
KEYWORDS			EST.	
SOURCE			Triticum aestivum (bread wheat)	
ORGANISM			Triticum aestivum	
REFERENCE			Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
AUTHORS			Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae	
JOURNAL			1 (bases 1 to 665)	
TITLE			Anderson,O.D., Chao,S., Crossman,C., Langridge,P., Lazo,G.R., Pham	
COMMENT			,J., Rauech,C.V., Sutton,T., Woot,J. and Wilson,C. The structure and function of the expressed portion of the wheat genomes - Meiotic anther cDNA library Unpublished Contact: Olin Anderson US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773 Fax: 5105595818 Email: andersen@pw.usda.gov Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: T7 primer. Location/Qualifiers 1..665 /organism="Triticum aestivum" /mol_type="mRNA" /cultivar="Chinese Spring" /db_xref="taxon:4565" /clone="WHB4048_E08_J16" /tissue_type="Anther" /dev_stage="Meiotic stages pre-meiosis-metaphase I" /lab_host="E.coli DH10B" /clone_id="wheat meiotic anther cDNA library" /note=Vector: pSPORT1; Site 1: SalI; Site 2: NotI; Plants were grown in a glasshouse. Anther meiotic stage was determined by removing anthers from individual primary flowers. One anther was sacrificed for microscopic staging, and if determined to be between (and including) meiotic stages pre-meiosis and metaphase I, the remaining two	
FEATURES				
source				

CA030713 500 bp mRNA linear EST 24-OCT-2002
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 DEFINITION 5-PRIME mRNA sequence.
 ACCESSION CA030713
 VERSION CA030713.1 GI:24326542
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticeae; Hordeum.
 1 (bases 1 to 500)
 Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
 EST sequencing and analysis in barley (2002)
 Unpublished
 Contact: Stein Nils
 Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3, 06466, Gatersleben, Germany
 Tel: 039482-5532
 Fax: 039482-5595
 Email: stein@ipk-gatersleben.de
 Insert Length: 500 Std Error: 0.00
 Plate: 7 row: 0 column: 11
 Seq primer: M3rev.
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 /note="Vector: Bluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."
 BASE COUNT 61 a 225 c 135 g 79 t
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 Query Match 51.8%; Score 426.2; DB 14; Length 500;
 Best local Similarity 96.7%; Pred. No. 9.3e-75;
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 DB 30 CACGCCACCGATGCGCGACGCGCTTCGCGAGCAGTAACGCGCCGGAAGCCGACCAAT 89
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QY 407 CGTGGCGCGCTTACCGACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 466
 DB 330 CGTGGCGCGCTTACCGACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 389
 QY 467 CGCGAGCTTCTCTCTCGCGCGCGCTTCTGAGCGCGCTGCG-CACACCCCAAGTTCTGCT 525
 DB 390 CGCGAGCTTCTCTCTCGCGCGCGCTTCTGAGCGCGCTGCG-CACACCCCAAGTTCTGCT 449
 QY 526 CGTGGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 565
 DB 450 CGTGGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 489
 RESULT 7
 CA637422 493 bp mRNA linear EST 23-NOV-2002
 LOCUS wrel.pk0004.c7 wrel Triticum aestivum cDNA clone wrel.pk0004.c7 5'
 DEFINITION end, mRNA sequence.
 ACCESSION CA637422
 VERSION CA637422.1 GI:25215718
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticeae; Triticum.
 1 (bases 1 to 493)
 Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
 Miao, G., Caraher, N. and Hanafey, M.K.
 Dupont Wheat cDNA Sequence
 Unpublished
 Contact: Scott V. Tingey
 Crop Genetics
 E. I. Dupont de Nemours and Company
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
 Tel: 302-631-2602
 Fax: 302-631-2607
 Email: Scott.V.Tingey@usa.dupont.com
 Seq primer: M3.
 Location/Qualifiers
 1..493
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /clone="wrel.pk0004.c7"
 /tissue_type="root"
 /clone_1ib="wrel"
 /note="Vector: Bluescript SK+; Site_1: EcoRI; Site_2: XhoI; Wheat (Triticum aestivum L.) root; 7 day old etiolated seedling"
 BASE COUNT 72 a 218 c 119 g 81 t 3 others
 ORIGIN
 Query Match 50.1%; Score 412; DB 14; Length 493;
 Best local Similarity 95.0%; Pred. No. 6.1e-72;
 Matches 458; Conservative 0; Mismatches 21; Indels 3; Gaps 3;
 QY 1 CTCTCTAACAACTCTCGTGTGTTTAAAGATCCGATCTCCCTTGCCTTCCCTCC 60
 DB 1 CTCTCTAACAACTCTCGTGTGTTTAAAGATCCGATCTCCCTTGCCTTCCCTCC 60
 QY 61 CTCTCTCTGATCTCTGACCACT 120
 DB 61 CTCTCTCTGATCTCTGACCACT 120
 QY 121 CCGGACGCGGCTTCTGCGAGCAGCAGCGCGCGGAGCGCAAGTCCGCGCGCGAGCA 180
 DB 121 CCGGACGCGGCTTCTGCGAGCAGCAGCGCGCGGAGCGCAAGTCCGCGCGCGAGCA 180
 QY 181 AGAGCGCGCGAGCTCTGCGATGATCTCCACCAAGAGCTGACGAGCGCAGCGCGCGG 240
 DB 181 AGAGCGCGCGAGCTCTGCGATGATCTCCACCAAGAGCTGACGAGCGCAGCGCGCGG 240

QY 241 ACCAGCTCTGATCTCCAGTCCGGGAGCGTCTACGAGTACGCTCCGCTGGGCGCCACC 300
 Db 241 ACCAGCTCTGATCTCCAGTCCGGGAGCGTCTACGAGTACGCTCCGCTGGGCGCCACC 300
 QY 301 -ACCCGGGCGGAGGTCCTGCTATCACCTTCGCGGCGGAGAGCGCCACGAGCTTC 359
 Db 301 AACCCGGGCGGAGGTCCTGCTATCACCTTCGCGGCGGAGAGCGCCACGAGCTTC 360
 QY 360 ATGGGCTTACC-ACCCGCTTCGCGGCGGAGCGCTTCCTCC-CCGCTTCTTGTGGCGCGC 417
 Db 361 ATGGGCTTACCACCCGAGTCTCGCGCGCGCTCTCCGAGCTTCTTGTGGCGCGC 420
 QY 418 TCACCGACTACACTGTCCCGCGCTCCGCGGAGCTTCGCGGCTCTCTCGCGAGCTCT 477
 Db 421 TCTCCGACTACAGCTCTCCCGCGCTCCGCGGAGCTTCGCGGAGCTCTCTCGCGAGTCT 480
 QY 478 CC 479
 Db 481 TC 482
 RESULT 8
 BQ238994 453 bp mRNA linear EST 03-MAY-2002
 LOCUS TA05038F05R TAB05 Triticum aestivum cDNA clone TA05038F05R, mRNA
 DEFINITION
 ACCESSION BQ238994
 VERSION BQ238994.1 GI:20434870
 KEYWORDS
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM
 REFERENCE
 AUTHORS Cloutier, S.
 TITLE Wheat functional genomics - Glenlea developing seeds cDNA libraries
 JOURNAL Unpublished
 COMMENT Contact: Dr. Sylvie Cloutier
 Cereal Research Centre, Agriculture and Agri-Food Canada
 195 Dufour Rd, Winnipeg, MB, Canada R3T 2M9
 Tel: (204) 983-2340
 Fax: (204) 983-4604
 Email: scloutier@agr.ca
 was cloned directionally, not all sequences generated with reverse
 primer were from the 5' end (same with forward primer and 3' end).
 Average insert size is >2.0 kb
 Plate: 038 row: F column: 05
 Seq primer: M13 Reverse.
 Location/Qualifiers
 1..453
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Glenlea"
 /db_xref="taxon:4565"
 /clone="TA05038F05R"
 /tissue_type="developing seeds"
 /dev_stage="5 days after anthesis"
 /lab_host="E. coli DH10B"
 /clone_lib="TAB05"
 /note="Vector: pSPORT-P (Invitrogen Technologies) ; Site_1:
 NotI; Site_2: MluI; mRNA obtained from wheat seeds of
 cultivar Glenlea 5 days post-anthesis"
 BASE COUNT 62 a 214 c 109 g 68 t
 ORIGIN
 Query Match 47.9%; Score 394.2; DB 13; Length 453;
 Best Local Similarity 94.8%; Pred. No. 2e-68; Indels 4; Gaps 1;
 Matches 419; Conservative 0; Mismatches 19; Indels 4; Gaps 1;
 QY 17 CGTGTCTTTTAAATCGATCTCCCTTCMCCCTCCCTCTCTCTCTAG- 72
 Db 12 CGTTCCTTTTAAATCGATCTCCCTTCGCGCTCCCTCTCTCTCTCTCC 71

QY 73 TCTGACCAACCCCTCTCGGCTCCAGCTAAATCGACGCAACCGATGACCGGAGCT 132
 Db 72 TCTGACCAACCCCTCTCGGCTCCAGCTAAATCGACGCAACCGATGACCGGAGCT 131
 QY 133 TCGCGAGCGCAACGCGCGCGGAGAGCGCAATGCGCGCGCGCAGCAAGAGCGCGCG 192
 Db 132 TCGCGAGCGCAACGCGCGCGGAGAGCGCAATGCGCGCGCGCAGCAAGAGCGCGCG 191
 QY 193 AGCTCCGATGATCTTCACCAAGAGACTGCAAGCGCGACCGCGCGGAGACCTTGA 252
 Db 192 AGCTCCGATGATCTTCACCAAGAGACTGCAAGCGCGACCGCGCGGAGACCTTGA 251
 QY 253 TCTGCATCTCCGCGGAGGAGTCTACAGTACGAGCTTCGCTGCGCGCAGCAACCGGCGCG 312
 Db 252 TCTGCATCTCCGCGGAGGAGTCTACAGTACGAGCTTCGCTGCGCGCAGCAACCGGCGCG 311
 QY 313 AGGTCCCGCTCATACCTTCGCGGCGCAGAGCGCACCGAGCTTCATGAGCTTACAC 372
 Db 312 AGGTCCCGCTCATACCTTCGCGGCGCAGAGCGCACCGAGCTTCATGAGCTTACAC 371
 QY 373 CGCCTTCGCTGCGCGCGCTCTCTCGCGCTTTCTGCGCGCGCTCAGCGACTACAG 432
 Db 372 CGCCTTCGCTGCGCGCGCTCTCTCGCGCTTTCTGCGCGCGCTCAGCGACTACAG 431
 QY 433 TCCCGCGCGCTCGCGGACTT 454
 Db 432 TACCCCGCGCTTCGAGACTT 453
 RESULT 9
 BQ605802 697 bp mRNA linear EST 25-JUN-2002
 LOCUS BR1.1370 wheat EST endosperm library Triticum aestivum cDNA 5',
 DEFINITION
 ACCESSION BQ605802
 VERSION BQ605802.1 GI:21554898
 KEYWORDS
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM
 REFERENCE
 AUTHORS Clarke, B., Lambrecht, M. and Rhee, S. Y.
 TITLE Arabidopsis genomic information for interpreting wheat EST
 JOURNAL sequences
 MEDLINE
 PUBMED 22478026
 12590341
 COMMENT Contact: Lambrecht M
 The Arabidopsis Information Resource
 Carnegie Institution of Washington, Dept. of Plant Biology
 260 Panama Street, Stanford, CA 94305, USA
 Tel: 1 650 325 1521 x 251
 Fax: 1 650 325 3748
 Email: rhees@coma.stanford.edu.
 Location/Qualifiers
 1..697
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Wynua"
 /db_xref="taxon:4565"
 /tissue_type="endosperm"
 /dev_stage="developing endosperm tissue 8, 10 and 12 DPA
 (days post anthesis)"
 /clone_lib="wheat EST endosperm library"
 BASE COUNT 114 a 217 c 177 g 189 t
 ORIGIN
 Query Match 41.6%; Score 342.2; DB 13; Length 697;
 Best Local Similarity 86.6%; Pred. No. 4.3e-58;
 Matches 388; Conservative 0; Mismatches 59; Indels 1; Gaps 1;

120 GCCCGACGAGGCTTCGCGGACGCAACGCGCGCGGAAAGCCGACGCAATGCGGCGCGAC 179
 1 GCCCGACGAGGCTTCGCGGACGCAACGCGCGCGGAAAGCCGACGCAATGCGGCGCGAC 60
 180 AAGACGCGCGCGAGCTCCGATGATCTTCACCAAGAGAGCTCCAGCGCGCGCGCG 239
 61 AAGACGCGCGCGAGCTCCGATGATCTTCACCAAGAGAGCTCCAGCGCGCGCGCG 120
 240 GACGACCTCTGATGATCTTCACCAAGAGAGCTCCAGCGCGCGCGCGCGCGCG 299
 121 GACGACCTCTGATGATCTTCACCAAGAGAGCTCCAGCGCGCGCGCGCGCGCG 180
 300 CACCGCGCGCGAGAGCTCCGCTCATCAGCTTCGCGCGCGCGCGCGCGCGCGCG 359
 181 CACCGCGCGCGAGAGCTCCGCTCATCAGCTTCGCGCGCGCGCGCGCGCGCGCG 240
 360 ATGAGCTTACACCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 419
 241 ATGAGCTTACACCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
 420 ACCGACTACAGTCTCCCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCG 479
 301 ACCGACTACAGTCTTCACCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
 480 TCCGCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 538
 361 TTCGCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
 539 GTGCTCTTCGATCGCGCTCTACTGCT 566
 421 GGGCTTTTGAATAGCCCTTATTGCT 448

RESULT 10
 LOCUS AY103762 1764 bp mRNA linear HTC 16-OCT-2002
 DEFINITION Zea mays PC0087385 mRNA sequence.
 ACCESSION AY103762
 VERSION AY103762.1 GI:21206840
 KEYWORDS HTC.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 1764)
 Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S.,
 Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
 Maize Mapping Project/DuPont Consensus Sequences for Design of
 Overgo Probes
 Unpublished (2002)
 2 (bases 1 to 1764)
 Coe, E.H.

REFERENCE JOURNAL
 TITLE Direct Submission
 AUTHORS Submitted (25-APR-2002) Maize Mapping Project, University of
 Missouri, Columbia, MO 65211, USA
 COMMENT If you are interested in getting corresponding physical clones,
 these are publicly available from ZmDB, www.zmdb.iastate.edu; TIGR,
 www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat
 Schnable, Iowa State, then clones may be requested from ZmDB:
 www.zmdb.iastate.edu.
 Location/Qualifiers
 1..1764
 /organism="Zea mays"
 /mol_type="mRNA"
 /db_xref="MaizeDB:634923"
 /db_xref="taxon:4577"
 /clone_11b="Maize Mapping Project/DuPont Consensus
 Library"
 /note="this sequence is part of a project of EST

assemblies resulting from the application of public
 contigs to seed Dupont contigs; this resource was
 assembled by Dupont as part of a collaboration for the
 overgo addressing of BACs in conjunction with the Maize
 Mapping Project"

Query Match 38.3%; Score 314.8; DB 11; Length 1764;
 Best Local Similarity 78.2%; Pred. No. 1.2e-52;
 Matches 417; Conservative 0; Mismatches 108; Indels 8; Gaps 3;

BASE COUNT 310 a 602 c 456 g 396 t
 ORIGIN
 82 CCCCTCTCGCGCTCCAGTAAATCCAGCCAGATGAGCCGCGCGCGCGCGCGCG 141
 27 CCTCCCGCGCTCCCTTCAATCAGACACCAAGCGGATCGAGCCAGCGCGCG 86
 142 CAACGCGCGCGAGCGGAGCGGATGCGCGCGCGCGCGCGCGCGCGCGCGCG 195
 87 CATGCGCGCGCTCTGATGATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 146
 136 TCCGATGATCTCCACCAAGAGCTGCGGCGCGCGCGCGCGCGCGCGCGCG 255
 147 TCCGATGATCTCTCCCAAGAGCTGCGGCGCGCGCGCGCGCGCGCGCGCG 206
 256 CCATCTCGCGGAGCGCTTACAGAGCTGCGGCGCGCGCGCGCGCGCGCGCG 315
 207 CCATCTCGCGGAGCGCTTACAGAGCTGCGGCGCGCGCGCGCGCGCGCGCG 266
 316 TCCGCTATCACTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 375
 267 TCCGCTATCACTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 326
 376 CCTCGGCGCGCGCGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 435
 327 CCTCGGCGCGCGCGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 386
 436 CCCCCGCTCGCGCGAGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 495
 387 CCCCCGCTCGCGCGAGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 446
 447 AACGCGTGGCG 506
 496 AGCGGCTGGG-CACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 554
 555 GCCTCTA-CTGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 606
 507 CGCTGTACTGTCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 559

RESULT 11
 LOCUS B1075898 634 bp mRNA linear EST 20-JUN-2001
 DEFINITION IP1 22.F11.b1 A002 Immature panicle 1 (IP1) Sorghum bicolor cDNA,
 mRNA sequence.
 ACCESSION B1075898
 VERSION B1075898.1 GI:14514555
 KEYWORDS EST.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 634)
 Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and Pratt
 L.H.

REFERENCE JOURNAL
 TITLE An EST database from Sorghum: developing preanthesis panicles
 AUTHORS Unpublished
 COMMENT Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210

QY 368 CCACCCGCGCTCGTGGCGCCGCTCTCTCGCGCTTCTTGTGTGGCGCGCTTCCAGCTACTA 427
 Db 258 CCACCGCGCTCGTGGCGCGCGCGCTCTCTCGCGCTTCTTGTGTGGCGCGCTTCCAGCTACTA 317
 QY 428 CACTGTCCCCCGCGCTCGCGGACTTCCGCGCGCTCTCTCGCGGAGCTTCTCTCGCGGG 487
 Db 318 CACCGCTCTCCCGCGCTCGCGGACTTCCGCGCGCTCTCTCGCGGAGCTTCTCTCGCGGG 377
 QY 488 CCTCTTGGAGGGGCTGGG-CAGACCCCGAAGTTCCGCTCTCTCGCGGAAATCTGTCTT 546
 Db 378 CCTCTTGGAGGGGCTGGGCGCCCGAAGTTCCAGCTCTCTCTCTCTCTCTCTCTT 437
 QY 547 CTGATTCGCGCTCTA-CTGCT 605
 Db 438 CTACCGCGCGCT 497
 QY 606 G 606
 Db 498 G 498

RESULT 13
 CC344270 576 bp DNA linear GSS 16-MAY-2003
 LOCUS OGMO60TV ZM 0.7.1.5 KB Zea mays genomic clone ZMMMA0385123,
 DEFINITION genomic survey sequence.
 CC344270
 VERSION CC344270.1 GI:30813676
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 576)
 WhiteIaw,C.A., Quackenbush,J., Van Aken,S., Uteerback,T., Resnick
 A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek
 R.W., Nurnberg,A., Robbins,D. and Lakey,N.
 Consortium for Maize Genomics
 Unpublished
 TITLE TIGR
 JOURNAL 9712 Medical Center Drive, Rockville, MD 20850, USA
 COMMENT Contact: Cathy WhiteIaw
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whiteIaw@tigr.org
 Seq primer: TF
 Class: sheared ends.
 Location/Qualifiers
 1..576
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_1ib="ZMMMA0385123"
 /clone_1ib="ZM 0.7.1.5 KB"
 /note="Vector: pBCK-; Site 1: HincII, 0.7-1.5 kb
 methylation filtered genomic DNA library"
 BASE COUNT 85 a 263 c 135 g 93 t
 ORIGIN

Query Match 35.2%; Score 289.8; DB 29; Length 576;
 Best Local Similarity 79.7%; Pred. No. 1e-47;
 Matches 372; Conservative 0; Mismatches 82; Indels 13; Gaps 2;

QY 57 CTCCCTTCTCTAGTCTGACCAACCCCTCTCTCGCGCTCAAGCTAATTCAGCGACCG 116
 Db 115 CTCCCACTTCCACATTTCTCCCGCTCTCTCGCGCTCTCAAGCTAATTCAGCGACCG 174
 QY 117 ATGGCCCGACGCGCTTGGCGGACGCAACGCGCGCGGAAAGCGACGCAATGCGCGCGC 176
 Db 175 AT-----AGGGGCGACGCGCGCGCAATGCGCGCTCTGCGGACGCAATGCGCGCGC 227

QY 177 AGCAAGA-----CGCGCGACGCTCGCATGATCTTCACCAAGAGCTGAGCGCAC 230
 Db 228 GGAAGAGCGCGGTGGCGCGGAGCGCTTGATCTCTCAAGAGCTTCGCGAGCAC 287
 QY 221 GCGCGCGGAGGACCTTGTGATCTTCATCTCGGAGAGCTTACAGAGCTTACGCGCTTG 290
 Db 288 GCGTCGCGCGGACCTTGTGATCTTCATCTCGGAGAGCTTACAGAGCTTACGCGCTTG 347
 QY 291 CTGCGCGCACACCGCGCGGCGGAGAGTCCCGCTATCACCTTCCGCGCGCAAGACGCGCAC 350
 Db 348 CTTCGCCACACCGCGCGGCGGAGAGTCCCGCTATCACCTTCCGCGCGGAGAGAGCGCAC 407
 QY 351 GAGCGCTTCATGAGCTTACACCGCGCTTCGCGCGCGCTCTCTCGCGCTTCTCTCTGTC 410
 Db 408 GACGCTTTCGCGCGCTTACACCGCGCTTCGCGCGCGCTCTCTCGCGCTTCTCTCTGTC 467
 QY 411 GCGCGCTTCACCGGACTTACGCTGTCCTCCCGCTTCGCGCGAGCTTCCGCGCTCTCTGTC 470
 Db 468 GCGCGCTTCGCGGACTTACGCTGTCCTCCCGCTTCGCGCGAGCTTCCGCGCTCTCTGTC 527
 QY 471 CAGCTCTCTCTCGCGCGGCTCTTTCGAGCGCGTTCGCGCACCGCCCAAG 517
 Db 528 CAGCTCTCTCTCGCGGCTCTTTCGAGCGCGTTCGCGCACCGCCCAAG 574

RESULT 14
 CA710447 478 bp mRNA linear EST 26-NOV-2002
 LOCUS wdk2c.pk015.k22 wdk2c Triticum aestivum cDNA clone wdk2c.pk015.k22
 DEFINITION 5' end, mRNA sequence.
 CA710447
 VERSION CA710447.1 GI:25432240
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 1 (bases 1 to 478)
 Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
 Miao,G., Caraher,N. and Hanafey,M.K.
 Dupont Wheat cDNA Sequence
 Unpublished
 TITLE Contact: Scott V. Tingey
 JOURNAL Crop Genetics
 COMMENT E. I. Dupont de Nemours and Company
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
 Tel: 302-631-2602
 Fax: 302-631-2607
 Email: Scott.V.Tingey@usa.dupont.com
 Seq primer: M13.
 Location/Qualifiers
 1..478
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /clone="wdk2c.pk015.k22"
 /tissue_type="kernel"
 /clone_1ib="wdk2c"
 /note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
 XhoI; Wheat (Triticum aestivum L.) developing kernel, 7
 days after anthesis."

BASE COUNT 67 a 199 c 111 g 78 t 23 others
 ORIGIN

Query Match 34.7%; Score 285.4; DB 14; Length 478;
 Best Local Similarity 87.8%; Pred. No. 7.7e-47;
 Matches 324; Conservative 0; Mismatches 42; Indels 3; Gaps 2;

QY 1 CTCCCTAACAACTCTCGTGTGTTTAAGATCGGATCTCCCTTCNCCCTTCCCTTC 60
 Db 14 CTCCCTAACAACTCTCGTGTGTTTAAGATCGGATCTCCCTTCCCTTCCCTTC 73

QY 61 CTTCTCTGAGTCTGACCACTCTCTGCGCTCCAGCTAAATCCAGCCACCGATGG 120
 DB 74 CTTCTCTGAGTCTGACCACTCTCTGCGCTCCAGCTAAATCCAGCCACCGATGG 133
 QY 121 CCGGCAAGGCTTCCGGGAGCAACGCGCGGGAAGCCGACGCAATCCCGCGCCAGCA 180
 DB 134 NCGGCAAGGCTTCCGGGAGCAACGCGCGGGAAGCCGACGCAATCCCGCGCCAGCA 193
 QY 181 AGGACCGCGGAGCTCCGATATCTCCACCAAGAGCTGACGAGCGCAAGCGCGCGCG 240
 DB 194 AGGACCGCGGAGCTCCGATATCTCCACCAAGAGCTGACGAGCGCAAGCGCGCGCG 253
 QY 241 AGGACCTTGATCTCCATCTCCGAGAGCTGAC-GAGCTCAAGCGCTGAGCTGCGCAC 299
 DB 254 AGGACCTTGATCTCCATCTCCGAGAGCTGACGAGCTGACGAGCTGAGCTGCGCAC 313
 QY 300 CAGCC--GGGCGGAGAGTCCGCTCATCACTCCGCGCGGAGAGCGCACCGAGCT 357
 DB 314 CAGCCCGGAGAGTCCGCTCATCACTCCGCGCGGAGAGCGCACCGAGCT 373
 QY 358 TCATGGCT 366
 DB 374 GNAAGCTT 382

RESULT 15

BG158998 400 bp mRNA linear EST 06-FEB-2001
 LOCUS RH122_41_d11_b1_A003 Rhizome2 (RH122) Sorghum proplinguunum cDNA, mRNA
 DEFINITION sequence.

ACCESSION BG158998
 VERSION BG158998.1 GI:12692662
 KEYWORDS EST.

SOURCE Sorghum proplinguunum
 ORGANISM Sorghum proplinguunum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 400)
 Cordonnier-Pratt, M.-M., Gingle, A., Petersen, A., Sudman, M. and Pratt
 L.H.

REFERENCE An EST database from Sorghum: Sorghum proplinguunum rhizomes
 AUTHORS Unpublished
 JOURNAL Contact: Cordonnier-Pratt MM
 COMMENT Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu
 Seq primer: JEN REV
 High quality sequence stop: 297
 POLY(A)=No.

FEATURES

source Location/Qualifiers
 1..400
 /organism="Sorghum proplinguunum"
 /mol_type="mRNA"
 /db_xref="taxon:132711"
 /clone_lib="Rhizome2 (RH122)"
 /note="Organ: Rhizome; Vector: pBluescript II from Lambda
 Zap II; Site 1: XhoI; Site 2: EcoRI; The library was made
 from poly-A RNA in the cloning vector Lambda Zap II.
 Clones to be sequenced were prepared by mass excision."

BASE COUNT

46 a 188 c 112 g 54 t

Query Match 34.5%; Score 283.6; DB 10; Length 400;
 Best Local Similarity 88.6%; Pred. No. 1.7e-46;
 Matches 318; Conservative 0; Mismatches 40; Indels 1; Gaps 1;

QY 182 GGAAGCGCGGAGCTCCGATGATCTCCACCAAGAGCTGAGCGAGCGCGCGCGGA 241
 DB 41 GGGCGCGGAGCTCCGATGATCTCCACCAAGAGCTCCGCGCGAGCGCGCGCGGA 100

QY 242 CGACTCTGAGATCTCCATCTCCGAGAGCTCTACAGAGCTACGCGCTGAGCGCGACCA 301
 DB 101 CGACTCTGAGATCTCCATCTCCGAGAGCTCTACAGAGCTACGCGCTGAGCGCGACCA 160
 QY 302 CCGGAGCGGAGGTCCTGCTATCACTCCGCGGAGAGAGCGCAAGAGCGCTTCAT 361
 DB 161 CCGGAGCGGAGGTCCTGCTATCACTCCGCGGAGAGAGCGCAAGAGCGCTTCAT 220
 QY 362 GAGCTACAGAGCGGCTCCGAGCGCGGCTCCGCGGCTTCGCTGAGCGCGCTCAC 421
 DB 221 GAGCTACAGAGCGGCTCCGAGCGCGGCTCCGCGGCTTCGCTGAGCGCGCTCAC 280
 QY 422 CGACTACAGGTCCTCCGCGGCTCCGCGGAGAGCTTCGCGGAGAGCTTCCTC 481
 DB 281 CGACTACAGGTCCTCCGCGGCTCCGCGGAGAGCTTCGCGGAGAGCTTCCTC 340
 QY 482 CCGGAGCGGTCCTGAGAGCGGTCGG-GACACCGGCAAGTCTGCTGTCGCAAGTCGG 539
 DB 341 CCGGAGCGGTCCTGAGAGCGGTCGGGCCACCGGCAAGTCTGCTGTCGCAAGTCGG 399

Search completed: December 31, 2003, 23:59:29
 Job time : 1259.26 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:49:12 ; Search time 40.8386 Seconds
(without alignments)
8894.970 Million cell updates/sec

Title: US-09-857-524B-16

Perfect score: 823
Sequence: 1 ccccttaacaaccgccgtt.....cgtnaagacttggttagcat 823

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/prodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCUTS_COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106.8	13.0	1702	4	US-08-934-254-26
2	75.2	9.1	4411529	3	US-09-103-840A-1
3	74.2	9.0	1926	4	US-09-249-585A-4
4	74.2	9.0	1931	2	US-09-130-114-2
5	73.4	8.9	7218	1	US-08-232-463-14
6	70.8	8.6	77536	4	US-09-410-551B-1
7	68.6	8.3	1881	3	US-09-434-288-5
8	68.4	8.3	4403765	4	US-09-103-840A-2
9	67.6	8.2	4403765	3	US-09-103-840A-2
10	67.6	8.2	4411529	3	US-09-103-840A-1
11	65.2	7.9	319	3	US-09-165-264-8
12	65	7.9	4488	3	US-08-406-030A-3
13	63.2	7.7	320	3	US-09-165-264-13
14	63	7.7	44377	2	US-08-804-227C-7
15	63	7.7	44377	2	US-08-804-198-1
16	62	7.5	12001	1	US-08-458-568A-11
17	61.8	7.5	833	2	US-08-403-852D-3
18	61.8	7.5	833	3	US-08-510-646B-3
19	61.8	7.5	833	3	US-09-231-818-3
20	61.8	7.5	4466	4	US-09-410-551B-20
21	61.8	7.5	4478	4	US-09-410-551B-16
22	61.8	7.5	4547	4	US-09-410-551B-22
23	61.8	7.5	4571	4	US-09-410-551B-18
24	61.8	7.5	5392	2	US-08-403-852D-1
25	61.8	7.5	5392	2	US-08-510-646B-1
26	61.8	7.5	5392	3	US-09-231-818-1
27	61.8	7.5	77536	4	US-09-410-551B-1

28	61.4	7.5	152331	3	US-09-128-155-16	Sequence 16, Appl
29	60.6	7.4	320	3	US-09-165-264-14	Sequence 14, Appl
30	60.6	7.4	1158	4	US-09-372-422A-21	Sequence 21, Appl
31	60.4	7.3	939	3	US-09-105-390-45	Sequence 45, Appl
32	60.4	7.3	1020	3	US-09-105-390-61	Sequence 61, Appl
33	60.4	7.3	1193	4	US-09-372-422A-23	Sequence 23, Appl
34	60.4	7.3	2612	3	US-09-105-390-7	Sequence 7, Appl
35	60.2	7.3	1717	4	US-09-048-888-2	Sequence 2, Appl
36	59.8	7.3	2481	4	US-09-894-998A-35	Sequence 35, Appl
37	59.8	7.3	6085	3	US-09-029-603-4	Sequence 4, Appl
38	59.6	7.2	318	3	US-09-165-264-12	Sequence 12, Appl
39	59.6	7.2	320	3	US-09-165-264-11	Sequence 11, Appl
40	59.6	7.2	675	3	US-08-998-416-723	Sequence 723, App
41	59.6	7.2	2064	1	US-08-343-428-1	Sequence 1, Appl
42	59.4	7.2	1896	4	US-09-311-626B-15	Sequence 15, Appl
43	59.2	7.2	1027	4	US-09-674-741-9	Sequence 9, Appl
44	59.2	7.2	1071	2	US-08-997-080-180	Sequence 180, App
45	59.2	7.2	1071	2	US-08-997-362-180	Sequence 180, App

ALIGNMENTS

RESULT 1
US-08-934-254-26
Sequence 26, Application US/08934254
Patent No. 6355861
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1702 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULAR TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1406
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1406
US-08-934-254-26
Query Match 13.0%; Score 106.8; DB 4; Length 1702;
Best Local Similarity 62.3%; Pred. No. 3.3e-13;

	Matches	187; Conservative	0; Mismatches	107; Indels	6; Gaps	1
QY	204	ATATCCACCAAGAGACTCGAGGCGGACACCGCGCGGAGAGACTCTGATCTTCACATCTCC				263
Db	72	ATCAAGCGGAGAGACTTCGCGCGCCACCAACAAATCGGAGATCTCTGAGATCTCCACAG				131
QY	264	GAGGAGCTTACAGACGTACACGCCCTGGCTGCGCCACCAACCGGCGCGGAGGTCCCGCTC				323
Db	132	GCGAAGGCTTACGACTGCTCTTCGGTGGGCGGAGACCCCGCGCGAGAGTCCCGCTC				191
QY	324	ATCAACCTCGCGCGGCGAGGACGCCACCGACGCTTCATGAGCCCTACACCGCGGCTCCCGG				383
Db	192	CTCAATCTGGCGCGGCGAGGACGTACACGACGCTTCATTTCGTACACCCCGGACAGGCG				251
QY	384	CGCCGCTCTTCGCGCGGCTTCTTGCTCGG-----CGGCTACACGACTACACTGTCCG				437
Db	252	TGGCGGCAATGTGATTCGCTCTTCAACGGGCTACTACTCAAGGACTTCGAAGTGTGG				311
QY	438	CCCGGCTCGCGGCAATTCGCGCGCGCTCCCTCGGCGAGCTCTCCGCGGCGGCTCTTCGAG				497
Db	312	GAGATCTCCAGAGACTACCGAGGCTTTTGAACGAGATGTCCGGTCCGGAATCTTCGAG				371

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RESULT 2
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007_00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

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	Query Match	9.1%	Score 75.2	DB 3	Length 4411529
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Qy	73	TCTGTACCAACCCTTCCTCGCGCTCCAGCTTAATCCAAGCCACCGATGGCCCGCACGGGCT	132		
Db	1218040	CCGGCG	1217981		
Qy	133	TCGGGGAACGAACGGCGCGCGGAAAGCGACGCAATGCGCGCGCGCACGAAGAAGCGCGCG	192		
Db	1217980	GCA	1217921		
Qy	193	ACGTCGCATGATCTCCACCAAGAGCTGACAGGCGACGCGCGCGCGACGACTCTTGA	252		
Db	1217920	CGGCGCGCAAGCGCGCGCGCATGCGCGTGCGCGGGGCGCGCGCGCGCGCTTAAAG	1217861		
Qy	253	TCTCCATTCGGGGAGCTTACGACGTCAGCGCCTTGCTGGCGCACCAACCGGGGCGG	312		
Db	1217860	GCGGCGG	1217801		
Qy	313	AGGTCGCGCTATCAACCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTATGGCGTAAACA	372		
Db	1217800	GCGG	1217741		

Qy	373	GGCCCTCGAGCGCGCGCTCTCCGCGCGCTTTTCTTCTGCGCGCGCTACAGGACTGAC	432
Db	1217740	CCGTTGGCGTTTACCCTGAGAGCCAGAGCCGCTTTTGTCCGCGCGCCCGCGCGCCACCG	1217681
Qy	433	TCGCCCGCGCTCCGCGGACTTTCGCGCGCTCTCTGCGGACGTCCTCTCGCGGGGCTCT	492
Db	1217680	TCCCGCGCGGCGCGCGCGCGCCACGACGCGCCACAGCTGGGGGTTGCTCTCGGCGCG	1217621
Qy	493	TCGAGCGCGTTCGGGACACCCCCAAAGTTCGTCTGTGTGGCAAAGTCNAGCTCTTTCGAT	552
Db	1217620	CCGGCGGCACCTGTCCCAACGCGCGCGCGCGGTCCCAACCGGACACCGCGCGCGCTGCTG	1217561
Qy	553	CGGCTCTAAGCTCTCTGCGCTGTCTAACAACCGGGGCGC	590
Db	1217560	CTGACGCACTTATCCCGGCGCTAAGCCCTTTTCGGCGGC	1217523

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RESULT 3
US-09-249-585A-4
; Sequence 4, Application US/09249585A
; Patent No. 6417002
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert
; TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
; FILE REFERENCE: 0867/0D905
; CURRENT APPLICATION NUMBER: US/09/249,585A
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Epstein Barr Virus
; FEATURES:
; NAME/KEY: misc feature
; LOCATION: (1)..(1926)
; OTHER INFORMATION: template strand of EBNA-1 DNA
US-09-249-585A-4

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[illegible]

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Query Match	9.08;	Score 74.2;	DB 2;	Length 1931;
Best Local Similarity	9.58;	Score 74.2;	DB 2;	Length 1931;

[illegible]

RESULT 5
US-08-232-463-14
Sequence 14, Application US/08232463
Patent No 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU

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? TELECOMMUNICATION INFORMATION
? TELEPHONE: (703)836-9300
?
? TELEFAX: (703)683-4109
?
?       TEXT: 899149
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? INFORMATION FOR SEQ ID NO: 14:
?
? SEQUENCE CHARACTERISTICS:
?     LENGTH: 7218 base pairs
?     TYPE: nucleic acid
?     STRANDEDNESS: single
?     TOPOLOGY: linear
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? IMMEDIATE SOURCE:
?
? CLONE: PTZgpt-F1s
US-08-232-463-14
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Query Match	8.9%;	Score 73.4;	DB 1;	Length 7218;
Best Local Similarity	3.6%;	Pred. No. 1.9e-06;		
Matches 14;	Conservative 234;	Mismatches 136;	Indels 0;	Gaps 0;

[illegible]

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RESULT 6
US-09-410-551B-1/C
Sequence 1, Application US/09410551B
Patent No. 6503737
GENERAL INFORMATION:
APPLICANT: KOSAN BIOSCIENCES, Inc.
APPLICANT: REEVES, CHRISTOPHER
APPLICANT: CHU, DANIEL
APPLICANT: KHOSLA, CHAITAN
APPLICANT: SANTI, DANIEL
APPLICANT: WU, KAI
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
FILE OF INVENTION: CONSTRUCTS THEREFOR
FILE REFERENCE: 30062-20026.00
CURRENT APPLICATION NUMBER: US/09/410,551B
CURRENT FILING DATE: 1999-10-01
PRIORITY APPLICATION NUMBER: US 60/139,650
PRIORITY FILING DATE: 1999-06-17
PRIORITY APPLICATION NUMBER: US 60/123,810
PRIORITY FILING DATE: 1999-03-11
PRIORITY APPLICATION NUMBER: US 60/102,748
PRIORITY FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 77536

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QY	125	CACGAGGCTTCGCGGACCGCAAGGCGGCCGGAAAGCCGACCAATGCGCGCCGACGACGAA	184
Db	2798912	CGCTGTGGCGGCCCAAGCGCGCGAGAGGCTCCCGCGCCGGGGGTCAACCGCGTCACCGCGCT	2798971
QY	185	CGCGCGCGGACGTCCGCGATATCTCCACCAAGAGAGCTGACGAGGCGCACGCGCCGCGGACGA	244
Db	2798972	CCCCGCGCATCATCTGCACATGACCGCGCGTACCGCGCGTTCGCGCGGCGCTCCGCGAGCCGC	2799033
QY	245	CCCTCGGATCTCCATCTTCGCGGGAGAGCTTAAGAGCTTACGCGCCCTTGCTGCGCCACACCC	304
Db	2799032	CGTACCGCGCAACGCGCGCGACACCGTGTGCTGCGCACTTGACCCGCGGGGTGCGGCCCCGC	2799091
QY	305	GGGCGGCGAGGATCCCGCTCATCACCCCTGCGCGGACGAGACGCAACGACGCGCTTCATGGC	364
Db	2799092	CGGCGCGCCCATCACCGCGCGGGGCCCGCGCTACCGCCCAACGCGCGCGACACCGCGCTTGC	2799151
QY	365	CTACCAACCGCGCTCCGTGCGCGCGCGCTCTCGCGGCTTCTTGTGCGGCGCGCTTCACCGA	424
Db	2799152	CGCCTTTCGCCGCGGCGCTCCAAACGCGCTTAGCGGCTGTGCGGCGCGGAGGAGGCCCTTGC	2799211
QY	425	CTACACTGTCCCCCGCGCTCTCGCGGAACTTTCGCGCGCTCTCTCGGCGACGCTTCTCCGC	484
Db	2799212	CGCGCGCGCACCACTAGCTCCGGGACCAACCGGACCGCACCGCGCGGCCCGCGCTTGCACCGG	2799271
QY	485	GGGCGCTTTCGAGCGCGGTGCGGACACCCCAAGTTCTCMTGC	526
Db	2799272	GTCACACGTCGCGCGGACACCGAACCCACCGCGCGCACCGGACTC	2799313

QY	125	CACGGGGCTTTCGGCGAGCCGAACGGCGCGCGAAGGCGAGCGCATGTGCGGCGCGCGACGAAGA	184
Db	2803459	CGCTGTGCGCGCCGAAGCGCGCGCGAGGCTCTCCGCGCGCGGGGGTCAACGGCCGTCAACGGCGGT	2803518
QY	185	CGCGCGCGGACGTCCGCATGATTTCTCCACCAAGAGCTGCAAGCGCAGCGCCGCGCGGACGA	244
Db	2803519	CCCCGCCATCATGTCCCATGTGACCGCGCGTCAACCGCGCTTTCGCGCGGAGCGCGCTCCGCGCGGCGCG	2803578
QY	245	CCCTGTGAGATCTGCATCTCGGGGGAGCGTTACGAGGTGACGCGCCCTGTGGCGGACGACCC	304
Db	2803579	CGTACCGCCCAAGCGCGCCCAACACCGTGGCTGCCGACTTAACCCGCGGGTGGCGGCGCGC	2803638
QY	305	GGGCGCGAGATGCCCGCTCATCAACCTTCGCGCGGACGACCGACCGACCGCTTCATGAGC	364
Db	2803639	CGGCGCGCGCATCAACCGCGCGGCGCGCGCTCAACCGCAAGCGCGCGGACACACCGCGCTTCG	2803698
QY	365	CTACCAACCGGCGCCTCGGTGCGCGCGGCTCTTCGCGCGCTTCTTGTGGCGCGCTCAACGA	424
Db	2803699	CGCCTTTCGCGCGGCGCTCTCAACGGCGCTCAAGGCTGTGGCGCGGAGGCGGCTTTCG	2803758
QY	425	CTACACTGTTCCTCCCGCGCTTCGCGCGACTTCGCGCGCTCTTGCGGAGACTTTCCTCCG	484
Db	2803759	CGCGCGCGCACCATGACTTCGCGACCAACCGGACCGCGCGGCGCCCGCCTTTCGACCGG	2803818
QY	485	GGGCTCTTTCGAGGCGGTGGGACACCGCCCAAGTTCTGTGCTC	526
Db	2803819	GTTCACCGTGTCCCGACACCGAACCGACCGGCGCGCACCGGCTC	2803860

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RESULT 11
US-09-165-264-8/c
Sequence 8, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiyiah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentrin Ver. 2.1
SEQ ID NO 8
LENGTH: 319
TYPE: DNA

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; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-8

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Query Match	7.9%;	Score 65.2;	DB 3;	Length 319;
Best Local Similarity	51.0%;	Pred. No. 6e-05;		
Matches 154;	Conservative	0;	Mismatches 148;	Indels 0;
			Gaps	0;

QY	213	AAGAGCTGCAGAGCCGACGCCCCGCGGAGCAACTGTGATCTTCATCTCCGAGACGTC	272
Db	313	AGGGTGTGAGAGACCC	254
QY	273	TACGACGTACGCGCTGTGCTGCGCACACCCGGGCGGAGAGTCCCGCTCATACCTTC	332
Db	253	CC	194
QY	333	GCGGACAGAGAGCCACGACGCTTTCATGAGCTTACACCGGCGCTCCGAGGAGCCGCTC	392
Db	193	CC	134
QY	393	CTCGGCGCTTCTTGCTGAGCGGCTCACGCACTACCTGTCCCCCGGCTTCGCGGAC	452
Db	133	CC	74
QY	453	TTCCGCGCGCTCTTCGCGAGCTTCCTCCGAGGAGCTTTCGAGGCGGTGCGACACCC	512
Db	73	CC	14
QY	513	CC 514	
Db	13	CC 12	

US-RESULT 12
US-08-406-030A-3/C
Sequence 3, Application US/08406030A
Patent No. 6270989
GENERAL INFORMATION:
APPLICANT: Treco, Douglas A.
APPLICANT: Heartlein, Michael W.
APPLICANT: Hauge, Brian M.
APPLICANT: Selden, Richard F
TITLE OF INVENTION: Protein Production and Delivery
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C
STREET: Two Milita Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,030A
FILING DATE: 17-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,391
FILING DATE: 13-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,586
FILING DATE: 03-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/911,533
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,840
FILING DATE: 05-NOV-1991

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PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/789,188
FILING DATE: 05-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11704
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09627
FILING DATE: 05-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TT795-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4488 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-406-030A-3

Query Match          7.9%; Score 65; DB 3; Length 4488;
Best Local Similarity 48.8%; Pred. No. 8.7e-05;
Matches 243; Conservative 0; Mismatches 241; Indels 14; Gaps 2

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Oy	31	GATCGAATCTCCCTTGNCCCTCCCTCCCTCTCTCTCTGAGTCTGACACACCTCTCTC	90
Db	2804	GCTCCCCCTTCCCTCCCGGCCCTCCCTCTCTCCCTGCGGGTCCAGCCCTCTCTCCCC	2745
Oy	91	GCCTCCAGCTAAATCCAGCCGCAACGAT-----GACCCGACAGGGCTTCCGGAGCG	142
Db	2744	TCCCCACCCGCGAATCCGGGCGGTGTGTGTGCTGGTGGATCCGCCCGGGCTTACGGGCCCC	2685
Oy	143	AACGGCCCGGAAACCGACGACGATGCGGGCCGCGACAGAGAGCGC-----GCCGACGT	196
Db	2684	TCCGCCAGCCCGCCGCCGCCGCCCTTGTGTGAGAGAGAGAGGCCCCCGGCCGGGGCTCCG	2625
Oy	197	CCGCATATCTCCACCAAGAGCTGCAAGCGCGACGCGCGCGGAGCAGACTTGGATCTC	256
Db	2624	GCGCGGGGCATTAACACGGGCGGAGCGGGCGCGCCCGGGGGCAGTAAAGCCGCTTACGGCCCG	2565
Oy	257	CATCTCCGGGGAGCTTACAGACGATCAGACGCCCTTGCTGGCGACACACCGGGCGGAGAGT	316
Db	2564	GGTAGAGGCCGCCGCCGCCCGGCTCTCTCCGGCCGCTCTCCGCCGCCGCCGCCGCCGCC	2505
Oy	317	CCGCGTCATCACTCTCGCCCGGCGAGAGCGCACGCGACTTTCATGGCTTACCAACCGCGC	376
Db	2504	GCCGACTTGGGGCGGCCCGGACGAGCCCTTGGCGGGACATGCCCGGCCCGGCCCGGCCG	2445
Oy	377	CTCCGTGGCCCGGCTCTCTCCGCGCGCTTCTTGTGTGGCGCGCGCTTACACGACTACATGTCC	436
Db	2444	CCGAGCCCTCTCCCGCGGACGCGCCCGCGCGCGGCTCTCGGCTCTCGACATCCCGCT	2385
Oy	437	CCCGGCTCCGCGCACTTCGCGCGCGCTCTTTCGCGCAGCTCTCTTCGCGGGCGCTTTCGA	496
Db	2384	CCCTCCCTCCGCGCGGCTCCGGCGCGCTCTCTCTCTCCCTCCCGAGTGTCCGTTGC	2325
Oy	497	GCAGGTGGGACACACCCG 514	
Db	2324	GTCATGCGGAGCCCTCTCC 2307	

RESULT 13
 US-09-165-264-13/C
 ; Sequence 13, Application US/09165264
 ; Patent No. 6197510
 ; GENERAL INFORMATION:
 ; APPLICANT: Vinayagamorthy, Thuraiayah
 ; TITLE OF INVENTION: Multi-loci Genomic Analysis

FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 13
LENGTH: 320
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer sequence
US-09-165-264-13

Query Match 7.7%; Score 63.2; DB 3; Length 320;
Best Local Similarity 50.0%; Pred. No. 0.00015;
Matches 158; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 199 GCATGATCTCCACCAAGAGCTGACAGCGCGCGCGGAGCACTCTGATCTCCA 258
DB 318 GCATGCGCTGCTCCACGTCCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 259
QY 259 TCTCCGGGAGCGTCTACGACGTACGCGCTGCTGCGCCACACCGGGGCGAGGTCC 318
DB 258 CC 199
QY 319 CGCTATCACCTCGCGGCGAGAGCGACGCGCTTACGCGCTACACCGCGCT 378
DB 198 CC 139
QY 379 CGGTGCGCGCGCTCTCTCGCGCGCTTCTGTCGCGCGCTACGCACTACGTCCCGC 438
DB 138 CC 79
QY 439 CGGCTCGCGCGCACTTCCGCGCGCTCTCTGCGCGCACTTCTCTCGGCGCTTGTGAGC 498
DB 78 CC 19
QY 499 GCGTGGGACACCGCC 514
DB 18 CCCCCCCCCCCCCC 3

RESULT 14

US-08-804-227C-7
Sequence 7, Application US/08804227C
Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: Dehoff, Bradley S.
APPLICANT: Kuhnstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT, 1501
STREET, LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231

TELECOMMUNICATION INFORMATION:

TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

FEATURE:
NAME/KEY: CDS
LOCATION: 350..14002

FEATURE:
NAME/KEY: CDS
LOCATION: 14046..20036

FEATURE:
NAME/KEY: CDS
LOCATION: 20110..31284

FEATURE:
NAME/KEY: CDS
LOCATION: 31329..36071

FEATURE:
NAME/KEY: CDS
LOCATION: 36155..41830

US-08-804-227C-7

Query Match 7.7%; Score 63; DB 2; Length 44377;
Best Local Similarity 50.5%; Pred. No. 0.00028;
Matches 153; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 182 GGAGCGCGCGGAGCTCCGATGATCTCCACCAAGAGCTGACAGCGCGCGCGGAG 241
DB 30714 GAGCGCGGAGCGCTGCGGAGCGCGCTGCGCGAGCGGTGGCGAGCTCCGCGAGGA 30773
QY 242 CGACCTTGATCTCATCTCGGAGCGCTACGACGTACAGCGCTGCGCGCGCA 301
DB 30774 ACGCACGACCGGCTGCTGCGCGCTGCTGCGGACGCGCGCTGCTGCGCGCA 30833
QY 302 CCGGCGCGGAGCTCCGCTATACCTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 361
DB 30834 CTCCGCGCGGAGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 30893
QY 362 GGCCTACGACCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 421
DB 30894 GCGCGTGAAGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 30953
QY 422 CGACTACACTGCCCCCGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 481
DB 30954 GGTCTTGAACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 31013
QY 482 CGC 484
DB 31014 GGC 31016

RESULT 15

US-08-804-198-1
Sequence 1, Application US/08804198
Patent No. 5945320
GENERAL INFORMATION:
APPLICANT: Burgelt, Stanley G.
APPLICANT: Kuhnstoss, Stuart A.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL, 1138
STREET, LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA

ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,198
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 350..14002
FEATURE:
NAME/KEY: CDS
LOCATION: 14046..20036
FEATURE:
NAME/KEY: CDS
LOCATION: 20110..31284
FEATURE:
NAME/KEY: CDS
LOCATION: 31329..36071
FEATURE:
NAME/KEY: CDS
LOCATION: 36155..41830
US-08-804-198-1

Query Match 7.7%; Score 63; DB 2; Length 44377;
Best Local Similarity 50.5%; Pred. No. 0.00028;
Matches 153; Conservative 0; Mismatches 150; Indels 0; Gaps 0;
QY 182 GGACGGCGCGGAGTCCGATGATCTCCACCAAGAGCTGACGCCGCGCGCGCA 241
Db 30714 GGACGGCGGAGCTCGGCGAGCGCTGCGCGAGCGGTGCGGACTCTCCGCGAGGA 30773
QY 242 CGACTCTGGATCTCCATCTCGGGGAGCTCTAAGAGTCAGCGCCCTGCTGCCACCA 301
Db 30774 AGCCCAAGACGGGCTGCTCGGCTGCTGCGGCGAACAAGTGCGCGGTACTGGGCCACGG 30833
QY 302 CCCGGGGCGGAGTCCGCTCATCACCTTCGCGCGCCAGAGCGCACGAGCGCTTCAAT 361
Db 30834 CTCGCGCGCGAGAGTCCGCGCCGACCGCGCTTCGCGAGGTGCGGTTGACTCGCTCAC 30893
QY 362 GGGCTACCAACCCCGCTCCGTGCGCCCGCTCTCCGCGCTTCTGCTCGGCGGCTTCAAT 421
Db 30894 GGCCTGTGAACCTCGCAACCGAATGGCGGGGTCAACGAGGCTCCCGCACCTT 30953
QY 422 CGACTACACTGTCCCGCGCTTCGCGCGCACTTCGCGCGCTTCGCGGAGCTTCTCTC 481
Db 30954 GGTCTTGACACACCCCGCGCGGCTGTCTCTGCACTGAGCGGCTGCTGGCCCG 31013
QY 482 CGC 484
Db 31014 GGC 31016

Search completed: January 1, 2004, 00:05:52
Job time: 63.8386 secs

LENGTH: 1702 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1406
FEATURE:
NAME/KEY: CDS
LOCATION: 48..1406
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-029-756-26

Query Match 13.0%; Score 106.8; DB 14; Length 1702;
Best Local Similarity 62.3%; Pred. No. 2,6e-18;
Matches 187; Conservative 0; Mismatches 107; Indels 6; Gaps 1;

QY 204 ATCTCCACCAAGAGCTGCAGCGCAGCGCGGAGCAGCCTGTGATCTCCATCTCC 263
DB 72 ATACCGCGGAGGAGCTCCCGCCGACACAGTCCGCGCATCTGTGATCTCCATCAG 131
QY 264 GGGAGCTCTACGACGTACGCGCCCTGCTGCGCCACCACTCCGCGGCGAGTCCGCTC 333
DB 132 GGCAGAGCTACGACTGCTCTCGGTGGGCGGAGCAGCCCGCGCGAGTCCGCTC 191
QY 324 ATACCTCGCGCGCGGAGGAGCGGAGCGGCGGCTTCACTGCGCTTCACTGCGGCTC 383
DB 192 CTAGTGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 251
QY 384 CGCGCGCTCTCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 437
DB 252 TGGCGGATGTGATCGGCTCTTCAACGCGGCTACTACTCAAGAGTCTGAGTCTG 311
QY 438 CGCGCTCGCGGAGCTTCCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 497
DB 312 GAGATCTCCAGGACTCTCCGAGGCTTTGACGAGATGTCTGCGGCTCTCTCTCTG 371

RESULT 2
US-10-292-798-1513/c
Sequence 1513, Application US/10292798
Publication No. US2003023583A1
GENERAL INFORMATION:
APPLICANT: SIWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1513
LENGTH: 3163
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
LOCATION: source
FEATURE:
LOCATION: (1) ..(3163)
FEATURE:
NAME/KEY: CDS
LOCATION: (201) ..(2963)
FEATURE:
NAME/KEY: modified_base
LOCATION: (556) ..(655)
OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:
NAME/KEY: modified base
LOCATION: (658) ..(669)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (671) ..(697)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (704) ..(707)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (709) ..(736)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (739) ..(743)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (745) ..(747)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (750) ..(750)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (752) ..(752)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (754) ..(756)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (761) ..(761)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (763) ..(763)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (818) ..(818)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (843) ..(843)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (892) ..(892)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (897) ..(897)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (920) ..(920)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (941) ..(941)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (993) ..(993)
OTHER INFORMATION: a, t, c, g, unknown or other

NAME/KEY: modified base	
LOCATION: (995)..(995)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified base	
LOCATION: (1066)..(1067)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified base	
LOCATION: (1082)..(1084)	
OTHER INFORMATION: a, t, c, g, unknown or other	
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NAME/KEY: modified base	
LOCATION: (1105)..(1107)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified base	
LOCATION: (1130)..(1130)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified base	
LOCATION: (1147)..(1147)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified base	
LOCATION: (1162)..(1162)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified base	
LOCATION: (1202)..(1202)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified base	
LOCATION: (1233)..(1233)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified base	
LOCATION: (1247)..(1248)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified base	
LOCATION: (1261)..(1261)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified base	
LOCATION: (1485)..(1485)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified base	
LOCATION: (1500)..(1500)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified base	
LOCATION: (1544)..(1544)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified base	
LOCATION: (1601)..(1601)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified base	
LOCATION: (1605)..(1605)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified base	
LOCATION: (1635)..(1635)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified base	
LOCATION: (1637)..(1637)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified base	

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1 LOCATION: (1654)..(1654)
2 OTHER INFORMATION: a, t, c, g, unknown or other
3
4 FEATURE:
5 NAME/KEY: modified_base
6 LOCATION: (1674)..(1674)
7 OTHER INFORMATION: a, t, c, g, unknown or other
8
9 FEATURE:
10 NAME/KEY: modified_base
11 LOCATION: (1695)..(1695)
12 OTHER INFORMATION: a, t, c, g, unknown or other
13
14 FEATURE:
15 NAME/KEY: modified_base
16 LOCATION: (1852)..(1852)
17 OTHER INFORMATION: a, t, c, g, unknown or other
18
19 FEATURE:
20 NAME/KEY: modified_base
21 LOCATION: (1866)..(1965)
22 OTHER INFORMATION: a, t, c, g, unknown or other
23
24 FEATURE:
25 NAME/KEY: modified_base
26 LOCATION: (1968)..(1980)
27 OTHER INFORMATION: a, t, c, g, unknown or other

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Query Match	10.6%;	Score 87;	DB 12;	Length 3163;
Best Local Similarity	33.3%;	Pred. No. 4e-13;		
Matches 230;	Conservative 0;	Mismatches 461;	Indels 0;	Gaps 0;

Oy	32	ATCGATCTCCCTTNCACCCCTCCCTCCCTCTCTCCGAGTCTGACACACCCCTCCG	91
Db	2552	ACCC	2493
Oy	92	CGCTCGAGCTAAATCCAAGCCACCGATGCGCCGACAGGGCTTTGCGGACGGCAAGCGCC	151
Db	2492	CCCCCAAAACGCMCNCNCCCCCNCNCCCCCCCCCCCCCCCCCCCCCCCCCCCC	2433
Oy	152	GGAAGCCGAGCGCAATGCCGGCCGCGACAGAAAGCGCGCGAGCTCGCATGATCTCCAC	211
Db	2432	NCC	2372
Oy	212	CAAGAGCTGAGCGGACGCGCGCGCGGAGACGCTGTGATCTCAATCTCCGGGAGAGT	271
Db	2372	CCCNMNCNCCAAACNCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	2313
Oy	272	CTACGAGTCAAGCGCTGTGCTGCGCAACAACCGGGGGCGAGAGTCCGCTCATCACCT	331
Db	2312	CCCCCCCCCCCCCCCCNCMCMCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	2255
Oy	332	CGCGGCGCAGAGCGCACCGACGCTTTATGGCTTACACCGGCTTCGTGCGCGGCT	391
Db	2252	CNCCNCC	2193
Oy	392	CTTCCGCGGCTTTCTTGCTGGCGCGGCTTCAACGATACGTGCCCCCGGCTCCGCGA	451
Db	2192	CCNCC	2133
Oy	452	CTTCCGCGGCTCTGCGCAGACTCTCTCGCGGGGCTTTGAGGCGGTGCGACAC	511
Db	2132	CCNCCNCC	2073
Oy	512	CCCAAGTTCTGCTGTCGCAAGTCNGTGTCTTTGCGATGGGCTCTACTCTCTCG	571
Db	2072	NNNNCCNCCNNN	2013
Oy	572	CTGCTCAACACCGGGGACACATGTTGGCGGGGGCTCATTTGGCTTATCTGTCAGTCGG	631
Db	2012	CCNN	1953
Oy	632	GCTGATTGGCATACTCGGACACAATACAGGACCTGCTCAAGCTCTGAGTGG	691
Db	1952	NN	1893
Oy	692	CTGGGAATGCTNACGGCTCGATCCTGGG	722

Db 1892 NNNNNNNNNNNNNNNNNNNNNNNNNNTTG3 1862

RESULT 3

US-10-017-161-1857/C

Sequence 1857, Application US/10017161

Publication No. US20030143668A1

GENERAL INFORMATION:

APPLICANT: SUMA, MAKIKO

APPLICANT: ASAI, KIYOSHI

APPLICANT: AKIYAMA, YUTAKA

APPLICANT: ABEURATANI, HIROYUKI

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 084335/0152

CURRENT APPLICATION NUMBER: US/10/017,161

PRIOR FILING DATE: 2002-12-18

PRIOR APPLICATION NUMBER: JP 2001/246789

NUMBER OF SEQ ID NOS: 2430

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1857

LENGTH: 3163

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: source

LOCATION: (1)..(3163)

FEATURE:

NAME/KEY: CDS

LOCATION: (201)..(2963)

FEATURE:

NAME/KEY: modified_base

LOCATION: (658)..(669)

OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:

NAME/KEY: modified_base

LOCATION: (671)..(697)

OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:

NAME/KEY: modified_base

LOCATION: (704)..(707)

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FEATURE:

NAME/KEY: modified_base

LOCATION: (739)..(743)

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FEATURE:

NAME/KEY: modified_base

LOCATION: (745)..(747)

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FEATURE:

NAME/KEY: modified_base

LOCATION: (750)

OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:

NAME/KEY: modified_base

LOCATION: (752)

OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:

NAME/KEY: modified_base

LOCATION: (754)..(756)

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FEATURE:

NAME/KEY: modified_base

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FEATURE:

NAME/KEY: modified_base

LOCATION: (763)

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NAME/KEY: modified_base

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NAME/KEY: modified_base

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NAME/KEY: modified_base

LOCATION: (897)

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NAME/KEY: modified_base

LOCATION: (920)

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NAME/KEY: modified_base

LOCATION: (941)

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FEATURE:

NAME/KEY: modified_base

LOCATION: (993)

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FEATURE:

NAME/KEY: modified_base

LOCATION: (995)

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FEATURE:

NAME/KEY: modified_base

LOCATION: (1066)..(1067)

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FEATURE:

NAME/KEY: modified_base

LOCATION: (1082)..(1084)

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FEATURE:

NAME/KEY: modified_base

LOCATION: (1105)..(1107)

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FEATURE:

NAME/KEY: modified_base

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FEATURE:

NAME/KEY: modified_base

LOCATION: (1147)

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FEATURE:

NAME/KEY: modified_base

LOCATION: (1162)

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FEATURE:

NAME/KEY: modified_base

LOCATION: (1202)

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NAME/KEY: modified_base

LOCATION: (1233)

OTHER INFORMATION: a, t, c, g, unknown or other

FEATURE:

NAME/KEY: modified_base

LOCATION: (1247)..(1248)

OTHER INFORMATION: a, t, c, g, unknown or other

[illegible][illegible]

[illegible]

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RESULT 5
US-10-032-393-8/c
; Sequence 8, Application US/10032393
; Publication No. US20030027286A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Wall, Daniel
; APPLICANT: Gross, Molly
; TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
; FILE REFERENCE: ELITRA.010A
; CURRENT APPLICATION NUMBER: US/10/032,393
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/259,434
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 09/948,993
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 12739
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vector pPEBP1
US-10-032-393-8

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Query Match	10.4%	Score 85.6;	DB 15;	Length 12739;
Best Local Similarity	47.0%;	Pred. No. 1e-12;		
Matches 262;	Conservative 0;	Mismatches 296;	Indels 0;	Gaps 0;
35 CGATCTCCCCCTTANCCCTCCCTCCCTCCGAGTCTGACACACCCCTCTCGAGC 94				

[illegible]

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RESULT 6
US-10-292-798-1191/c
; Sequence 1191, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABRATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 08435/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1191
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
; FEATURE:
; LOCATION: (1)..(3133)
; FEATURE:
; LOCATION: (1)..(3133)
; NAME/KEY: CDS
; LOCATION: (201)..(2933)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(118)

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NAME/KEY: modified base
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FEATURE:
NAME/KEY: modified base
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LOCATION: (229)..(229)
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FEATURE:
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LOCATION: (231)..(232)
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FEATURE:
NAME/KEY: modified base
LOCATION: (238)..(239)
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FEATURE:
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FEATURE:
NAME/KEY: modified base
LOCATION: (265)..(270)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (272)..(276)
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FEATURE:
NAME/KEY: modified base
LOCATION: (282)..(283)
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FEATURE:
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FEATURE:
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FEATURE:	
NAME/KEY: modified_base	
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OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (229)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (231) .. (232)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (238) .. (239)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (242)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (245)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (248) .. (260)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (265) .. (270)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (272) .. (276)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (278)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (282) .. (283)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (287) .. (290)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (302) .. (306)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	

LOCATION: (311) ..(313)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (323) ..(324)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (336) ..(341)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (345) ..(353)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (365) ..(368)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (370)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (374) ..(375)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (379) ..(385)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (387) ..(388)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (390) ..(393)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
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FEATURE:	
NAME/KEY: modified_base	
LOCATION: (397)	
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FEATURE:	
NAME/KEY: modified_base	
LOCATION: (400) ..(402)	
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NAME/KEY: modified_base	
LOCATION: (409)	
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FEATURE:	
NAME/KEY: modified_base	

Query Match	10.3%	Score 84.8	DB 13	Length 3133
Best Local Similarity	34.1%	Pred. No. 1.5e-12		
Matches 219	0	Mismatches 424	Indels 0	Gaps 0

[illegible]

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FEATURE:
NAME/KEY: modified base
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FEATURE:
NAME/KEY: modified base
LOCATION: (168) ..(168)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (172) ..(172)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (189) ..(189)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (191) ..(193)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (196) ..(196)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:

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2 NAME/KEY: modified_base
3 LOCATION: (214) ..(214)
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5 FEATURE:
6 NAME/KEY: modified_base
7 LOCATION: (218) ..(218)
8 OTHER INFORMATION: a, t, c, g, unknown or other
9 FEATURE:
10 NAME/KEY: modified_base
11 LOCATION: (221) ..(221)
12 OTHER INFORMATION: a, t, c, g, unknown or other
13 FEATURE:
14 NAME/KEY: modified_base
15 LOCATION: (225) ..(226)
16 OTHER INFORMATION: a, t, c, g, unknown or other
17 FEATURE:
18 NAME/KEY: modified_base
19 LOCATION: (229) ..(329)
20 OTHER INFORMATION: a, t, c, g, unknown or other
21 FEATURE:
22 NAME/KEY: modified_base
23 LOCATION: (232) ..(232)
24 OTHER INFORMATION: a, t, c, g, unknown or other
25 FEATURE:
26 NAME/KEY: modified_base
27 LOCATION: (235) ..(236)
28 OTHER INFORMATION: a, t, c, g, unknown or other
29 FEATURE:
30 NAME/KEY: modified_base
31 LOCATION: (246) ..(246)
32 OTHER INFORMATION: a, t, c, g, unknown or other
33 FEATURE:
34 NAME/KEY: modified_base
35 LOCATION: (248) ..(252)
36 OTHER INFORMATION: a, t, c, g, unknown or other
37 FEATURE:
38 NAME/KEY: modified_base
39 LOCATION: (256) ..(257)

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?	LOCATION: (261)..(263)
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?	FEATURE:
?	NAME/KEY: modified_base
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?	FEATURE:
?	NAME/KEY: modified_base
?	LOCATION: (283)..(285)
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?	FEATURE:
?	NAME/KEY: modified_base
?	LOCATION: (298)..(300)
?	OTHER INFORMATION: a, t, c, g, unknown or other
?	FEATURE:
?	NAME/KEY: modified_base
?	LOCATION: (302)..(302)
?	OTHER INFORMATION: a, t, c, g, unknown or other
?	FEATURE:
?	NAME/KEY: modified_base
?	LOCATION: (307)..(307)
?	OTHER INFORMATION: a, t, c, g, unknown or other
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?	NAME/KEY: modified_base
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?	FEATURE:
?	NAME/KEY: modified_base
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?	FEATURE:
?	NAME/KEY: modified_base
?	LOCATION: (339)..(339)
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?	NAME/KEY: modified_base
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?	OTHER INFORMATION: a, t, c, g, unknown or other
?	FEATURE:
?	NAME/KEY: modified_base
?	LOCATION: (357)..(357)
?	OTHER INFORMATION: a, t, c, g, unknown or other
?	FEATURE:
?	NAME/KEY: modified_base
?	LOCATION: (359)..(359)
?	OTHER INFORMATION: a, t, c, g, unknown or other
?	FEATURE:
?	NAME/KEY: modified_base
?	LOCATION: (362)..(362)
?	OTHER INFORMATION: a, t, c, g, unknown or other

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1  FEATURE:
2  NAME/KEY: modified base
3  LOCATION: (365)..(365)
4  OTHER INFORMATION: a, t, c, g, unknown or other
5  FEATURE:
6  NAME/KEY: modified base
7  LOCATION: (367)..(368)
8  OTHER INFORMATION: a, t, c, g, unknown or other
9  FEATURE:
10 NAME/KEY: modified base
11 LOCATION: (370)..(373)
12 OTHER INFORMATION: a, t, c, g, unknown or other
13 FEATURE:
14 NAME/KEY: modified base
15 LOCATION: (376)..(378)
16 OTHER INFORMATION: a, t, c, g, unknown or other

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Query Match	9.5%	Score 78.2	DB 12	Length 5452
Best Local Similarity	35.1%	Pred. No. 8	2e-11	
Matches 189, Conservative	0	Mismatches 345	Indels 0	Gaps 0

[illegible]

RESULT 9
US-10-017-161-1481/C
Sequence 1481, Application US/10017161
Publication No. US20030143668A1
GENERAL INFORMATION:
APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABDULHAKIM, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 08435/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIORITY APPLICATION NUMBER: JP 2001/246789
PRIORITY FILING DATE: 2001-06-18

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NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1481
LENGTH: 5452
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
LOCATION: source
FEATURE:
LOCATION: (1)..(5452)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(5252)
FEATURE:
NAME/KEY: modified_base
LOCATION: (1)..(140)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (145)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (147)..(148)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (162)
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FEATURE:
NAME/KEY: modified_base
LOCATION: (165)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (168)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
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[illegible]

Oy		467	CGGACACTCTCCTCCGGAGGAGCTTTCGTGAAGCGGTGGACACCCCCAAGTCTCTGC	526
Dd		4437	CNCNNNNNNNCCNCCCCCCCCCCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCC	4378
Oy		527	GTCGCAAAATCNGTGCTTTCTGTGATGGAGCTCTACTGCTCTCGCTGTCAACACC	584
Dd		4377	CCCCNNNNNNNNNNNNNNCCCNCCCCGCCNCCNCCNCCNCCNCCNCCNCCNCC	4320
 RESULT 10 US-09-804-682-29 Sequence 29, Application US/09804682 Patent No. US20020106765A1 GENERAL INFORMATION: APPLICANT: Kinders, Robert TITLE OF INVENTION: PAL-18 POLYPEPTIDES, NUCLEIC ACIDS TITLE OF INVENTION: CODING THE SAME AND METHODS FOR SCREENING FOR OR FILE REFERENCE: 130001.406 CURRENT APPLICATION NUMBER: US/09/804,682 CURRENT FILING DATE: 2001-03-12 NUMBER OF SEQ ID NOS: 174 SOFTWARE: FastSeq for Windows Version 4.0 SEQ ID NO 29 LENGTH: 1064 TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc feature LOCATION: 5, 6, 16, 21, 24, 25, 33, 39, 72, 110, 209, 214, 231, 232, LOCATION: 235, 237, 238, 244, 245, 246, 256, 282, 292, 297, 306, 319, LOCATION: 321, 323, 330, 334, 340, 349, 354, 355, 363, 372, 376, 378, LOCATION: 397, 405, 432, 437, 454, 455, 457, 458, 459, 468, 470 OTHER INFORMATION: n = A,T,C or G NAME/KEY: misc feature LOCATION: 485, 487, 488, 494, 496, 499, 511, 524, 527, 552, 557, 562, LOCATION: 583, 600, 611, 613, 623, 624, 652, 654, 674, 681, 687, 691, LOCATION: 694, 701, 713, 716, 720, 721, 725, 731, 734, 735, 739, 743, LOCATION: 744, 781, 782, 785, 789, 799, 803, 821, 823, 847, 852 OTHER INFORMATION: n = A,T,C or G NAME/KEY: misc feature LOCATION: 858, 878, 884, 886, 896, 897, 901, 917, 926, 932, 939, 948, LOCATION: 957, 961, 965, 981, 993, 1001, 1002, 1005, 1011, 1018, LOCATION: 1043, 1047, 1049, 1051, 1054, 1056 OTHER INFORMATION: n = A,T,C or G US-09-804-682-29				
 Query Match 9.4%; Score 77.2; DB 10; Length 1064; Best Local Similarity 4.0%; Pred. No. 1.3e-10; Matches 238; Conservative 0; Mismatches 312; Indels 4; Gaps 1.				
Oy		39	CTCCCCTTNCCTCCCTCTCTCTCTCTGAGTCTGATCACACCCTCTCGGAGCTCA	98
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Oy		99	GCTAATTCACAGCCAGCATGGCCCGACGCGGCTTGGCGACGGAAGCGCGCGGAGAGCC	158
Dd		575	CCCCCTCTNTTCTCCCTCTCCCTCCCTCCCTCCCTCCCTCCNCCNCCNCCNCCNCCCTCC	634
Oy		159	GACGCAATGCGGCGCGGACAGAAGAGCGCGCGAGCTGCGATGATTTCCACAAGAGG	218
Dd		635	TCCCCCCCCCCCCCCCCCNCCNCCCCCTCTCCGCCNCCNCCNCCNCCNCCNCCNCCNCC	694
Oy		219	CTGAGGCGACGCGCGCGCGGAGACCTTGATTTTCATTTCCGGGAGAGTCTAGAC	278
Dd		695	CCCCCNCNCCCTTACCTTCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC	754
Oy		279	GTAAGGCGCTGCGGCGGACACACCGGAGGAGGATCCCGCTATACACCTCGCGGCG	338
Dd		755	CTACCCCTCTTCTCCCTCTCCCTCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC	810

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NAME/KEY: modified_base
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NAME/KEY: modified_base
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FEATURE:
NAME/KEY: modified_base


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; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDES ENCODING THE FKBP GENE OF THE FK-520 POLYKETIDE SYNTH
; TITLE OF INVENTION: GENE CLUSTER
; FILE REFERENCE: 30062-20026.11
; CURRENT APPLICATION NUMBER: US/09/940,316B
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/410,551
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 77536
; TYPE: DNA
; ORGANISM: Streptomyces hygroscopicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52275) ... (71465)
; US-09-940-316B-1

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Query Match 8.6%; Score 70.8; DB 13; Length 77536;

Best Local Similarity 49.2%; Pred. No. 8.5e-09; Matches 186; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

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QY 135 GCGAGCGCAACGCGCGCGAAGCGCAATGCGCGCGCGCAAGAGAGCGCGCGAC 194
DB 14484 GTGACGACATGCGCGCGAGTCCGCGCGCGCGCGCAATGAGCGCGCGAGACACAC 14425
QY 195 GTCCGCGATGATCTTCACCAAGAGCTGACAGCGCGCGCGCGCGAGCACTTGATC 254
DB 14424 GCGAAGATGCTCTCAAGGATCCCGCGCGCGCGCGCGAGCGCGCGCGCGCGATCACC 14365
QY 255 TCATCTCCGCGGAGCGTCTAGAGCTACAGCGCGCGCGCGCGCGCGCGCGCGAG 314
DB 14364 GCGGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14305
QY 315 GTCCGCGCTATCACTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 374
DB 14304 CTCCTCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14245
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DB 14244 GCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14185
QY 435 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 494
DB 14184 TTCCACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14125
QY 495 GAGCGCGTGGCGACACCC 512
DB 14124 GACACGCTCTCAACACC 14107

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RESULT 15

US-10-184-644-332/C

; Sequence 332, Application US/10184644

; Publication No. US20030044930A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

```

; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 332
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-184-644-332

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Query Match 8.6%; Score 70.4; DB 15; Length 520;

Best Local Similarity 26.9%; Pred. No. 7.5e-09; Matches 84; Conservative 61; Mismatches 167; Indels 0; Gaps 0;

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QY 211 CCAAGAGCTGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 270
DB 434 YCYNSSGB.YBBSN.CY.CM.CMBC.CSSCMBC.HCM.CT.C.TCM.CT.C.SC.CM 375
QY 271 TCTAGAGCTGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 330
DB 374 BCT.C.BCS.CMYC.C.CAHCMSCM.CATC.SC.SC.CTYC.SCTSC.CMTC.DCB 315
QY 331 TCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 390
DB 314 TC..C.BC..C.C.HCMTC..CT.C.C.YC.HCMSC.TC..CKBCTHMKCYHMSC. 255
QY 391 TCCTCGCGCGCTCTCTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 450
DB 254 .C.HCM.CMCA.CM.C.CCHCMSCM.C.C.ACMTC.MC.TC..C.CT.CMBC..C. 195
QY 451 ACTTCGCGCGCGCTCTCTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 510
DB 194 .CS.CATCHYCKTMTCM.T..C..C.TC.KCKTMDC..C.TC..CM.Y.KC.N.A.NH 135
QY 511 CCGCAAGTTCCT 522
DB 134 BY..D.DSBYB 123

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Search completed: January 1, 2004, 05:19:45
Job time : 216.271 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 : Search time 10.4957 Seconds
(without alignments)
1724.030 Million cell updates/sec

Title: US-09-857-524b-17

Perfect score: 592
Sequence: 1 MPAAKADADVMISTKEIQ.....ADFRLLAQLSSAGHFERYG 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	592	100.0	114	21	AA71556
2	588	99.3	469	21	AA71555
3	501	84.6	462	21	AA71552
4	274.5	46.4	448	21	AA71551
5	274.5	46.4	458	21	AA71548
6	271.5	45.9	450	21	AA71554
7	269.5	45.5	450	24	ABG73418
8	266	44.9	452	23	AAU79851
9	266	44.9	452	24	ABG73416

10	261	44.1	448	24	ABG73417
11	258	43.6	448	19	AA98455
12	258	43.6	448	17	AA67471
13	258	43.6	448	20	AA98430
14	258	43.6	448	21	AA951349
15	258	43.6	448	23	AAU79830
16	258	43.6	448	24	ABG73095
17	255.5	43.2	449	21	AA629290
18	250.5	42.3	449	20	AA951333
19	249	42.1	446	21	AA985122
20	236.5	39.9	449	21	AA607392
21	236.5	39.9	449	21	AA953861
22	236.5	39.9	449	21	AA951334
23	236.5	39.9	517	21	AA607391
24	195	32.9	477	23	ABG73600
25	195	32.9	477	23	AB984275
26	193.5	32.7	459	23	AAE22063
27	192	32.4	53	21	AA983236
28	175.5	29.6	135	21	AA623317
29	173	29.2	53	21	AA983242
30	169.5	28.6	134	21	AA607989
31	167.5	28.3	126	21	AA623318
32	166.5	28.1	140	21	AA624685
33	166.5	28.1	140	21	AA637798
34	166.5	28.1	200	21	AA654881
35	164	27.7	904	14	AA641757
36	162.5	27.4	95	21	AA6319062
37	161.5	27.3	873	23	AB606014
38	161	27.2	453	24	AAE31900
39	160.5	27.1	116	21	AA632671
40	160.5	27.1	509	24	AAU07348
41	159.5	26.9	801	21	AA638590
42	159.5	26.9	905	21	AA638589
43	159.5	26.9	917	21	AA638588
44	157.5	26.6	126	21	AA611407
45	157.5	26.6	126	21	AA611408

ALIGNMENTS

RESULT 1	
AA71556	
AA71556 standard; Protein; 114 AA.	
AA71556;	
12-OCT-2000 (first entry)	
Wheat sphingolipid desaturase #2.	
Wheat; sphingolipid desaturase; membrane-bound desaturase;	
transgenic plant; fatty acid.	
Triticum aestivum.	
WO200032790-A2.	
08-JUN-2000.	
02-DEC-1999; 99WO-US28589.	
03-DEC-1998; 98US-0110784.	
(DUPO) DU PONT DE NEMOURS & CO E I.	
Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;	
WPI, 2000-412336/35.	
N-PSDB; AAD01354.	
Polynucleotide encoding delta-6 desaturase enzyme useful for producing	
transgenic plants and for producing antibodies specific to which is	

PT useful for screening cDNA expression libraries -
 XX
 PS Claim 10; Page 57; 57pp; English.
 XX
 CC The present sequence is a sphingolipid desaturase
 CC from clone wrel.pk004.c7 isolated from wheat etiolated
 CC seedling root cDNA library, wrel.
 CC The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is also useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
 CC
 XX
 SQ Sequence 114 AA;
 Query Match 100.0%; Score 592; DB 21; Length 114;
 Best Local Similarity 100.0%; Pred. No. 5,5e-62;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPASKDAADVMTSTKELOAHAAADDLWISGDDYDVTWMLRHHPGSEVPLITLAGOD 60
 DB 1 MPASKDAADVMTSTKELOAHAAADDLWISGDDYDVTWMLRHHPGSEVPLITLAGOD 60
 QY 61 ATDAFMAHPPSVRPLLRFFVGRITDYTVPPASADFRRLAQLSSAGLFEYRG 114
 DB 61 ATDAFMAHPPSVRPLLRFFVGRITDYTVPPASADFRRLAQLSSAGLFEYRG 114
 RESULT 2
 AA71555
 ID AA71555 standard; Protein; 469 AA.
 AC AA71555;
 XX
 DT 12-OCT-2000 (first entry)
 XX
 DE Wheat sphingolipid desaturase #1.
 XX
 KM Wheat; sphingolipid desaturase; membrane-bound desaturase;
 KM transgenic plant; fatty acid.
 XX
 OS Triticum aestivum.
 OS
 PN WO200032790-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 02-DEC-1999; 99WO-US28589.
 XX
 PT 03-DEC-1998; 98US-0110784.
 PR
 XX
 PS (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;
 XX
 DR WPI; 2000-412336/35.
 DR N-PSDB; AAD01353.
 XX
 PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries -
 XX
 PS Example 4; Page 49-50; 57pp; English.
 XX
 CC The present sequence is a sphingolipid desaturase
 CC from clone wrel.pk004.c7;is isolated from wheat etiolated
 CC seedling root cDNA library, wrel.
 CC The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is also useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is useful as primer or probe for screening cDNA libraries to

CC isolate desired full-length cDNA clones.
 XX
 SQ Sequence 469 AA;
 Query Match 99.3%; Score 588; DB 21; Length 469;
 Best Local Similarity 99.1%; Pred. No. 9,4e-61;
 Matches 113; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPASKDAADVMTSTKELOAHAAADDLWISGDDYDVTWMLRHHPGSEVPLITLAGOD 60
 DB 17 MPASKDAADVMTSTKELOAHAAADDLWISGDDYDVTWMLRHHPGSEVPLITLAGOD 76
 QY 61 ATDAFMAHPPSVRPLLRFFVGRITDYTVPPASADFRRLAQLSSAGLFEYRG 114
 DB 77 ATDAFMAHPPSVRPLLRFFVGRITDYTVPPASADFRRLAQLSSAGLFEYRG 130
 RESULT 3
 AA71552
 ID AA71552 standard; Protein; 462 AA.
 AC AA71552;
 XX
 DT 12-OCT-2000 (first entry)
 XX
 DE Corn sphingolipid desaturase.
 XX
 KM Corn; sphingolipid desaturase; membrane-bound desaturase;
 KM transgenic plant; fatty acid.
 XX
 OS Zea mays.
 OS
 PN WO200032790-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 02-DEC-1999; 99WO-US28589.
 XX
 PT 03-DEC-1998; 98US-0110784.
 PR
 XX
 PS (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Cahoon EB, Cahoon RE, Hiltz WD, Kinney AJ;
 XX
 DR WPI; 2000-412336/35.
 DR N-PSDB; AAD01350.
 XX
 PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries -
 XX
 PS Claim 10; Page 42-43; 57pp; English.
 XX
 CC The present sequence is a sphingolipid desaturase
 CC from clone cdeic.pk001.08;is isolated from corn developing
 CC embryo cDNA library, cdeic. The present sequence is useful for producing
 CC transgenic plants having altered levels of sphingolipid desaturase which
 CC in turn would alter the fatty acid composition. The enzyme is also useful
 CC for producing polyclonal or monoclonal antibodies. The polynucleotide
 CC is useful as primer or probe for screening cDNA libraries to
 CC isolate desired full-length cDNA clones.
 CC
 XX
 SQ Sequence 462 AA;
 Query Match 84.6%; Score 501; DB 21; Length 462;
 Best Local Similarity 83.2%; Pred. No. 1,8e-50;
 Matches 94; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
 QY 2 PAASKDAADVMTSTKELOAHAAADDLWISGDDYDVTWMLRHHPGSEVPLITLAGOD 61
 DB 11 PGDAAGADVMTSTKELOAHAAADDLWISGDDYDVTWMLRHHPGSEVPLITLAGOD 70
 QY 62 TDAFMAHPPSVRPLLRFFVGRITDYTVPPASADFRRLAQLSSAGLFEYRG 114

Db 71 TDAFAAHPSPARPLRRFFVGRSLSDYAVSPASADYRRLAQLSSAGLFFRVG 123

RESULT 4
AA71551
ID AA71551 standard; Protein; 448 AA.

XX AC AA71551;
XX DT 12-OCT-2000 (first entry)

XX DE Florida bitterbush delta-6 fatty acid desaturase.

XX KM Florida bitterbush; delta-6 fatty acid desaturase; tartronic acid;
XX KM transgenic plant; fatty acid; membrane-bound desaturase.

XX OS Picramnia pentandra.

XX PN WO200032790-A2.

XX PD 08-JUN-2000.

XX PF 02-DEC-1999; 99WO-US28589.

XX PR 03-DEC-1998; 98US-0110784.

XX PA (DUPO) DU PONT DE NEMOURS & CO E. I.

XX PI Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;

XX PS WPI; 2000-412336/35.

XX DR N-PSDB; AAD01349.

XX PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
XX PT transgenic plants and for producing antibodies specific to which is
XX PT useful for screening cDNA expression libraries

XX PS Claim 10; Page 40-41; 57pp; English.

XX CC The present sequence is a delta-6 fatty acid desaturase protein sequence
XX CC from clone pps.p0011.d5, is isolated from Florida bitterbush developing
XX CC seed cDNA library, pps. The delta-6 desaturase enzyme catalyzes the
XX CC formation of tartronic acid, a fatty acid that has a triple bond at the
XX CC delta-6 carbon. The present sequence is useful for producing
XX CC transgenic plants having altered levels of delta-6 desaturase which
XX CC in turn would alter the fatty acid composition. The enzyme is also useful
XX CC for producing polyclonal or monoclonal antibodies. The polynucleotide
XX CC is useful as primer or probe for screening cDNA libraries to
XX CC isolate desired full-length cDNA clones.

XX SO Sequence 448 AA;

Query Match 46.4%; Score 274.5; DB 21; Length 448;
Best Local Similarity 51.0%; Pred. No. 9, 8e-24;

Matches 52; Conservative 16; Mismatches 33; Indels 1; Gaps 1;

QY 14 ISCKEIOAADAADLWISISGDYVDTVMRHHGGEVPLITLAGODATDAFMAVHPV 73

DB 8 ISQADIAKAKQPDLMISIKGVYDLSKWTKEHPGELPLSPAGODVDATFAVHPGTA 67

QY 74 RPLLRFPVVG-RLTDYVPPASADFRRLAQLSSAGLFFRVG 114

DB 68 WQYLDKFFFTGYVQDYVSEMSKDYRRLLVSEFSKMGLEFKTPG 109

RESULT 5
AA71548
ID AA71548 standard; Protein; 458 AA.

XX AC AA71548;

XX DT 27-APR-2000 (first entry)

XX DE Sphingolipid desaturase protein.

XX KM Sphingolipid desaturase; sld; sphingobase; ceramide; capnoid;

XX KM transgenic plant; crop plant; delta-8-unsaturated long-chain base;

XX KM tolerance; resistance; soil salinity; ion stress; toxicity; drought;

XX KM cold; frost; phytopathogenic microorganism; flowering time; cosmetic;

XX KM pharmaceutical; food; chemical raw material.

XX OS Unidentified.

XX PN DE19828850-A1.

XX PD 30-DEC-1999.

XX PF 27-JUN-1998; 98DE-1028850.

XX PR 27-JUN-1998; 98DE-1028850.

XX PA (GVSE-) GVS GES ERWERB & VERM LANDWIRTSCHAFTLICH.

XX PI Heinz E, Zaehring U, Schmidt H, Sperling P;

XX DR WPI; 2000-127549/12.

XX DR N-PSDB; AA244851.

XX PT New sphingolipid desaturase that selectively introduces double bond
XX PT into sphingolipids and capnoids

XX PS Disclosure; Fig 15; 62pp; German.

XX CC This invention describes a novel sphingolipid desaturase that selectively
XX CC introduces a double bond into the sphingobase of the ceramide residue of
XX CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
XX CC desaturase, or a vector containing the DNA sequence, can be used to
XX CC produce transgenic plants, especially crop plants, with an increased or
XX CC decreased delta-8-unsaturated long-chain base content or an altered
XX CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
XX CC compensate for a delta-8-unsaturated long-chain base deficiency, to
XX CC exclude production of delta-8-unsaturated bases, to increase tolerance
XX CC or resistance to soil salinity, ion stress or toxicity, drought, wet
XX CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
XX CC alter size growth and flowering time. Cells, transgenic organisms or
XX CC plants containing the DNA sequence can be used to produce sphingolipids
XX CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
XX CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
XX CC materials. This sequence represents a sphingolipid desaturase protein
XX CC described in the method of the invention.

XX SO Sequence 458 AA;

Query Match 46.4%; Score 274.5; DB 21; Length 458;
Best Local Similarity 50.0%; Pred. No. 1e-23;

Matches 52; Conservative 19; Mismatches 32; Indels 1; Gaps 1;

QY 12 RMISTKEIOAADAADLWISISGDYVDTVMRHHGGEVPLITLAGODATDAFMAVHP 71

DB 17 KYTTSKELKRNPNMDLWISIKGVYNTVMKKEHPGGAFLINLAGODVDATFAVHPG 76

QY 72 SVRPLLRFPVVG-RLTDYVPPASADFRRLAQLSSAGLFFRVG 114

DB 77 TWMKLDKLFYGYHLKDYVSDISRDYRLASLPAKAGFEKKG 120

RESULT 6
AA71554
ID AA71554 standard; Protein; 450 AA.

XX AC AA71554;

XX DT 12-OCT-2000 (first entry)

XX DE Soybean sphingolipid desaturase #2.

```
XX Soybean; sphingolipid desaturase; membrane-bound desaturase;  
KW transgenic plant; fatty acid.  
OS Glycine max.  
FN WO200032790-A2.  
PD  
PP 08-JUN-2000.  
PR 02-DEC-1999; 99WO-US28589.  
PS 03-DEC-1998; 98US-0110784.  
RA (DUPO ) DU PONT DE NEMOURS & CO E I.  
RI Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ,  
DR MPI: 2000-412336/35.  
RN N-PADB: AAD01352.  
RT Polynucleotide encoding delta-6 desaturase enzyme useful for producing  
PT transgenic plants and for producing antibodies specific to which is  
PX useful for screening cDNA expression libraries -  
PY  
PS Claim 10; Page 47-48; 57pp; English.  
CC The present sequence is a sphingolipid desaturase  
CC from clone ssl.pK0017.b4.fis isolated from soybean seedling CDNA  
CC library, ssl. The present sequence is useful for producing  
CC transgenic plants having altered levels of sphingolipid desaturase which  
CC in turn would alter the fatty acid composition. The enzyme is also useful  
CC for producing polyclonal or monoclonal antibodies. The polynucleotide  
CC is useful as primer or probe for screening cDNA libraries to  
CX isolate desired full-length CDNA clones.  
SQ Sequence 450 AA:  
  
Query Match 45.9%; Score 271.5; DB 21; Length 450;  
Best Local Similarity 48.1%; Pred.No. 2,2e-23;  
Matches 50; Conservative 21; Mismatches 32; Indels 1; Gaps 1
```

OY 12 RMISKELQAHAAADDLMWISGVDVDTTPMLRHHPGEVPRLITLAGDAPAFMAHYRP 71
. : . : . : | | | | | : : . : . : | | | | | : : | | | | |
DY 9 KYTSEELEKHNGKEGDLMWSIQKYNNSDWKHEHFGDVDPLSNLAGDDVTDAFTAYHG 68
OY 72 SVRPLELRFPVG-RLTDTVTPPASDPFRLLAQLSSAGLFERVG 114
DB 69 TAWSHLEKFPTYGHLSDFPKVSFVSDVKKLASEFKGLFLFCYG 112

RESULT 7
ABG73418
ID ABG73418 standard; Protein; 450 AA.

AC ABG73418;
XX
DE 16-APR-2003 (first entry)
DT XX
Evening primrose delta-6-desaturase #2.
DE
Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower; soybean;
KW maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
KM octadecatrienoic acid; alpha-linolenic acid; delta-15-desaturase;
evening primrose.
XX
OOenothera biennis.
OS
US2002108147-A1.
XX
PN 08-AUG-2002.
FD
21-DEC-2001; 2001US-0029756.
PF

XX		PR	13-OCT-1992;	92US-0959952.
XX		BR	19-SEP-1997;	97US-0934254.
XX		PR	10-OCT-1991;	91US-0774475.
XX		PR	08-JAN-1992;	92US-0817919.
XX		PR	14-SEP-1994;	94US-0307382.
XX		PR	28-JAN-1997;	97US-0789936.
PA	(THOM/) THOMAS T L.			
XX		P1	Thomas TL;	
XX		DR	WPI; 2003-066659/06.	
XX		PT	Novel nucleic acid encoding evening primrose delta-6-desaturase, useful for producing plant with increased gamma linolenic acid content, and for inducing octadecatetraenoic acid production in plant -	
PS	Example 15; Fig 11; 55pp; English.			
XX		CC	The invention relates to a nucleic acid encoding an evening primrose delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful for producing a plant (such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant) with increased gamma-linolenic acid (GLA) content by transforming a plant cell with the nucleic acid or vector and regenerating a plant with increased GLA content from the plant cell, for inducing or increasing production of GLA in an organism lacking in or producing low levels of GLA and for inducing production of octadecatetraenoic acid in at least one of a plant deficient or lacking in or producing low levels of octadecatetraenoic acid, a bacterium which produces alpha-linolenic acid or a bacterium which exhibits a delta-15-desaturase activity on a GLA substrate. This sequence represents an evening primrose delta-6-desaturase polypeptide.	
SQ	Sequence 450 AA;			
OY	Query Match 45.5%; Score 269.5; DB 24; Length 450; Best Local Similarity 51.0%; Pred. No. 3.8e-23; Matches 53; Conservative 17; Mismatches 33; Indels 1; Gaps 1;			
DG	12 RMISTKELQAAADDLTISIGPVVTVPMILHHPGSEVPRLTLTGODATDAFMAYNRP 71 7 KYTTAEPLRRRNKSGDLMWSIQGVYDVSRMAAHNPGEVPLMLAGQDVTDAFIATNPG 66			
DG	72 SVREPLRRFFVG-RLTDTYTPPASADFRLLLAQLSAGLPERVG 114 67 TAMRHLDPLFTGYLYLKDFEVSEISKDYRRLINEMSRSGIREKKG 110			
RESULT 8				
ID	AU79851 standard; Protein: 452 AA.			
AC	AU79851;			
XX				
DT	15-JUL-2002 (first entry)			
DE	Evening primrose delta6-desaturase.			
KX	delta6-desaturase; sunflower; soybean; maize; tobacco;			
KW	peanut; carrot; oil seed rape; gamma linolenic acid; GLA;			
XX	chilling tolerance; evening primrose.			
OS	Oenothera biennis.			
PN	US6355861-B1.			
PD	12-MAR-2002.			
PF	19-SEP-1997; 97US-0934254.			
PR	13-OCT-1992; 92US-0959952.			

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PR 10-OCT-1991; 91US-0774475.
PR 08-JAN-1992; 92US-0817919.
PR 14-SEP-1994; 94US-0307382.
PR 28-JAN-1997; 97US-0789936.
XX
PA (RHON ) RHONE-POULENC AGROCHIMIE.
XX
PI Thomas TL;
XX
DR WPI; 2002-380944/41.
DR N-PSDB; ABX49503.
XX
PT Novel nucleic acid encoding evening primrose delta6-desaturase which
PT converts linoletic acid to gamma linoletic acid useful for producing
PT gamma linoletic acid in transgenic plant or bacteria
XX
PS Claim 3; Column 45-48; 53pp; English.
XX
CC The invention describes an isolated nucleic acid encoding an evening
CC primrose delta6-desaturase. The nucleic acid and a vector expressing the
CC nucleic acid are useful for producing a plant such as sunflower, soybean,
CC maize, tobacco, peanut, carrot or oil seed rape plant, with increased
CC gamma linoletic acid (GLA) content, and also for inducing or increasing
CC production of GLA in a bacteria or plant deficient, lacking in or
CC producing low levels of GLA. The nucleic acid is also useful for inducing
CC chilling tolerance in plants. This is the amino acid sequence of the
CC evening primrose delta6 desaturase involved in the production of gamma
CC linoletic acid.
XX
SQ Sequence 452 AA;
XX
Query Match 44.9%; Score 266; DB 23; Length 452;
Best Local Similarity 49.5%; Pred. No. 1e-22;
Matches 52; Conservative 18; Mismatches 33; Indels 2; Gaps 1;
QY 12 RMISTKELOAHAAADDLWISISGVDVTPMLRHHHGGEVPLTTLAGODATDAFMAYHPP 71
DB 7 KXITMEDLRHHKSGDLWISIGKYYDCSRMAHEHGGEVPLSLAGQVDTAFIYHNG 66
QY 72 SVRPLLRFFVG-RITDYTPPASADPFRLLAQSSAGLPERVG 114
DB 67 TAWRHLDPLFTGYYYLKDFEVEISIKDYRRLNEMSRSGIFPKKG 111
XX
RESULT 9
ABG73416
ID ABG73416 standard; Protein; 452 AA.
XX
AC ABG73416;
XX
DT 16-APR-2003 (first entry)
XX
DE Evening primrose delta-6-desaturase #1.
XX
KW Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower; soybean;
KW maize; tobacco; peanut; carrot; oil seed rape; gamma-linoletic acid; GLA;
KW octadecateetraenoic acid; alpha-linoletic acid; delta-15-desaturase;
KW evening primrose.
XX
XX
OS Oenochera biennis.
XX
PN US2002108147-A1.
XX
PD 08-AUG-2002.
XX
PF 21-DEC-2001; 2001US-0029756.
XX
PR 13-OCT-1992; 92US-0959952.
PR 19-SEP-1997; 97US-0934254.
PR 10-OCT-1991; 91US-0774475.
PR 08-JAN-1992; 92US-0817919.
PR 14-SEP-1994; 94US-0307382.
PR 28-JAN-1997; 97US-0789936.

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XX
PA (THOM/) THOMAS T L.
XX
PI Thomas TL;
XX
DR WPI; 2003-06659/06.
DR N-PSDB; ABX15367.
XX
PT Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
PT for producing plant with increased gamma linoletic acid content, and
PT for inducing octadecateetraenoic acid production in plant
XX
PS Claim 3; Fig 10; 55pp; English.
XX
CC The invention relates to a nucleic acid encoding an evening primrose
CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
CC for producing a plant (such as sunflower, soybean, maize, tobacco,
CC peanut, carrot or oil seed rape plant) with increased gamma-linoletic
CC acid (GLA) content by transforming a plant cell with the nucleic acid or
CC vector and regenerating a plant with increased GLA content from the plant
CC cell, for inducing or increasing production of GLA in an organism lacking
CC in or producing low levels of GLA and for inducing production of
CC octadecateetraenoic acid in at least one of a plant deficient or lacking
CC in or producing low levels of octadecateetraenoic acid, a bacterium which
CC produces alpha-linoletic acid or a bacterium which exhibits a
CC delta-15-desaturase activity on a GLA substrate. This sequence represents
CC an evening primrose delta-6-desaturase polypeptide.
XX
SQ Sequence 452 AA;
XX
Query Match 44.9%; Score 266; DB 24; Length 452;
Best Local Similarity 49.5%; Pred. No. 1e-22;
Matches 52; Conservative 18; Mismatches 33; Indels 2; Gaps 1;
QY 12 RMISTKELOAHAAADDLWISISGVDVTPMLRHHHGGEVPLTTLAGODATDAFMAYHPP 71
DB 7 KXITMEDLRHHKSGDLWISIGKYYDCSRMAHEHGGEVPLSLAGQVDTAFIYHNG 66
QY 72 SVRPLLRFFVG-RITDYTPPASADPFRLLAQSSAGLPERVG 114
DB 67 TAWRHLDPLFTGYYYLKDFEVEISIKDYRRLNEMSRSGIFPKKG 111
XX
RESULT 10
ABG73417
ID ABG73417 standard; Protein; 448 AA.
XX
AC ABG73417;
XX
DT 16-APR-2003 (first entry)
XX
DE Borage delta-6-desaturase #2.
XX
KW Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower; soybean;
KW maize; tobacco; peanut; carrot; oil seed rape; gamma-linoletic acid; GLA;
KW octadecateetraenoic acid; alpha-linoletic acid; delta-15-desaturase;
KW borage.
XX
XX
OS Borage officinalis.
XX
PN US2002108147-A1.
XX
PD 08-AUG-2002.
XX
PF 21-DEC-2001; 2001US-0029756.
XX
PR 13-OCT-1992; 92US-0959952.
PR 19-SEP-1997; 97US-0934254.
PR 10-OCT-1991; 91US-0774475.
PR 08-JAN-1992; 92US-0817919.
PR 14-SEP-1994; 94US-0307382.
PR 28-JAN-1997; 97US-0789936.

```

XX (THOM/) THOMAS T L.
 XX Thomas TL;
 PI WPI; 2003-066659/06.
 DR Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
 PT for producing plant with increased gamma linolenic acid content, and
 PT for inducing octadecatetraenoic acid production in plant -
 XX Example 15; Fig 11; 55pp; English.
 PS The invention relates to a nucleic acid encoding an evening primrose
 CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
 CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
 CC for producing a plant (such as sunflower, soybean, maize, tobacco,
 CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
 CC acid (GLA) content by transforming a plant cell with the nucleic acid or
 CC vector and regenerating a plant with increased GLA content from the plant
 CC cell, for inducing or increasing production of GLA in an organism lacking
 CC in or producing low levels of GLA and for inducing production of
 CC octadecatetraenoic acid in at least one of a plant deficient or lacking
 CC in or producing low levels of octadecatetraenoic acid, a bacterium which
 CC produces alpha-linolenic acid or a bacterium which exhibits a
 CC delta-15-desaturase activity on a GLA substrate. This sequence represents
 CC a borage delta-6-desaturase polypeptide.
 XX
 SQ Sequence 448 AA;
 Query Match 44.1%; Score 261; DB 24; Length 448;
 Best Local Similarity 47.7%; Pred. No. 3.9e-22;
 Matches 52; Conservative 20; Mismatches 35; Indels 2; Gaps 2;
 QY 8 AADV-RMISTKELQAAADDLWISISGDVYDTPWLRHHPGGEVPLITLAGODATDAPM 66
 DB 2 AAQIKKTYITSDKLNHDKPGDLWISIQGKAYDVSDWKHPGGSFPLKSLAGOEVTDAV 61
 QY 67 AYHPPSVRLRLRRFPVG-RLTDYVPPASADFRRLAQLSSAGLFEKRVG 114
 DB 62 AFHPASTWKNLDFFTGYTLKDYSEVSKDYRKLVEFSKGLYDKKG 110

RESULT 11
 AAR98455 standard; Protein; 448 AA.
 AC AAR98455;
 DT 15-SEP-1996 (first entry)
 XX Borage delta-6-desaturase.
 DE Borage delta-6-desaturase.
 XX Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;
 KM polyunsaturated fatty acid; octadecatetraenoic acid;
 KM chilling resistance; oilseed.
 XX Borage officinalis.
 OS Borage officinalis.
 FH Key
 FT Region Location/Qualifiers
 FT 156..163 /note= "His-rich metal binding motif"
 FT 196..200 /note= "His-rich metal binding motif"
 FT /label= Metal_box-1
 FT 372..377 /label= Metal_box-2
 FT Region /label= Metal_box-2
 XX
 PN MO9621022-A2.
 XX
 PD 11-JUL-1996.
 XX
 PF 28-DEC-1995; 95WO-IB01167.
 XX

PR 30-DEC-1994; 94US-0366779.
 XX (RHON) RHONE POULENC AGROCHIMIE.
 PA Freyessinet GL, Nuccio M, Numborg AN, Reddy AS, Thomas TL;
 XX WPI; 1996-333997/33.
 DR N-PSDB; AAT30395.
 DR Transgenic plants comprising the borage delta-6-desaturase gene -
 PT show increased production of gamma linolenic acid and having
 PT increased resistance to chilling
 XX Claim 3; Page 52-53; 75pp; English.
 PS Borage delta-6-desaturase (AAR98455) catalyses the conversion of
 CC linoleic acid to gamma-linolenic acid (GLA). Its sequence was
 CC deduced from that of the delta-6-desaturase gene (AAT30395) isolated
 CC from a borage membrane-bound polysomal library. The sequence is
 CC distinct from that of Synchocystis delta-6-desaturase (AAR98456).
 CC Expression of the desaturase in transgenic plants, esp. sunflower,
 CC soybean, maize, tobacco, peanut, carrot or oilseed rape, results in
 CC increased GLA prodn. Alteration of the plant membrane lipids as a
 CC result of expression of the desaturase may also result in increased
 CC resistance to chilling.
 XX
 SQ Sequence 448 AA;
 Query Match 43.6%; Score 258; DB 17; Length 448;
 Best Local Similarity 46.8%; Pred. No. 8.7e-22;
 Matches 51; Conservative 21; Mismatches 35; Indels 2; Gaps 2;
 QY 8 AADV-RMISTKELQAAADDLWISISGDVYDTPWLRHHPGGEVPLITLAGODATDAPM 66
 DB 2 AAQIKKTYITSDKLNHDKPGDLWISIQGKAYDVSDWKHPGGSFPLKSLAGOEVTDAV 61
 QY 67 AYHPPSVRLRLRRFPVG-RLTDYVPPASADFRRLAQLSSAGLFEKRVG 114
 DB 62 AFHPASTWKNLDFFTGYTLKDYSEVSKDYRKLVEFSKGLYDKKG 110

RESULT 12
 AAM67471 standard; Protein; 448 AA.
 AC AAM67471;
 DT 02-MAR-1999 (first entry)
 XX Borage delta-6 desaturase protein.
 DE Borage delta-6 desaturase protein.
 XX Upstream region; regulatory region; sunflower; albumin; seed; expression;
 KM lipid metabolism; delta-6 desaturase; transgenic plant.
 XX Borage officinalis.
 OS Borage officinalis.
 FH Key
 FT Region Location/Qualifiers
 FT 40..44 /note= "cytochrome b5 haem-binding motif"
 FT 156..163 /note= "His-rich metal binding motif"
 FT 196..200 /note= "His-rich metal binding motif"
 FT /note= "His-rich metal binding motif"
 FT 373..377 /note= "His-rich metal binding motif"
 FT Domain /note= "His-rich metal binding motif"
 XX
 PN MO9845460-A1.
 XX
 PD 15-OCT-1998.
 XX
 PF 09-APR-1998; 98WO-US07178.
 XX
 PF 09-APR-1997; 97US-0831570.
 XX

XX (RHON) RHONE-FOULENC AGROCHIMIE.
 XX Beremand PD, Nunberg AN, Thomas TL;
 PI WPI; 1998-583201/49.
 DR N-PSDB; AAV34398.
 XX
 PT New sunflower albumin 5' regulatory region - useful for directing
 PT altered lipid metabolism in plant seeds
 XX
 PS Example 2; Fig 1; 38pp; English.
 XX
 CC This sequence corresponds to the borage (*Borago officinalis*) delta-6
 CC desaturase enzyme. The encoding lipid metabolism gene is an example
 CC of a heterologous gene which can be expressed at high levels in a
 CC seed-specific manner in transgenic plants, when placed under control
 CC of the sunflower albumin gene 5' regulatory region (AAV34397).
 CC
 SQ Sequence 448 AA;
 Query Match 43.6%; Score 258; DB 19; Length 448;
 Best Local Similarity 46.8%; Pred. No. 8.7e-22;
 Matches 51; Conservative 21; Mismatches 35; Indels 2; Gaps 2;
 QY 8 AADV-RMISTKELQAAADLMIISGVDVTPMLRHHPGSEVPLITLAGODATDAM 66
 DB 2 AAQIKYITSDLEKNDKPGDLWISIQKAYVSDVWKDHPGSPFLKSLAGOEVTDAV 61
 QY 67 AVHPSPVRPLRRFFVG-RLTDYTPPASADFRRLAQLSAGLPERVG 114
 DB 62 AFHPASTWKNLDKFPFGYLLKDYSEVSKDYRKLVFEFSKXGLYDKG 110
 RESULT 13
 AAV98130
 ID AAV98130 standard; Protein; 448 AA.
 XX
 AC AAV98130;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Borage delta-6 desaturase.
 XX
 KW Delta-6 desaturase; borage; oleosin; At521; promoter;
 KW transgenic plant; seed; lipid; fatty acid; oilseed; vegetable oil;
 KW gamma-linolenic acid; octadecatetraenoic acid.
 XX
 OS Borago officinalis.
 XX
 PH Key Location/Qualifiers
 FT Binding-site 40..44 /note= "cytochrome b5 haem-binding motif"
 FT Binding-site 156..163 /note= "metal binding, histidine-rich motif"
 FT Binding-site 196..200 /note= "metal binding, histidine-rich motif"
 FT Binding-site 373..377 /note= "metal binding, histidine-rich motif"
 FT Binding-site /note= "metal binding, histidine-rich motif"
 XX
 PN WO9845461-A1.
 XX
 PD 15-OCT-1998.
 XX
 PF 09-APR-1998; 98WO-US07179.
 XX
 PR 09-APR-1997; 97US-0831575.
 XX
 XX (RHON) RHONE-FOULENC AGROCHIMIE.
 XX Li Z, Thomas TL;
 PI WPI; 1999-180333/15.
 DR

DR N-PSDB; AAX24917.
 XX
 PT Nucleic acid containing oleosin 5'-regulatory region - useful for
 PT modulating fatty acid synthesis and lipid metabolism in plants,
 PT particularly to increase content of gamma-linolenic acid
 XX
 PS Example 2; Page 61; 101pp; English.
 XX
 CC The present sequence is borage delta-6 desaturase, an enzyme that
 CC catalyses the conversion of linoleic acid to gamma-linolenic acid
 CC (GLA). Delta-6 desaturase cDNA (see AAX24917) was isolated from a
 CC borage membrane-bound polyosomal cDNA library using a partial clone,
 CC obtained from an EST database search, as probe. The borage delta-6
 CC desaturase nucleic acid can be operably linked to the seed-specific
 CC 5' regulatory region (see AAX24916) of the Arabidopsis thaliana
 CC oleosin At521 gene in claimed expression cassettes of the invention.
 CC Transgenic plants, e.g. sunflower, soybean, maize, tobacco, cotton,
 CC peanut, oilseed rape or Arabidopsis are obtained that show increased
 CC levels of GLA or octadecatetraenoic acid. The levels of desirable
 CC fatty acids in oilseed crops can be manipulated to provide seed
 CC oils of use in human health and industrial applications.
 CC
 SQ Sequence 448 AA;
 Query Match 43.6%; Score 258; DB 20; Length 448;
 Best Local Similarity 46.8%; Pred. No. 8.7e-22;
 Matches 51; Conservative 21; Mismatches 35; Indels 2; Gaps 2;
 QY 8 AADV-RMISTKELQAAADLMIISGVDVTPMLRHHPGSEVPLITLAGODATDAM 66
 DB 2 AAQIKYITSDLEKNDKPGDLWISIQKAYVSDVWKDHPGSPFLKSLAGOEVTDAV 61
 QY 67 AVHPSPVRPLRRFFVG-RLTDYTPPASADFRRLAQLSAGLPERVG 114
 DB 62 AFHPASTWKNLDKFPFGYLLKDYSEVSKDYRKLVFEFSKXGLYDKG 110
 RESULT 14
 AAY51349
 ID AAY51349 standard; Protein; 448 AA.
 XX
 AC AAY51349;
 XX
 DT 27-APR-2000 (first entry)
 XX
 DE Sunflower HADES protein.
 XX
 KW Sunflower lipid desaturase; sld1; sphingobase; ceramide;
 KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
 KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
 KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
 KW pharmaceutical; food; chemical raw material.
 XX
 OS Helianthus annuus.
 XX
 PN DE19828850-A1.
 XX
 PD 30-DEC-1999.
 XX
 PF 27-JUN-1998; 98DE-1028850.
 XX
 PR 27-JUN-1998; 98DE-1028850.
 XX
 XX (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
 XX Heinz B, Zaehring U, Schmidt H, Sperling P;
 PI WPI; 2000-127549/12.
 XX
 XX New sphingolipid desaturase that selectively introduces double bond
 XX into sphingolipids and ceranoids -
 PS Disclosure; Page 33-34; 62pp; German.

XX This invention describes a novel sphingolipid desaturase that selectively
 CC introduces a double bond into the sphingobase of the ceramide residue of
 CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
 CC desaturase, or a vector containing the DNA sequence, can be used to
 CC produce transgenic plants, especially crop plants, with an increased or
 CC decreased delta-8-unsaturated long-chain base content or an altered
 CC delta-8-unsaturated long-chain base cis/trans ratio, especially to
 CC compensate for a delta-8-unsaturated long-chain base deficiency, to
 CC exclude production of delta-8-unsaturated bases, to increase tolerance
 CC or resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 CC alter size growth and flowering time. Cells, transgenic organisms or
 CC plants containing the DNA sequence can be used to produce sphingolipids
 CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
 CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 CC materials. This sequence represents a desaturase protein, HADES, isolated
 CC from *Helianthus annuus* (sunflower) which is used in the method of the
 CC invention.

XX
 SQ Sequence 448 AA;

Query Match 43.6%; Score 258; DB 21; Length 448;
 Best Local Similarity 46.8%; Pred. No. 8,7e-22;
 Matches 51; Conservative 21; Mismatches 35; Indels 2; Gaps 2;

QY 8 AADV-EMISTKEIQAHAAADDLWISGVDYDTPWLRHHPGGEVPLITLAGDADTAFM 66
 Db 2 AAQIKKYITSDELKNDKPDGLWISIQKAYDVSDWKDPGSPFLKSLAGGEVTDADFV 61
 QY 67 AYHPPSVRLRLRRFVG-RLTDYTPPASADPRLLAQLSSAGLPERVG 114
 Db 62 AFHPASTWKMLDKFETGYLYLKDVSVSEVSKDYRKLVFEFSKMGLYDKKG 110

RESULT 15
 AAU79830

ID AAU79830 standard; Protein; 448 AA.

XX AAU79830;

DT 15-JUL-2002 (first entry)

DE Borago officinalis delta6-desaturase.

XX KW delta6-desaturase; sunflower; soybean; maize; tobacco;

KW peanut; carrot; oil seed rape; gamma linolenic acid; GLA;

XX KW chilling tolerance; borage.

OS Borago officinalis.

XX FH Key Location/Qualifiers

FT Region 156..163 /label= Lipid_box

FT Region 196..200 /label= Metal_box_1

FT Region 372..377 /label= Metal_box_2

XX US6355861-B1.

PD 12-MAR-2002.

PF 19-SEP-1997; 97US-0934254.

PR 13-OCT-1992; 92US-0959952.

PR 10-OCT-1991; 91US-0774475.

PR 08-JAN-1992; 92US-0817919.

PR 14-SEP-1994; 94US-0307382.

PR 28-JAN-1997; 97US-0789936.

XX (RHON) RHONE-POULENC AGROCHIMIE.

PI Thomas TL;

DR WPI: 2002-380944/1.

DR N-PSDB; ABR49502.

XX Novel nucleic acid encoding evening primrose delta6-desaturase which

PT converts linolenic acid to gamma linolenic acid useful for producing

PT gamma linolenic acid in transgenic plant or bacteria

XX Example 9; Column 31-34; 53pp; English.

XX The invention describes an isolated nucleic acid encoding an evening
 CC primrose Delta6-desaturase. The nucleic acid and a vector expressing the
 CC nucleic acid are useful for producing a plant such as sunflower, soybean,
 CC maize, tobacco, peanut, carrot or oil seed rape plant, with increased
 CC gamma linolenic acid (GLA) content, and also for inducing or increasing
 CC production of GLA in a bacteria or plant deficient, lacking in or
 CC producing low levels of GLA. The nucleic acid is also useful for inducing
 CC chilling tolerance in plants. This is the amino acid sequence of the
 CC borage delta6 desaturase involved in the production of gamma linoleic
 CC acid.

XX
 SQ Sequence 448 AA;

Query Match 43.6%; Score 258; DB 23; Length 448;
 Best Local Similarity 46.8%; Pred. No. 8,7e-22;
 Matches 51; Conservative 21; Mismatches 35; Indels 2; Gaps 2;

QY 8 AADV-EMISTKEIQAHAAADDLWISGVDYDTPWLRHHPGGEVPLITLAGDADTAFM 66
 Db 2 AAQIKKYITSDELKNDKPDGLWISIQKAYDVSDWKDPGSPFLKSLAGGEVTDADFV 61
 QY 67 AYHPPSVRLRLRRFVG-RLTDYTPPASADPRLLAQLSSAGLPERVG 114
 Db 62 AFHPASTWKMLDKFETGYLYLKDVSVSEVSKDYRKLVFEFSKMGLYDKKG 110

Search completed: January 1, 2004, 06:36:55
 Job time : 11.4957 secs

Nature 408, 816-820, 2000
 A:Author: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luroe, J.S.; Malt, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Schatz, G.; Schatz, G.; Schatz, G.;
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; WUID:21016719; PMID:11130712
 A:Accession: A86390
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-135 <STO>
 A:Cross-references: GB:AE005172; NID:g9797763; PIDN:AAF98581.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1
 C:Superfamily: cytochrome b5; cytochrome b5 core homology
 C:Keywords: heme; iron; metalloprotein
 F:40/64/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 29.6%; Score 175.5; DB 2; Length 135;
 Best Local Similarity 35.1%; Pred. No. 3 6e-11;
 Matches 40; Conservative 22; Mismatches 43; Indels 9; Gaps 3;

QY 1 MPASKDAADVMIISTKELQAHAAADLWISGVDYDTYPMLRHHPGGEVPLITLADG 60
 DB 1 MPTLTK-----LYSWEBAATHNKODDCWVVDGKYVDVSSVDEHGGDDVLLAVAGKD 54

QY 61 ATDAFM-AVHPSPVRLRRFFVGRITDVTVP--PASAPFRLLADLSAGLFE 111
 DB 55 ATDDFEDAGSHKDAKRLMKRYFGEIDBSLPEIPRLKTYKKDQPDQSVQKLF 108

RESULT 7
 SS2857
 nitrate reductase (NADH) (EC 1.7.1.1) - *Beauveria bassiana*
 C:Species: *Beauveria bassiana*
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
 C:Accession: SS2857
 R:Maurel, P.
 submitted to the EMBL Data Library, February 1995
 A:Reference number: SS2857
 A:Accession: SS2857
 A:Molecule type: DNA
 A:Residues: 1-894 <MAN>
 A:Cross-references: EMBL:X84950; NID:g693925; PIDN:CAA59336.1; PID:g693926
 C:Genetics:
 A:introns: 593/1
 C:Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 red
 C:Keywords: heme; iron; metalloprotein; molybdenum; molybdopterin; oxidoreductase; phosph
 F:62-467/Domain: molybdopterin-binding domain homology <PCO>
 F:535-609/Domain: cytochrome b5 core homology <CB5>
 F:645-894/Domain: cytochrome-b5 reductase homology <CBR>
 F:169/Binding site: molybdopterin (Cys) (covalent) #status predicted
 F:570/593/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 29.4%; Score 174; DB 2; Length 894;
 Best Local Similarity 40.3%; Pred. No. 4.3e-10;
 Matches 31; Conservative 18; Mismatches 28; Indels 0; Gaps 0;

QY 11 VMISTKELQAHAAADLWISGVDYDTYPMLRHHPGGEVPLITLADGATDAFM 70
 DB 535 VRIISLELKAHGEHMEPFFVNGHYNGTPYLDNHPGATSIINAAADATDEEFTIHS 594

QY 71 PSVRLRRFFVGRITDVTVP 87
 DB 595 ENAKAMMPQYHIGTLND 611

RESULT 8
 TS2469
 cytochrome b5 [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 01-Dec-2000

C:Accession: TS2469
 R:Fukuchi-Mizutani, M.; Mizutani, M.; Tanaka, Y.; Kusumi, T.; Ohta, D.
 Plant Physiol. 119, 353-361, 1999
 A:Title: Microsomal Electron Transfer in Higher Plants: Cloning and Heterologous Express
 A:Reference number: Z52574
 A:Accession: TS2469
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-134 <FUK>
 A:Cross-references: EMBL:AB007801; PIDN:CAB17231.1
 C:Superfamily: cytochrome b5; cytochrome b5 core homology
 C:Keywords: heme; iron; metalloprotein
 F:40/64/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 28.6%; Score 169.5; DB 2; Length 134;
 Best Local Similarity 36.5%; Pred. No. 1.5e-10;
 Matches 31; Conservative 23; Mismatches 30; Indels 1; Gaps 1;

QY 8 AADVMIISTKELQAHAAADLWISGVDYDTYPMLRHHPGGEVPLITLADGATDAFM 66
 DB 2 SSDRVLSPFEVSKNKTKDCWLIISGKYVDYTPMDHPRGDDVLLSTGKDATNDFD 61

QY 67 AVHPSPVRLRRFFVGRITDVTVP 91
 DB 62 VGHSDTARDMDKRYFGEIDSSVP 86

RESULT 9
 T14454
 cytochrome b5 - wild cabbage
 C:Species: *Brassica oleracea* (wild cabbage)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
 C:Accession: T14454
 R:Kearns, E.V.; Keck, P.; Somerville, C.R.
 submitted to the EMBL Data Library, March 1992
 A:Description: Nucleotide sequence of cDNA for cytochrome b5 from cauliflower (*Brassica*
 A:Reference number: Z18100
 A:Accession: T14454
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-134 <KEA>
 A:Cross-references: EMBL:M87514; NID:g167139; PID:g167140
 C:Function:
 A:Description: acts as electron carrier for membrane-bound oxygenases
 C:Superfamily: cytochrome b5; cytochrome b5 core homology
 C:Keywords: electron transfer; heme; iron; membrane protein; metalloprotein
 F:5-80/Domain: cytochrome b5 core homology <CB5>
 F:40/64/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 28.5%; Score 168.5; DB 2; Length 134;
 Best Local Similarity 35.3%; Pred. No. 1.9e-10;
 Matches 30; Conservative 23; Mismatches 31; Indels 1; Gaps 1;

QY 8 AADVMIISTKELQAHAAADLWISGVDYDTYPMLRHHPGGEVPLITLADGATDAFM 66
 DB 2 ABEKYLGEHVSQNKTKDCWLIISGKYVDYTPMDHPRGDDVLLSTGKDATNDFD 61

QY 67 AVHPSPVRLRRFFVGRITDVTVP 91
 DB 62 VGHSDTARDMDKRYFGEIDSSVP 86

RESULT 10
 RDNTNT
 nitrate reductase (NADH) (EC 1.7.1.1) nia-1 - common tobacco
 C:Species: *Nicotiana tabacum* (common tobacco)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 03-Jun-2002
 C:Accession: S04838; S05696
 R:Vaucheret, H.; Kromerberger, J.; Rouze, P.; Caboche, M.
 Plant Mol. Biol. 12, 597-600, 1989
 A:Title: Complete nucleotide sequence of the two homeologous tobacco nitrate reductase ge
 A:Reference number: S04838
 A:Accession: S04838

A: Molecule type: DNA
A: Residues: 1-904 <VAD>
A: Cross-references: EMBL:X14058
R: Rouze, P.
submitted to the EMBL Data Library, January 1989
A: Reference number: S05696
A: Accession: S05696
A: Molecule type: DNA
A: Residues: 1-35, 'P', 37-904 <ROU>
A: Cross-references: EMBL:X14058; NID: g19888; PIDN: CAA32216.1; PID: g19889
C: Genetics:
A: Gene: nla-1
A: Introns: 338/1; 385/1; 462/3
C: Complex: homodimer
C: Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 red
C: Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron;
E: 79-471/Domain: molybdopterin-binding domain homology <PCO>
E: 531-605/Domain: cytochrome b5 core homology <CB5>
E: 654-904/Domain: cytochrome-b5 reductase homology <CBR>
E: 183/Binding site: molybdopterin (Cys) (covalent) #status predicted
F: 442/Disulfide bonds: interchain #status predicted
F: 566, 589/Binding site: heme iron (His) (axial ligands) #status predicted
F: 718, 876/Binding site: NAD (Tyr, Cys) #status predicted
E: 755/Binding site: FAD (Tyr) #status predicted

Query Match	28.2%	Score 167	DB 1	Length 904
Best Local Similarity	35.7%	Pred No. 2.4e-09		
Matches 40	Conservative 15	Mismatches 43	Indels 14	Gaps 3

```

QY      1 MPAAKSDADVYRMISTIKELQYHAAADDLMISIGDVYDVTPLNRHHPGGEVPLITLACGD 60
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      527 MNTASK-----MYSNSEVVRKHSAPSASAWIYHGHIVDATRFLKDHGSGDSLILNAGTD 580

```

```

QY      61 ATDAFMAYHPSPVRLRRFFVGRLL--TDYVPP-----ASADFRLLAQL 104
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      581 CTEFPDAIHSDAKKLLSEFRISLLTTGYTSDSPGNSVHGSSSFSSFLAPI 632

```

RESULT 11

T52468
cytochrome b5 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 01-Dec-2000
C:Accession: T52468
R:Fukuchi-Mizutani, M.; Mizutani, M.; Tanaka, Y.; Kusumi, T.; Ohta, D.
Plant Physiol. 119, 353-361, 1999
A:Title: Microsomal Electron Transfer in Higher Plants: Cloning and Heterologous Expression
A:Reference number: 225274
A:Accession: T52468
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-140 <FUK>
A:Cross-references: EMBL:AB007802; PIDN:CAB17232.1
C:Superfamily: cytochrome b5; cytochrome b5 core homology
C:Keywords: heme, iron; metalloprotein
F:40.64/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match	28.1%	Score 166.5	DB 2	Length 140
Best Local Similarity	39.8%	Pred. No. 3.3e-10		
Matches 33	Conservative 17	Mismatches 32		Indels 1
				Gaps 1

Dy 10 DVRMTSTKELQAAADDLWISGVDVDTVPMLRHHPGGEVPLITLAGDQATDAEM-AY 68
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 4 DGKVFLTSEVSQHSSAKDCMIIDGKYVDYTKFLLDDHPCGDDEVILSTGKQATDDDEFDVG 63

```
QY      69 HPPSVRPLRLRRFFVGRGLTDYTP 91
          |  ::::: |||
Db      64 HSSTAKAMLDEYYVGIDITATVP 86
```

RESULT 12
S46306
cytochrome b5 - common tobacco

C:Species: Nicotiana tabacum (common tobacco)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #ext_change 05-May-2000
C:Accession: S46306; S33157
R:Smith, M.A.; Stobart, A.K.; Shewry, P.R.; Napier, J.A.
Plant Mol. Biol. 25, 527-537, 1994
A>Title: Tobacco cytochrome b(5): cDNA isolation, expression analysis and in vitro protein
A:Reference number: S46306; MUID:94325476; PMID:8049375
A:Accession: S46306
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-139 <SMI>
A:Cross-references: EMBL:X71441; NID:g296385; PIDD:CA50575.1; PIDD:g296386
A:Superfamily: cytochrome b5; cytochrome b5 core homology
C:Keywords: heme; iron; metalloprotein
F:8-63/Domain: cytochrome b5 core homology <CS>
F:43,67/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match	28.0%	Score 165.5	DB 2	Length 139
Best Local Similarity	39.8%	Pred. No. 4	1e-10	
Matches 33	Conservative 16	Mismatches 33	Indels 1	Gaps 1

```

QY      10 DVKMTSTKELOAAHAADDLMTISGDVYDTPMLRHHGEGVEPLITLAGDQATDAEM-AY 688
      :  ::  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      7  ETKVFLLAEVSGHNNAKDCWLIVISGKYDVTKFLDDHGGDEVLVLSATGQATDDPEDVG 666

```

Qy 69 HPPSVRPLLRFFVGLTDYTP 91
67 HSSSARAMLDEYYVGDIDSATIP 89

RESULT 13
S16292

C:Species: *Neurospora crassa*
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 03-Jun-2002
C:Accession: S16292; S07176; S34796; S37298

A;Title:

A:Reference number: S16292; PMID:91287699; PMID:1829499
A:Accession: S16292
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-982 <MOL>
A:Note: the authors translated the codon CGC for residue 140 as Pro
R,Le,K.H.D., Lederer, F.
EMBO J. 2, 1905-1914, 1983
A:Title: On the presence of a heme-binding domain homologous to cytochrome b5 in Neurospora crassa
A:Reference number: S07176
A:Accession: S07176
A:Molecule type: Protein
A:Residues: 'D',622-623,'Y',624,'IK',627,'Y',628,'XNKKX',635,'LILHYKK',643,'DL',646,'K',647
C:Genetics:
A:Gene: nit-3
A:Introns: 675/1
C:Complex: homodimer
C:Superfamily: nitrate reductase (NADH); cytochrome b5 core homolog; cytochrome-b5 reductase family; nitrate reductase (NADH); cytochrome b5 core homolog; cytochrome-b5 reductase family

F:121-548 Domain: molybdopterine-binding domain homology <PCO>
F:611-691/Domain: cytochrome b5 core homology <CB5>
E:728-982/Domain: cytochrome-b5 reductase homology <CBR>
728/982/Domain: cytochrome-b5 reductase homology <CBR>

Feature	Value
F:499/Disulfide bonds:	interchain #status predicted
F:652,675/Binding site:	heme iron (His) (axial ligands) #status predicted
F:796,956/Binding site:	NADP (Lys, Cys) #status predicted

Query Match	28.0%;	Score 165.5;	DB 1;	Length 982;
Best Local Similarity	33.3%;	Pred. No. 3.8e-09;		

Q7 DAADVRMISTKEIQAHAADDLMISIGDYDVTPLRHHPGGEVPLITLAGODATDAFM 66

Db 613 DEKVTLLTLEELRQHDGEEBFWVNGVYNGTPTLEHGPAGASITGAGQDVTDEFL 672
 QY 67 AYHPSVRPLLRPFVGRLT-----DYTVPPASAD 96
 Db 673 AIHSENAKAWMPYTHIGTLPSAPALAKSSSTSDPALSD 711

RESULT 14

NRTNNS

nitrate reductase (NADH) (EC 1.7.1.1) nia-2 - common tobacco

C/Species: Nicotiana tabacum (common tobacco)

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 03-Jun-2002

C/Accession: S04839; S25375; S22779

R/Vaucheret, H.; Kronenberger, J.; Rouze, P.; Caboche, M.

Plant Mol. Biol. 12, 597-600, 1989

A/Title: Complete nucleotide sequence of the two homeologous tobacco nitrate reductase g

A/Reference number: S04838

A/Accession: S04839

A/Molecule type: DNA

A/Residues: 1-904 <NAU>

A/Cross-references: EMBL:X14059; NID:G19890; PIDN:CAA2217.1; PID:G19891

R/Galangau, F.; Cherel, I.; Deng, M.; Meyer, C.; Moutaux, T.; Rouze, P.; Vaucheret, H.;

Curr. Top. Plant Biochem. Physiol. 7, 26-34, 1988

A/Title: Nitrate reductase expression in tobacco and tomato.

A/Reference number: S25375

A/Accession: S25375

A/Molecule type: DNA

A/Residues: 1-904 <CAL>

A/Calza, R.; Hutterer, E.; Vincenz, M.; Rouze, P.; Galangau, F.; Vaucheret, H.; Cherel,

Mol. Gen. Genet. 209, 552-562, 1997

A/Title: Cloning of DNA fragments complementary to tobacco nitrate reductase mRNA and en

A/Reference number: S22779

A/Accession: S22779

A/Molecule type: mRNA

A/Residues: 171-724 <CAL>

A/Cross-references: EMBL:X06134; NID:G19894; PIDN:CAA29497.1; PID:G929750

C/Genetics:

A/Introns: 338/1; 385/1; 462/3

C/Complex: homodimer

C/Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 red

C/Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron;

F/79-471/Domain: molybdopterin-binding domain homology <PCO>

F/531-605/Domain: cytochrome b5 core homology <CB5>

F/554-904/Domain: cytochrome-b5 reductase homology <CBR>

F/483/Binding site: molybdopterin (Cys) (covalent) #status predicted

F/422/Disulfide bonds: interchain #status predicted

F/566,589/Binding site: heme iron (His) (axial ligand) #status predicted

F/718,876/Binding site: NAD (Lys, Cys) #status predicted

F/758/Binding site: FAD (Tyr) #status predicted

Query Match 27.7%; Score 164; DB 1; Length 904;

Best Local Similarity 35.7%; Pred. No. 4.9e-09;

Matches 40; Conservative 15; Mismatches 43; Indels 14; Gaps 3;

QY 1 MPASADADVWRISTKEQAHAAADDLMISIGDVYVTPWLRHHPGCEVPLITLAGOD 60
 Db 527 KNTASK-----MYSSEVAKSHSSADSAMWITVHGHTYDATRFLKDHGGTDSITLINAGTD 580
 QY 61 ATDAFMAVHPSPVPLLRPFVGRLT--TDYTVPP-----ASADFRLLAQL 104
 Db 581 CTEFPAIHSDKAKKLLDEPRIGELITGTSTSDSPGNSVHGSSSFSSFLAPI 632

RESULT 15

T00796

cytochrome b5 At2g32720 [similarity] - Arabidopsis thaliana

N/Alternate names: protein F24L7.14

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 02-Mar-2001

C/Accession: T00796; F84736

R/Rounsaey, S.D.; Lin, X.; Kechum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul

submitted to the EMBL Data Library, February 1998

A/Description: Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence.
 A/Reference number: Z14204

A/Accession: T00796

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-134 <ROU>

A/Cross-references: EMBL:AC003974; NID:G2914688; PIDN:AAC04491.1; PID:G2914701

A/Experimental source: cultivar Columbia

R/Lin, X.; Kaul, S.; Rounsaey, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;

eues, D.; Nierman, W.C.; White, O.; Eilen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J.

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: F84736

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-134 <STO>

A/Cross-references: GB:A8002093; NID:G2914701; PIDN:AAC04491.1; GSPDB:GN00139

C/Genetics:

A/Map position: 2

A/Introns: 29/3; 52/1

C/Superfamily: cytochrome b5; cytochrome b5 core homology

C/Keywords: heme; iron; metalloprotein

F/5-80/Domain: cytochrome b5 core homology <CB5>

F/40,64/Binding site: heme iron (His) (axial ligand) #status predicted

Query Match 27.6%; Score 163.5; DB 2; Length 134;

Best Local Similarity 37.3%; Pred. No. 6.4e-10;

Matches 31; Conservative 19; Mismatches 32; Indels 1; Gaps 1;

QY 10 DYRMISTKELQAHAAADDLMISIGDVYVTPWLRHHPGCEVPLITLAGODATDAPM-AY 68
 Db 4 EAKIFLSEVSRHNOAHDQWIVNGRVYVTKFLBDHPGDDVLLSTGKDATDPEVVG 63
 QY 69 HPSVVRPLLRPFVGRLTDTYVP 91
 Db 64 HSESAREMMEQYVGEIDPTIP 86

Search completed: January 1, 2004, 06:39:43
 Job time : 4.29068 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 2.5084 Seconds
(without alignments)
2137.240 Million cell updates/sec

Title: US-09-857-524B-17

Sequence: 1 MPASADADVMISTKEIQ.....ADFRLLAQLSAGLFRVIG 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	177	29.9	905 1 NIA_FUSOX	P39863 fusarium ox
2	174	29.4	894 1 NIA_BEABA	P43100 beaveria b
3	169.5	28.6	134 1 CYB5_1ARATH	Q42342 arabidopsis
4	168.5	28.5	134 1 CYB5_BRAOL	P40934 brassica ol
5	167	28.2	904 1 NIA1_TORAC	P11605 nicotiana t
6	165.5	28.0	136 1 CYB5_TORAC	P49058 nicotiana t
7	165.5	28.0	136 1 CYB5_TORAC	P49058 nicotiana t
8	164	27.7	904 1 NIA2_TORAC	P08619 neuropept
9	163.5	27.6	134 1 CYB5_1ARATH	P48845 arabidopsis
10	161.5	27.3	891 1 NIA7_HORVU	P27968 hordeum vul
11	161	27.2	318 1 NIA_CHLVU	Q01170 chlorella v
12	159.5	26.9	909 1 NIA_PETMY	P36859 petunia hyb
13	159.5	26.9	917 1 NIA1_1ARATH	P11832 arabidopsis
14	159	26.9	881 1 NIA1_P1HAVU	P29865 phaseolus v
15	158.5	26.8	444 1 FADS_BRAE	Q0867 brachydanio
16	157	26.5	890 1 NIA2_P1HAVU	P39866 phaseolus v
17	157	26.5	926 1 NIA_SPTOL	P23312 spinacia ol
18	156	26.4	864 1 NIA_VOLCA	P36841 volvox cart
19	155.5	26.3	135 1 CYB5_TORAC	P49059 nicotiana t
20	153	25.8	900 1 NIA_LOTJA	P39869 lotus japon
21	152.5	25.8	893 1 NIA_TLEPMC	P36842 leptophaer
22	152	25.7	911 1 NIA1_BRANA	P39867 brassica na
23	152	25.7	911 1 NIA1_LYCS	P17570 lycopersico
24	151	25.5	917 1 NIA2_1ARATH	P11035 arabidopsis
25	150.5	25.4	132 1 CYB5_BOROF	Q04354 borago offi
26	149.5	25.3	137 1 CYB5_ORYSA	P49100 oryza sativ
27	149.5	25.3	146 1 CYM5_RAT	P40166 rattus norv
28	148	25.0	920 1 NIA_TICTIN	P43101 cichorium i
29	147	24.8	573 1 CYB2_HANAN	P09437 hansenula a
30	147	24.8	911 1 NIA2_BRANA	P39868 brassica na
31	146.5	24.7	916 1 NIA1_ORYSA	P16081 oryza sativ
32	145	24.5	890 1 NIA2_SOYBN	P39870 glycine max
33	145	24.5	898 1 NIA_BEYVE	P27783 betula verr

34	143.5	24.2	129 1 CYB2_SCHPO	Q9uen6 schizosacch
35	143.5	24.2	131 1 CYB5_RHIST	Q9hfc1 rhizopus st
36	142.5	24.1	147 1 YDAA_SCHPO	Q10352 echizosacch
37	142.5	24.1	908 1 NIA_USTMA	Q05531 ustilago ma
38	142	24.0	130 1 CYB5_MORAP	Q9y706 mortierella
39	142	24.0	886 1 NIA1_SOYBN	P54233 glycine max
40	142	24.0	889 1 NIA1_MAIZE	P49102 zea mays (m
41	141.5	23.9	135 1 CYB5_CUSRE	P49097 cuscuta ref
42	140	23.6	859 1 NIA_PICAN	P49050 picchia angu
43	139.5	23.6	134 1 CYB5_DROME	Q9v4n3 drosophila
44	139.5	23.6	621 1 NIA1_MAIZE	P17571 zea mays (m
45	139	23.5	912 1 NIA2_HORVU	P27969 hordeum vul

ALIGNMENTS

RESULT 1	NIA_FUSOX	STANDARD;	PRT;	905 AA.
ID	NIA_FUSOX			
AC	P39863,			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Nitrate reductase [NADPH] (EC 1.7.1.3) (NR).			
GN	NIA.			
OS	Fusarium oxysporum.			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.			
OX	NCBI_TaxId=5507;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=F0M24;			
RA	MEDLINE=93380674; PubMed=8370541;			
RT	Diolez A., Langin T., Gerlinger C., Brygoo Y., Daboussi M.-J.;			
RT	"The nia gene of Fusarium oxysporum: isolation, sequence and			
RT	development of a homologous transformation system.";			
RL	Gene 131:61-67(1993).			
CC	- FUNCTION: Nitrate reductase is a key enzyme involved in the first			
CC	step of nitrate assimilation in plants, fungi and bacteria.			
CC	- CATALYTIC ACTIVITY: Nitrite + NADP(+) + H(2)O = nitrate + NADPH.			
CC	- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)			
CC	AND ONE MOLYBDENUM ATOM.			
CC	- SUBUNIT: Homodimer (by similarity).			
CC	- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE			
CC	N-TERMINAL DOMAIN.			
CC	- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.			
CC	- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE			
CC	C-TERMINAL DOMAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.1sb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; Z22549; CA80270.1; -			
DR	PIR; J0803; J0803.			
DR	HSSP; P04166; 1EUR.			
DR	InterPro; IPR001199; Cyt_B5.			
DR	InterPro; IPR001834; Cyt_B5_reductase.			
DR	InterPro; IPR000572; Burk_Mb_oxred.			
DR	InterPro; IPR001709; PPN_Cyt_reductase.			
DR	InterPro; IPR005066; Mo-co dimer.			
DR	InterPro; IPR001433; Oxred_FAD/NAD(P).			
DR	Pfam; PF00970; FAD_binding_6; 1.			
DR	Pfam; PF00173; heme_1; 1.			
DR	Pfam; PF03404; Mo-co_dimer; 1.			
DR	Pfam; PF00175; NAD_binding_1; 1.			
DR	Pfam; PF00174; oxidored_mol_yb; 1.			
DR	PRINTS; PR00406; CYTB5RDYASE.			

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DR PRINTS; PR00363; CYTOCHROME B5.
DR PRINTS; PR00407; EUMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR PRODOM; PD000612; Cyt_B5_1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS00255; CYTOCHROME_B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KM Oxidoreductase; Flavoprotein; FAD; NADP; Heme; Molybdenum;
Nitrates assimilation..
KW DOMAIN 3
FT METAL 179 179 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 230 230 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 428 428 INTERCHAIN (POTENTIAL).
FT DOMAIN 550 620 HEME-BINDING (BY SIMILARITY).
FT METAL 581 581 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 604 604 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT DOMAIN 645 905 FLAVIN-BINDING DOMAIN (BY SIMILARITY).
FT NP BIND 875 884 NADP (BY SIMILARITY).
SQ SEQUENCE 905 AA; 101898 MW; D5DE23F7971ACDA CRC64;

Query Match 29.9%; Score 177; DB 1; Length 905;
Best Local Similarity 38.8%; Pred. No. 4.8e-11;
Matches 33; Conservative 16; Mismatches 34; Indels 0; Gaps 0;

QY 12 RMISTKELQAHAAADLMISGVDVDTPLMRHHPGGEVPLITLAGODATDAPMAVHP 71
DB 547 RKTIELKAKHSGEEMFVVKGEVDTCTPLSGHGAASIFGAAGDATEREEMHSE 606
QY 72 SVRPLRRFFVGRITDVTVPASD 96
DB 607 NAKAMLPYHIGLDESRALISGD 631

RESULT 2
NIA_BEABA STANDARD; PRT; 894 AA.
ID NIA_BEABA
AC P43100;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase (NADPH) (EC 1.7.1.3) (NR).
GN NIA.
OS Beauveria baasiana (Trichothium shioteae).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Cordycaps.
OX NCBI_TaxID=16275;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BB147;
RA Maurer P.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NADP(+) + H2O = nitrate + NADPH.
CC -1- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
CC AND ONE MOLYBDENUM ATOM.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X84950; CAAS9336.1; -.
CC PIR; S52857; S52857.

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DR HSSP; P04166; 1EUB.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR001834; Cyt_B5_reductase.
DR InterPro; IPR000572; Euk_Mb_oxred.
DR InterPro; IPR001709; FPN_cyt_reductase.
DR InterPro; IPR005066; Mo-co_dimer.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00970; FAD binding_6; 1.
DR Pfam; PF00173; heme 1; 1.
DR Pfam; PF03404; Mo-co_dimer; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR Pfam; PF00174; oxidored_molyb; 1.
DR PRINTS; PR00406; CYTB5RDYASE.
DR PRINTS; PR00363; CYTOCHROME B5.
DR PRINTS; PR00371; FPNCR.
DR PRODOM; PD000612; Cyt_B5_1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS00255; CYTOCHROME_B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KM Oxidoreductase; Flavoprotein; FAD; NADP; Heme; Molybdenum;
Nitrates assimilation..
KW METAL 169 169 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 220 220 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 418 418 INTERCHAIN (POTENTIAL).
FT METAL 570 570 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 593 593 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 894 AA; 99934 MW; D0ED234FB1B1322B CRC64;

Query Match 29.4%; Score 174; DB 1; Length 894;
Best Local Similarity 40.3%; Pred. No. 9.9e-11;
Matches 31; Conservative 18; Mismatches 28; Indels 0; Gaps 0;

QY 11 YRMISTKELQAHAAADLMISGVDVDTPLMRHHPGGEVPLITLAGODATDAPMAVHP 70
DB 535 VRLISLEELKAKHSGEEMFVVKGEVDTCTPLSGHGAATSTINAAQDATEREEMHIS 594
QY 71 PSVRPLRRFFVGRITDVTVPASD 87
DB 595 ENAKAMMPYHIGLITLND 611

RESULT 3
CY51_ARATH STANDARD; PRT; 134 AA.
ID CY51_ARATH
AC Q42342; Q9S805;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome b5 isoform 1.
GN AT5G53560 OR MNC6.10.
OS Arabidopsis thaliana (Mouse-ear cress). Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta; Eudicotyledons; core eudicots; Rosidae;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=99097071; PubMed=9880378;
RA Fukuchi-Mizutani M., Mizutani M., Tanaka Y., Kusumi T., Ohta D.;
RT "Microsomal electron transfer in higher plants: cloning and
RT heterologous expression of NADH-cytochrome betas reductase from
RT Arabidopsis.";
RL Plant Physiol. 119:353-361 (1999).
CC [2]
CC SEQUENCE FROM N.A.
CC STRAIN=cv. Columbia;
CC MEDLINE=99087489; PubMed=9872454;
CC Nakamura Y., Sato S., Asamizu E., Kaneko T., Kocani H., Miyajima N.,
CC Tabata S.;
CC "Structural analysis of Arabidopsis thaliana chromosome 5. VII.
CC Sequence features of the regions of 1,013,767 bp covered by sixteen

```

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RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:297-308(1998).
RN [3]
RP SEQUENCE OF 1-113 FROM N.A.
RC STRAIN=cv, Columbia;
RA Cooke R., Laudie M., Raynal M., Delyen M.;
RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
CC carrier for several membrane bound oxygenases (By Similarity).
CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE, BOUND TO THE
CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC -----
DR EMBL; AB007801; BAA74839.1; -
DR EMBL; AB015476; BAB09732.1; -
DR EMBL; F20001; CAA23377.1; -
DR PIR; T52469; T52469.
DR HSBP; P00171; IEHB.
DR InterPro; IPR001199; Cyt_B5.
DR Pfam; PF00173; heme_1; 1.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR ProDom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Electron transport; Transmembrane; Heme; Iron; Mitochondrion;
KW Multigene family.
FT FT 107 127 POTENTIAL.
FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT CONFLICT 1 3 MSS -> ARA (IN REF. 3).
SQ SEQUENCE 134 AA; 15084 MW; 9CC01C60F7C873FD CRC64;
Query March 28.6%; Score 169.5; DB 1; Length 134;
Best Local Similarity 36.5%; Pred. No. 3.5e-11;
Matches 31; Conservative 23; Mismatches 30; Indels 1; Gaps 1;
QY 8 AADVPMSTKELQAAHAADIMISIGDVTVPWLRHHPGGEVPLTLIAGQATDAFM- 66
Db 2 SSDSKVLSFEVSVSGNKTCKDMLISGKVTYVTFPMDDHPGDEVLSSTGKATINPDD 61
QY 67 AYPPSVPLRLRRFPVGLRDITYVP 91
Db 62 VGHSDTARDMDMKYFGEIDSSVVP 86
RESULT 4
CYB5_BRAOL STANDARD; PRT; 134 AA.
AC P40934;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome b5.
GN CYB5.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids II; Brassicales; Brassicaceae; Brassica.
OC NCBI_taxonomy=3712;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 6-47 AND 75-89.
RC STRAIN=cv, Cauliflora;
RA Kearns E.V., Keck P., Somerville C.R.;
RT "Nucleotide sequence of cDNA for cytochrome b5 from cauliflower
(Brassica oleracea L.).";

```

```

RL Plant Physiol. 99:1254-1257(1992)
CC -1- FUNCTION: Membrane bound hemoprotein which function as an electron
CC carrier for several membrane bound oxygenase.
CC -1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CC CYTOSOLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC -----
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CC
CC EMBL; M87514; AAA3290.1; -.
CC PIR; T14454; T14454.
CC DR HSSP; P00171; 1EH8.
CC DR InterPro; IPR001199; Cyt_B5.
CC DR Pfam; PF00173; heme_1; 1.
CC DR PRINTS; PR00363; CYTOCHROME_B5.
CC DR ProDom; PD000612; Cyt_B5; 1.
CC DR PROSITE; PSS00255; CYTOCHROME_B5_1; 1.
CC DR PROSITE; PSS00191; CYTOCHROME_B5_2; 1.
CC KW Electron transport; Transmembrane; Heme; Iron; Microsome.
CC TRANSMEM 107 127
CC METAL 40 40 POTENTIAL.
CC METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC VARIANT 5 5 K -> N
CC SEQUENCE 134 AA; 15062 MW; 764DC24A4CDD591 CRC64;

```

	Query Match	28.5%	Score 168.5;	DB 1;	Length 134;	
	Best Local Similarity	35.3%	Pred. No. 4,4e-11;			
	Matches	30;	Conservative	22;	Mismatches	31; Indels 1; Gaps 1,
Cy	8 AADVRISTKELOAHAAADDLMISGSDYDVTPTMLRNHPGGVEPLITLAGODATDAFM-	66				
	::: :::					
	::: :::					
Oy	67 AYHPSVRPLLRPFVGRLDTVP 91					
	::: :::					
Dd	62 VGHSDTRADMMEKYIGEIDSTIVP 86					
	::: :::					
RESULT 5						
NIAL TOBAC						
ID	NIAL TOBAC	STANDARD;	PRT;	904 AA.		
AC	P116D5;					
DT	01-OCT-1989 (Rel. 12, Created)					
DT	01-OCT-1989 (Rel. 12, Last sequence update)					
DT	28-FEB-2003 (Rel. 41, Last annotation update)					
DE	Nitrate reductase [NADH] 1 (EC 1.7.1.1) (NR1).					
DN	NIAI.					
OS	Nicotiana tabacum (Common tobacco).					
OC	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;					
OC	Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.					
OX	NCBI_TaxID=4097;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=cv. Xanthi; TISSUE=leaf;					
RA	Vauchereet H., Kronenberger J., Fouze P., Caboche M.;					
RT	"complete nucleotide sequence of the two homeologous tobacco nitrate					
RL	reductase genes.";					
PL	Plant Mol. Biol. 12:597-600(1989).					
CC	- FUNCTION: Nitrate reductase is a key enzyme involved in the first					
CC	step of nitrate assimilation in plants, fungi and bacteria.					
CC	- CATALYTIC ACTIVITY: Nitrite + NAD(+)+ H(2)O = nitrate + NADH.					
CC	- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,					
CC	HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME					
CC	GROUP IS CALLED CYTOCHROME B-557.					
CC	- ENZYME REGULATION: REGULATED BY THE NITROGEN SOURCE AND CONTROLLED					
CC	BY THE CIRCADIAN RHYTHM.					

CC -1- SUBUNIT: Homodimer.
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 CC N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
 CC C-TERMINAL DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X14058; CA32216.1; -.
 CC F1R; S04838; RDNNT.
 CC HSP; P15771; ZCND.
 CC InterPro: IPR001199; Cyt_B5.
 CC InterPro: IPR001834; Cyt_B5_reductase.
 CC InterPro: IPR000572; Bk_Mb_oxrd.
 CC InterPro: IPR001709; PPN_Cyt_redctse.
 CC InterPro: IPR005066; Mo-co_dimer.
 CC InterPro: IPR001433; Oxrd_FAD/NAD(p).
 CC Pfam: PF00970; FAD_binding_6; 1.
 CC Pfam: PF00173; heme_1; 1.
 CC Pfam: PF03404; Mo-co_dimer; 1.
 CC Pfam: PF00175; NAD_binding_1; 1.
 CC Pfam: PF00174; oxidored_melb; 1.
 CC PRINTS: PR00406; CYTB5RDTASE.
 CC PRINTS: PR00363; CYTOCHROMEBS.
 CC PRINTS: PR00407; EMOPTERIN.
 CC PRINTS: PR00371; FPNCR.
 CC ProDom: PD000612; Cyt_B5; 1.
 CC ProSite: PS00191; CYTOCHROME_B5_1; 1.
 CC ProSite: PS50255; CYTOCHROME_B5_2; 1.
 CC ProSite: PS00559; MOLYBDOPTERIN_EUK; 1.
 CC KX Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
 CC Nitrate assimilation; Multigene family;
 CC FT METAL 183 183 MOLYBDENUM-PTERIN (POTENTIAL).
 CC FT METAL 237 237 MOLYBDENUM-PTERIN (POTENTIAL).
 CC FT DISULFID 422 422 INTERCHAIN (POTENTIAL).
 CC FT METAL 566 566 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC FT METAL 589 589 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC SQ SEQUENCE 904 AA; 101907 MW; 85642BDA723EE154 CRC64;
 CC
 CC Query Match 28.2%; Score 167; DB 1; Length 904;
 CC Best Local Similarity 35.7%; Pred. No. 5.6e-10;
 CC Matches 40; Conservative 15; Mismatches 43; Indels 14; Gaps 3;
 CC
 CC QY 1 MPASKADAVRMSTKELQAAADLMTISGDVYDVTPMLRHGGEVPLITLAGOD 60
 CC DB 527 MNTSK-----MYSSEVRGSSADSAWIIHGHIYDARPLRDLHGSSDSITINAGTD 580
 CC QY 61 ATDAFMAHPSPVRLRPFVGRLT--TDYTPP-----ASADFRLLAQL 104
 CC DB 581 CTEFEDAIHDKAKKLEFRIGELITGTTSDFGNSVHGSSSFSLAPI 632
 CC
 CC RESULT 6
 CC CYB5_TOBAC STANDARD; PRT; 136 AA.
 CC ID CYB5_TOBAC
 CC DT 01-FEB-1996 (Rel. 33, Created)
 CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Cytochrome b5.
 CC OS Nicotiana tabacum (Common tobacco).
 CC OC Burkholderia, Vibrionaceae, Streptococcus, Embryophyta, Tracheophyta;
 CC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC OC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.
 CC NCBI_TaxId=4097;
 CC RX [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RX MEDLINE=94325476; PubMed=8049375;
 RA Smith M.A., Stobart A.K., Shewry P.R., Napier J.A.;
 RT Tobacco cytochrome b5: cDNA isolation, expression analysis and in
 RT vitro protein targeting.";
 RL Plant Mol. Biol. 25:527-537 (1994).
 CC -1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
 CC FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
 CC OXYGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY
 CC DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH IN
 CC THE DEVELOPING SEED IS UTILIZED FOR MEMBRANE SYNTHESIS AND IN THE
 CC DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE
 CC LIPIDS. IS INVOLVED IN THE REDUCTION OF CYTOCHROME P-450 AND
 CC MAY THEREFORE BE INVOLVED IN FLAVONOID BIOSYNTHESIS IN THE PETALS.
 CC -1- SUBCELLULAR LOCATION: MICROSOAL MEMBRANE. BOUND TO THE
 CC CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: IS HIGHLY EXPRESSED IN DEVELOPING SEEDS,
 CC MODERATELY EXPRESSED IN FLOWERS, AND IS EXPRESSED AT LOW
 CC LEVELS IN THE LEAF.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X71441; CA50575.1; ALT_INIT.
 CC EMBL: X68140; CA448240.1; -.
 CC HSP; P04166; 1BSM.
 CC InterPro: IPR001199; Cyt_B5.
 CC InterPro: IPR00173; heme_1; 1.
 CC ProDom: PD000612; Cyt_B5; 1.
 CC ProSite: PS00191; CYTOCHROME_B5_1; 1.
 CC ProSite: PS50255; CYTOCHROME_B5_2; 1.
 CC DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 CC KX Electron transport; Transmembrane; Heme; Iron; Microsome;
 CC Multigene family.
 CC FT TRANSMEM 107 127 POTENTIAL.
 CC FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC FT CONFLICT 10 11 LA -> EF (IN REF. 1; CA448240).
 CC FT CONFLICT 105 105 MISSING (IN REF. 1; CA448240).
 CC SQ SEQUENCE 136 AA; 14979 MW; DACE9EA695B2835F CRC64;
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 CC Query Match 28.0%; Score 165.5; DB 1; Length 136;
 CC Best Local Similarity 39.8%; Pred. No. 9.4e-11;
 CC Matches 33; Conservative 16; Mismatches 33; Indels 1; Gaps 1;
 CC
 CC QY 10 DVAMISTKELQAAADLMTISGDVYDVTPMLRHGGEVPLITLAGODATDAFM-AY 68
 CC DB 4 ETRVFTIAEVSQINNAKDCMLVYSGRYDVYTFLLDHPGDEVLATSKDATTDEPDVG 63
 CC QY 69 HPSVRLRPFVGRITDYTP 91
 CC DB 64 HSSAPAMDEYVGDISATIP 86
 CC
 CC RESULT 7
 CC NIA_NEUCR STANDARD; PRT; 982 AA.
 CC ID NIA_NEUCR
 CC DT 01-AUG-1988 (Rel. 08, Created)
 CC DT 01-MAY-1992 (Rel. 22, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Nitrate reductase [NADPH] (EC 1.7.1.3) (NR).
 CC GN NIT-3.
 CC OS Neurospora crassa.
 CC OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 CC NCBI_TaxId=5141;
 CC RX [1]

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=74-OR23-1A / FGSC 987;
 RX MEDLINE=91287699; PubMed=1829499;
 RA Okamoto P.M., Fu Y.-H., Marzluf G.A.;
 RT "Nit-3, the structural gene of nitrate reductase in *Neurospora crassa*: nucleotide sequence and regulation of mRNA synthesis and turnover."
 RL Mol. Gen. Genet. 227:213-223(1991).
 RN [2]
 RP PRELIMINARY PARTIAL SEQUENCE AROUND HIS-652.
 RA Le K.H.D., Lederer F.;
 RT "On the presence of a heme-binding domain homologous to cytochrome b5 in *Neurospora crassa* assimilatory nitrate reductase."
 RL EMBO J. 2:1909-1914(1983).
 RN [3]
 RP MUTANTS.
 RC STRAIN=74-OR23-1A / FGSC 987;
 RX MEDLINE=93241176; PubMed=8479443;
 RA Okamoto P.M., Garrett R.H., Marzluf G.A.;
 RT "Molecular characterization of conventional and new repeat-induced mutants of nit-3, the structural gene that encodes nitrate reductase in *Neurospora crassa*."
 RL Mol. Gen. Genet. 238:81-90(1993).
 RN [4]
 RP MUTAGENESIS.
 RC MEDLINE=93360901; PubMed=8355655;
 RA Okamoto P.M., Marzluf G.A.;
 RT "Nitrate reductase of *Neurospora crassa*: the functional role of individual amino acids in the heme domain as examined by site-directed mutagenesis."
 RL Mol. Gen. Genet. 240:221-230(1993).
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NADPH(+) + H(2)O = nitrate + NADPH.
 CC -1- COFACTOR: EACH SUBUNIT CONTAINS 1 EQUIVALENT OF FAD, HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME GROUP IS CALLED CYTOCHROME B-557.
 CC -1- PATHWAY: Nitrate assimilation (denitrification).
 CC -1- SUBUNIT: Homodimer.
 CC -1- INDUCTION: ITS EXPRESSION IS HIGHLY REGULATED AND RESPONDS RAPIDLY TO NITRATE INDUCTION AND TO NITROGEN REPRESSION.
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE C-TERMINAL DOMAIN.
 CC -----
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 CC -----
 CC EMBL, X61303; CAA43600.1; --
 CC HSSP, P00171; 1F03.
 DR InterPro: IPR001199; Cyt B5.
 DR InterPro: IPR001834; Cyt B5 reductase.
 DR InterPro: IPR000572; Btk_Mb_oxred.
 DR InterPro: IPR005066; Mo-co_dimer.
 DR InterPro: IPR001433; Oxred_FAD/NAD(P).
 DR Pfam: PF00970; FAD_binding_6; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR Pfam: PF03404; Mo-co_dimer; 1.
 DR Pfam: PF00175; NAD_binding_1; 1.
 DR Pfam: PF00174; oxidored_mol_yb; 1.
 DR PRINTS; PRO0406; CYTBSRDRASE.
 DR PRINTS; PRO0363; CYTOCHROMEBS.
 DR PRINTS; PRO0407; EUMOPTERIN.
 DR ProDom; PD000612; Cyt B5; 1.
 DR PROSITE, PS00191; CYTOCHROME_B5_1; 1.

DR PROSITE, PS0255; CYTOCHROME B5_2; 1.
 DR PROSITE, PS00559; MOLYBDOPTERIN_EUK; 1.
 KM Oxidoreductase; Flavoprotein; FAD; NADP; Heme; Molybdenum;
 KM Nitrate assimilation.
 FT METAL 240 240
 FT METAL 295 295
 FT DISULFID 499 499
 FT DOMAIN 621 691
 FT METAL 652 652
 FT METAL 675 675
 FT METAL 718 962
 FT NP_BIND 952 961
 FT MUTAGEN 652 652
 FT MUTAGEN 675 675
 SQ SEQUENCE 982 AA; 108432 MW; B7638C031B19687F CRC64;
 Query Match 28.0%; Score 165.5; DB 1; Length 982;
 Best Local Similarity 33.3%; Pred. No. 8.9e-10;
 Matches 33; Conservative 19; Mismatches 38; Indels 9; Gaps 1;
 QY 7 DAADVMTKELQAAADDLWISSGVYDVTPLRHNGGEVPLITLAGDADTAPM 66
 DB 613 DEKVTPLITLLELRQHDGESEPFVNVGQVNGTPEPLFGHFGAASITGAAGDVTDFL 672
 QY 67 AYHPSVRPLRRPFVGRLT-----DYTPPSAD 96
 DB 673 AIHSEKAKMPTYHIGTITPSAPALAKSSITSDPALSD 711
 RESULT 8
 NIA2_TOBAC STANDARD; PRT; 904 AA.
 ID NIA2_TOBAC
 AC P08509;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Nitrate reductase [NADH] 2 (EC 1.7.1.1) (NR2).
 GN NIA2.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxId=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Xanthi; TISSUE=Leaf;
 RA Vaucheret H., Kronenberger J., Rouze P., Caboche M.;
 RT "Complete nucleotide sequence of the two homologous tobacco nitrate reductase genes."
 RL Plant Mol. Biol. 12:597-600(1989).
 RN [2]
 RP SEQUENCE OF 171-724 FROM N.A.
 RA Calza R., Hutterer B., Vincenz M., Rouze P., Galanau F.,
 RA Vaucheret H., Cherel I., Meyer C., Kronenberger J., Caboche M.;
 RT "Cloning of DNA fragments complementary to tobacco nitrate reductase mRNA and encoding epitopes common to the nitrate reductases from higher plants."
 RL Mol. Genet. 209:552-562(1987).
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NADPH(+) + H(2)O = nitrate + NADH.
 CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD, HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME GROUP IS CALLED CYTOCHROME B-557.
 CC -1- ENZYME REGULATION: REGULATED BY THE NITROGEN SOURCE AND CONTROLLED BY THE CIRCADIAN RHYTHM.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE C-TERMINAL DOMAIN.
 CC -----


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RT barley.";
RL Mol. Genet. 228:329-334(1991).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(P)+ + H2O = nitrate +
CC NAD(P)H.
CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
CC GROUP IS CALLED CYTOCHROME B-557.
CC -1- SUBUNIT: Homodimer.
CC -1- INDUCTION: By nitrate.
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X60173; CAA42739.1; -.
DR PIR: S16895; RBHNP.
DR HSSP: P17571; 2CND.
DR InterPro: IPR001199; Cyt_B5.
DR InterPro: IPR001834; Cyt_B5_reductase.
DR InterPro: IPR000572; Euk_Mb_oxred.
DR InterPro: IPR001709; FPN_Mb_reductase.
DR InterPro: IPR005066; Mo-co_dimer.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR InterPro: IPR001221; Phe_hydroxylase.
DR Pfam: PF00970; FAD_binding_6; 1.
DR Pfam: PF00173; heme_1; 1.
DR Pfam: PF03404; Mo-co_dimer; 1.
DR Pfam: PF00175; NAD_binding_1; 1.
DR Pfam: PF00174; oxidored_molyd; 1.
DR PRINTS: PR00406; CYTB5RDYASE.
DR PRINTS: PR00363; CYTOCHROMEBS.
DR PRINTS: PR00407; EUMOPTERIN.
DR PRINTS: PR00371; PPNCR.
DR PRINTS: PR00410; PHEHYDRYLASE.
DR PRODOM: PD000612; Cyt_B5; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS0255; CYTOCHROME_B5_2; 1.
DR PROSITE: PS00559; MOLYBDOPTERIN_EUK; 1.
DR Oxidoreductase; Flavoprotein; FAD; NAD; NADP; Heme; Molybdenum;
DR Nitrate assimilation; Multigene family.
DR METAL 168 168 MOLYBDENUM-PTERIN (POTENTIAL).
DR METAL 221 221 MOLYBDENUM-PTERIN (POTENTIAL).
DR DISULFID 406 406 INTERCHAIN (POTENTIAL).
DR METAL 550 550 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
DR METAL 573 573 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
DR SEQUENCE 891 AA; 96630 MW; AA47EC52FC1EF3D3 CRC64;

Query Match 27.3%; Score 161.5; DB 1; Length 891;
Best Local Similarity 35.6%; Pred. No. 2.1e-09;
Matches 37; Conservative 16; Mismatches 44; Indels 7; Gaps 2;

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ID NIA_CHLVU STANDARD; PRT; 318 AA.
AC 001170;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR) (Fragment).
OS Chlorella vulgaris.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Chlorella.
OX NCBI_TaxID=3077;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=91354204; PubMed=1883330;
RA Camons A.C., Iida N., Solomonson L.P.;
RT "Expression of a cDNA clone encoding the haem-binding domain of
RT Chlorella nitrate reductase."
RL Biochem. J. 278:203-209(1991).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(P)+ + H2O = nitrate + NADH.
CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
CC GROUP IS CALLED CYTOCHROME B-557.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56771; CAA0090.1; -.
DR PIR: S17197; S17197.
DR HSSP: P04166; 1BSM.
DR InterPro: IPR001199; Cyt_B5.
DR InterPro: IPR000572; Euk_Mb_oxred.
DR InterPro: IPR005066; Mo-co_dimer.
DR Pfam: PF00173; heme_1; 1.
DR Pfam: PF03404; Mo-co_dimer; 1.
DR PRINTS: PR00363; CYTOCHROMEBS.
DR PRINTS: PR00407; EUMOPTERIN.
DR PRODOM: PD000612; Cyt_B5; 1.
DR PROSITE: PS00191; CYTOCHROME_B5_1; 1.
DR PROSITE: PS0255; CYTOCHROME_B5_2; 1.
DR PROSITE: PS00559; MOLYBDOPTERIN_EUK; PARTIAL.
DR Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
DR Nitrate assimilation.
DR METAL 251 251 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
DR METAL 274 274 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
DR NON TER 318 318
DR SEQUENCE 318 AA; 34830 MW; E60D82FE1E98292A CRC64;

Query Match 27.2%; Score 161; DB 1; Length 318;
Best Local Similarity 33.0%; Pred. No. 7.5e-10;
Matches 29; Conservative 18; Mismatches 41; Indels 0; Gaps 0;

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RESULT 11
NIA_CHLVU

RESULT 12
 ID NIA_PETHY STANDARD; PRT; 909 AA.
 AC P36859;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR).
 GN NIA.
 OS Petunia hybrida (Petunia).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Solanales; Solanaceae; Petunia.
 OC NCBI_Taxid=4102;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. TLR13; Tissue=Leaf;
 RX MEDLINE=9392981; PubMed=8514183;
 RA Salanoubat M., Ha D.B.D.;
 RT "Analysis of the petunia nitrate reductase apoenzyme-encoding gene: a
 first step for sequence modification analysis.";
 RL Gene 128:147-154 (1993).
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
 step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
 CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
 HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
 GROUP IS CALLED CYTOCHROME B-557.
 CC -1- ENZYME REGULATION: REGULATED BY THE NITROGEN SOURCE AND CONTROLLED
 BY THE CIRCADIAN RHYTHM.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- DEVELOPMENTAL STAGE: MAXIMUM EXPRESSION 2 HOURS AFTER SUNRISE. LOW
 EXPRESSION FOUND 2 HOURS BEFORE AND 8 HOURS AFTER SUNRISE.
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -1- SIMILARITY: To FAD/MAD-BINDING CYTOCHROME REDUCTASES IN THE
 C-TERMINAL DOMAIN.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: U13691; AAA3713.1; --
 CC HSSP: P17571; 2CND.
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR001834; Cyt_B5 reductase.
 DR InterPro: IPR000572; Euk_Mb_oxred.
 DR InterPro: IPR001709; FPN_Cyt_reductase.
 DR InterPro: IPR005066; Mo-co_dimer.
 DR InterPro: IPR001433; Oxred_FAD/NAD(P).
 DR Pfam: PF00970; FAD binding_6; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR Pfam: PF03404; Mo-co_dimer; 1.
 DR Pfam: PF00175; NAD binding_1; 1.
 DR Pfam: PF00174; Oxidored_molyb; 1.
 DR PRINTS: PR00406; CYTBSRDYASE.
 DR PRINTS: PR00363; CYTOCHROMEBS.
 DR PRINTS: PR00407; EUMOPTERIN.
 DR PRINTS: PR00371; FPNCR.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProSITE: PS00191; CYTOCHROME_B5_1; 1.
 DR ProSITE: PS0255; CYTOCHROME_B5_2; 1.
 DR PROSITE: PS00559; MOLYBDOPTERIN_EUK; 1.
 DR KMW: Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
 KM Nitrate assimilation; Multigene family.
 FT METAL 187 187 MOLYBDENUM-PTERIN (POTENTIAL).
 FT METAL 241 241 MOLYBDENUM-PTERIN (POTENTIAL).
 FT DISULFID 426 426 INTERCHAIN (POTENTIAL).

FT METAL 570 570 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 593 593 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 909 AA; 102376 MW; 502C706F6563E706 CRC64;
 Query Match 26.9%; Score 159.5; DB 1; Length 909;
 Best Local Similarity 36.3%; Pred. No. 3.6e-09;
 Matches 41; Conservative 14; Mismatches 43; Indels 15; Gaps 3;
 QY 1 MPASKADADVIRISIKELQAAADLMISIGDYDVTPLRHHPGGEVPLITLAGOP 60
 DB 531 MNTASK-----MYSSEVKKNSADSAMIIYGHVYDTRFLKDPGGIDSLINAGTD 584
 QY 61 ATDAFAPAYHPSPVRLRRPFVGRLT--TDYVPPA-----SADFRRLAQL 104
 DB 585 CTEEPDAIHSDDAKKLLLEDPRIGELITTYGTSSSPNNSVHSSSFGFLAP1 637
 RESULT 13
 ID NIAI_ARATH STANDARD; PRT; 917 AA.
 AC P11832; O9CA18;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Nitrate reductase [NADH] 1 (EC 1.7.1.1) (NR1).
 GN NIAI OR AT1677760 OR T3288.9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosidia II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.; VARIANT THR-198, AND HERBICIDE RESISTANCE.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=93287999; PubMed=8510658;
 RA Wilkinson J.Q., Crawford N.M.;
 RT "Identification and characterization of a chlorate-resistant mutant
 RT of Arabidopsis thaliana with mutations in both nitrate reductase
 RT structural genes NIA1 and NIA2.";
 RL Mol. Gen. Genet. 239:289-297 (1993).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=cv. Columbia;
 RC MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federpspiel N.A., Kaul S.,
 RA White O., Alonso J., Alcafi H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Benlier E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Greasy T.H., Dewar K.,
 RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Feng B., Fujii C.Y.,
 RA Gali J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremetskaia I., Kutz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Malt R., Marshall A.,
 RA Miltiescher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Tortum M.J., Town C.D.,
 RA Utenhake T., Van Aken S., Vayberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Frazer C.M., Ventler J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 408:816-820 (2000).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=cv. Columbia;
 RC Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 RT SSP consortium (Salk/Stanford/PGSC).";
 RN Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 342-360 AND 525-917 FROM N.A.
 RX MEDLINE=89091069; PubMed=2905260;

Cheng C., Dewdney J., Nam H., den Boer B.G.W., Goodman H.M.;
 "A new locus (NIA 1) in Arabidopsis thaliana encoding nitrate
 reductase.";
 EMBO J. 7:3309-3314 (1988).
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
 CC step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
 CC -1- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD,
 CC HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
 CC GROUP IS CALLED CYTOCHROME B-557.
 CC -1- SUBUNIT: Homodimer.
 CC -1- TISSUE SPECIFICITY: ROOT, LEAF, AND SHOOT.
 CC -1- MISCELLANEOUS: WHEN MUTATED CONFERS RESISTANCE TO THE HERBICIDE
 CC CHLORATE.
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 CC N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 CYTOCHROME B5 HEME-BINDING DOMAIN.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
 CC C-TERMINAL DOMAIN.
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 CC -----
 DR EMBL; AC012193; AAG51627.1; -;
 DR EMBL; AY090950; AAM13997.1; -;
 DR EMBL; AF424624; AAL1617.1; -;
 DR EMBL; X13434; CAA31786.1; -;
 DR EMBL; X13436; CAA31786.1; -;
 DR PIR; E96807; E96807.
 DR PIR; S35228; S35228.
 DR HSSP; P17571; 2CND.
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR001834; Cyt_B5_reductase.
 DR InterPro: IPR000572; Euk_Mb_oxred.
 DR InterPro: IPR001709; FPN_cyt_reductase.
 DR InterPro: IPR005066; Mo-co_dimer.
 DR InterPro: IPR001433; Oxred_FAD/NAD(P).
 DR InterPro: IPR001221; Phe_hydroxylase.
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR Pfam; PF03404; Mo-co_dimer; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR Pfam; PF00174; oxidored_molyb; 1.
 DR PRINTS; PR00406; CYTB5RDTASE.
 DR PRINTS; PR00363; CYTB5RDTASE.
 DR PRINTS; PR00407; EUMOPTERIN.
 DR PRINTS; PR00371; FPNCR.
 DR PRINTS; PR00410; PHEHYDRXLAZE.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE; PS02255; CYTOCHROME_B5_2; 1.
 DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
 DR Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
 DR Nitrate assimilation; Multigene family; Herbicide resistance.
 DR METAL; 197; MOLYBDENUM-PTERIN (POTENTIAL).
 DR METAL; 251; MOLYBDENUM-PTERIN (POTENTIAL).
 DR METAL; 251; MOLYBDENUM-PTERIN (POTENTIAL).
 DR METAL; 436; INTERCHAIN (POTENTIAL).
 DR METAL; 580; IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 DR METAL; 603; IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 DR VARIANT; 198; A -> T (LOSS OF ACTIVITY).
 DR VARIANT; 17; A -> R (IN REF. 1).
 DR CONFLICT; 17; A -> R (IN REF. 1).
 DR SEQUENCE; 917 AA; 103040 MW; 6F3ED46B9F63825 CR64;

Query Match 26.9%; Score 159.5; DB 1; Length 917;
 Best Local Similarity 35.1%; Pred. No. 3; 6e-09;
 Matches 39; Conservative 16; Mismatches 43; Indels 13; Gaps 3;
 QY 1 MPAAKADADVMISTPELQAAADDLWISIGDYDVTPLRHHGGEVPLITLAGOD 60
 DB 541 MNTASK-----MYSISEVRKNTADSMIYHGHITDCTRFKHPGGTDSLINAGTD 594
 QY 61 ATDAFMAVHPSPVRLRRFPVGRLLTDYVPP-----ASADFRLLAQL 104
 DB 595 CEEFPAIRSDAKKLLLEDYRIGELLITGYDSSPNVSVGASNFGGLAPV 645
 RESULT 14
 ID NIA1 PHAVU STANDARD; PRT; 881 AA.
 AC P39865;
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Nitrate reductase [NADH] 1 (EC 1.7.1.1) (NR-1).
 GN NIA1 OR NR1.
 OS Phaseolus vulgaris (kidney bean) (French bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosid 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
 OX NCBI_TaxID=3885;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Saxa; TISSUE=Shoot;
 RA Hoff T., Stummann B.W., Henningsen K.W.;
 RT "Cloning and expression of a gene encoding a root specific nitrate
 RT reductase in bean (Phaseolus vulgaris).";
 RL Physiol. Plantarum 82:197-204(1991).
 CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
 CC step of nitrate assimilation in plants, fungi and bacteria.
 CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
 CC -1- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
 CC AND ONE MOLYBDENUM ATOM.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
 CC N-TERMINAL DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 CYTOCHROME B5 HEME-BINDING DOMAIN.
 CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
 CC C-TERMINAL DOMAIN.
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 CC -----
 DR EMBL; X53603; CAA37672.1; -;
 DR PIR; S25445; S25445.
 DR HSSP; P17571; 2CND.
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR001834; Cyt_B5_reductase.
 DR InterPro: IPR000572; Euk_Mb_oxred.
 DR InterPro: IPR001709; FPN_cyt_reductase.
 DR InterPro: IPR005066; Mo-co_dimer.
 DR InterPro: IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR Pfam; PF03404; Mo-co_dimer; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR Pfam; PF00174; oxidored_molyb; 1.
 DR PRINTS; PR00406; CYTB5RDTASE.
 DR PRINTS; PR00363; CYTB5RDTASE.
 DR PRINTS; PR00407; EUMOPTERIN.
 DR PRINTS; PR00371; FPNCR.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE; PS02255; CYTOCHROME_B5_2; 1.
 DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
 DR Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;

KW Nitrate assimilation; Multigene family.
 FT METAL 167 167 MOLYBDENUM-PTERIN (POTENTIAL).
 FT METAL 221 221 MOLYBDENUM-PTERIN (POTENTIAL).
 FT DISULFID 406 406 INTERCHAIN (POTENTIAL).
 FT METAL 550 550 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 573 573 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 881 AA; 99222 MW; A212A1288BAEE661 CRC64;
 Query Match 26.8%; Score 159; DB 1; Length 881;
 Best Local Similarity 38.1%; Pred. No. 3.9e-09;
 Matches 32; Conservative 16; Mismatches 34; Indels 2; Gaps 1;
 QY 15 STEKQAHAAADLWISGVDVTPWLRHHPGGEVPLITLAGODATDAFMAYHPSPVR 74
 DB 519 SLSEVRHNRNRDAMITVNHVYDCTRFKDHFGEGSILNAGCTCTEEFEALHSKAK 578
 QY 75 PLRRPFVGRLLTDYTPPASAD 96
 DB 579 KMLEDYRIGELMTDYSDDSSN 602
 RESULT 15
 FADS_BRARE STANDARD; PRT; 444 AA.
 ID FADS_BRARE
 AC QDEX7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Delta-5/delta-6 fatty acid desaturase (EC 1.14.19.-).
 GN FADS2 OR FADS6.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCBI_TaxID=7935;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=21592990; PubMed=11724940;
 RA Hastings N., Agaba M., Tocher D.R., Leaver M.J., Dick J.R.,
 RA Sargent J.R., Teale A.J.;
 RT "A vertebrate fatty acid desaturase with delta5 and delta6
 RT activities";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:14304-14309(2001).
 CC -1- FUNCTION: Fatty acid desaturase with both delta-5 and delta-6
 CC activities. May represent a component of the polyunsaturated fatty
 CC acid biosynthesis pathway.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
 CC -----
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 CC -----
 CC DR EMBL; AF309556; AAG25710.1; -;
 DR HSSP; P00173; IJEX.
 DR ZFIN; ZDB-GENE-011212-1; fads2.
 DR InterPro; IPR001199; Cyt B5.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR Pfam; PF00173; heme_1; 1.
 DR ProDom; PD000612; Cyt B5; 1.
 DR ProDom; PD001081; FA_desat_fam; 2.
 DR PROSITE; PS00191; CYTOCHROME_B5_1; FALSE_NEG.
 DR PROSITE; PS0235; CYTOCHROME_B5_2; 1.
 KW Fatty acid biosynthesis; Oxidoreductase; Heme.
 FT DOMAIN 18 95 HEME-BINDING.
 FT METAL 53 53 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

FT METAL 76 76 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 444 AA; 52032 MW; 6AA25A1DC1DC0F65 CRC64;
 Query Match 26.8%; Score 158.5; DB 1; Length 444;
 Best Local Similarity 35.2%; Pred. No. 2e-09;
 Matches 37; Conservative 18; Mismatches 39; Indels 11; Gaps 3;
 QY 17 KETQAHAAADLWISGVDVTPWLRHHPGGEVPLITLAGODATDAFMAYHP--PSVR 74
 DB 24 EYQKTKHGDQVYVERKYNVSCVKNHFGGLRILGHVAGEDATDAFTAPHPNQLVR 83
 QY 75 PLRRPFVGRLLTDYTPPAS-----ADFRLLAQLSSAGLFE 111
 DB 84 KYLKPLLIGEL-EASEPSQDRQNALVEDFRALRERLAECCFK 127
 Search completed: January 1, 2004, 06:30:57
 Job time : 3.5084 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49 ; Search time 10.2316 Seconds
(without alignments)
2875.205 Million cell updates/sec

Title: US-09-857-524B-17
Perfect score: 592
Sequence: 1 MPAAKADADVMISTKELQ.....ADFRRLAQLASAGLPERVQ 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	592	100.0	469	10	Q92TUB
2	306	51.7	446	10	Q81LD7
3	282.5	47.7	446	10	Q9FR82
4	274.5	46.4	458	10	Q43469
5	267.5	45.2	448	10	Q8VZ21
6	263.5	44.5	448	10	Q8VZ22
7	262.5	44.5	446	10	Q92T79
8	258	43.6	448	10	Q9SNU5
9	258	43.6	448	10	Q04353
10	250.5	42.3	449	10	Q92RPH
11	249	42.1	448	10	Q8L717
12	236.5	39.9	449	10	Q8LB96
13	236.5	39.9	449	10	Q92RPH
14	195	32.7	477	10	Q8RXB0
15	193.5	32.7	459	10	Q944W4
16	180	30.4	464	5	Q9Y1W0

17	178.5	30.2	929	3	Q8J259	Q8J259 tuber borch
18	177	29.9	445	13	Q90ZB9	Q90ZB9 oreochromis
19	177	29.9	907	3	Q92237	Q92237 gibberella
20	175.5	29.6	135	10	Q9FDW8	Q9FDW8 arabidopsis
21	173	29.2	891	3	Q00101	Q00101 phaeosphaer
22	172.5	29.1	445	13	Q8Y644	Q8Y644 sparus aura
23	169.5	28.6	452	13	Q8UTM5	Q8UTM5 oncorhynch
24	169.5	28.6	467	5	Q96099	Q96099 dicystostei
25	169.5	28.6	870	3	Q9P942	Q9P942 hansenula a
26	168.5	28.5	444	13	Q9P942	Q9P942 cyprinus ca
27	167.5	28.3	134	10	Q8H293	Q8H293 ananas como
28	166.5	28.1	140	10	Q92WT2	Q92WT2 arabidopsis
29	165.5	28.0	134	10	Q48618	Q48618 olea europ
30	165.5	28.0	454	13	Q98SW7	Q98SW7 oncorhynch
31	161.5	27.3	873	3	Q8X1X0	Q8X1X0 monascus an
32	161	27.2	882	10	Q9SDY3	Q9SDY3 chlamydomon
33	160.5	27.1	454	13	Q90ZB8	Q90ZB8 oncorhynch
34	160	27.0	877	10	Q42497	Q42497 chlorella v
35	160	27.0	983	3	Q96VE8	Q96VE8 ustilago ma
36	159.5	26.9	892	3	Q13486	Q13486 metarhizium
37	159.5	26.9	915	10	Q43042	Q43042 petunia hyb
38	155.5	26.3	134	10	Q94HX5	Q94HX5 oryza sativ
39	155	26.2	914	10	Q9PFC2	Q9PFC2 ricinus com
40	154.5	26.1	89	5	Q8SY77	Q8SY77 diosiphila
41	154.5	26.1	132	10	Q24651	Q24651 olea europ
42	154.5	26.1	477	10	Q8H0N8	Q8H0N8 phytophthor
43	154	26.0	486	11	Q9P924	Q9P924 rattus norv
44	153.5	25.9	456	10	Q944W3	Q944W3 pythium itr
45	152.5	25.8	386	4	Q96H07	Q96H07 homo sapien

ALIGNMENTS

RESULT 1	ID	Q92TUB	PRELIMINARY;	PRT;	469 AA.
AC	Q92TUB	01-MAY-1999 (T-EMBLrel. 10, Created)			
DT	01-MAY-1999 (T-EMBLrel. 10, Last sequence update)				
DT	01-MAR-2003 (T-EMBLrel. 23, Last annotation update)				
DE	S276.				
GN	S276.				
OS	Triticum aestivum (wheat).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;				
OC	Triticaceae; Triticum.				
OX	NCBI_TaxID=4565;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=cv. ET3;				
RA	Delhaize E., Hebb D.M., Gardner R.C., Richards K.D.;				
RT	"Aluminum tolerance in yeast conferred by over-expression of wheat				
RT	genes.";				
RL	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.				
CC	-1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.				
DR	EMBL; AF031194; AAD10250.1; -				
DR	HSSP; P00171; I150.				
DR	InterPro; IPR001199; Cyt B5.				
DR	InterPro; IPR005804; PA_decat fam.				
DR	InterPro; IPR001092; H1H_basitc.				
DR	Pfam; PF00487; PA_decatase; 1.				
DR	Pfam; PF00173; heme_1; 1.				
DR	PRINTS; PR00363; CYTOCHROME B5.				
DR	ProDom; PD000612; Cyt B5; 1.				
DR	ProDom; PD001081; PA_decat fam; 1.				
DR	PROSITE; PS50255; CYTOCHROME_B5_2; 1.				
DR	PROSITE; PS00038; H1H_1; 1.				
KW	Heme.				
SQ	SEQUENCE 469 AA; 52617 MW; 16F223CC1F79740D CRC64;				
Query Match	100.0%;	Score 592;	DB 10;	Length 469;	
Best Local Similarity	100.0%;	Pred. NO. 3.1e-54;			

Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASKCAADVRMTSTKELQAAADLMISGSDVYDTPWLRHNGGVEPLTTAGOD 60
 DB 17 MPASKCAADVRMTSTKELQAAADLMISGSDVYDTPWLRHNGGVEPLTTAGOD 76

QY 61 ATDAFMAVHPSPVRLRRFFVGLTDTYVPPASADFRRLAQLSSAGLPERVG 114
 DB 77 ATDAFMAVHPSPVRLRRFFVGLTDTYVPPASADFRRLAQLSSAGLPERVG 130

RESULT 2
 Q8LBD7
 ID Q8LBD7 PRELIMINARY; PRT; 446 AA.
 AC Q8LBD7
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DE Sphingolipid long chain base delta 8 desaturase.
 OS Aquilegia vulgaris.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
 OC Ranunculaceae; Aquilegia.
 OC NCBI_TaxID=3451;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Longman A.J., Michaelson L.V., Napier J.A.;
 RT "Isolation and characterization of a cDNA encoding a delta 8
 sphingolipid desaturase from Aquilegia vulgaris."
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AF406816; AAN03619.1; -
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR PRINTS: PR00363; CYTOCHROME_B5.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 446 AA; 51273 MW; 76366DDB0EB956D09 CRC64;

Query Match 51.7%; Score 306; DB 10; Length 446;
 Best Local Similarity 51.5%; Pred. No. 5.3e-24;
 Matches 53; Conservative 22; Mismatches 28; Indels 0; Gaps 0;

QY 12 RMISTKELQAAADLMISGSDVYDTPWLRHNGGVEPLTTAGODATDAFMAVHP 71
 DB 6 REITSEELKHKHKGDIWISIQGKIYVSEWIKDHPGSEAPLNLAAQDVTDAFVHPG 65

QY 72 SVRPLRRFFVGLTDTYVPPASADFRRLAQLSSAGLPERVG 114
 DB 66 SAWKYLDFKFTGLKDYLTISVSKDYRKLVAFESKAGLYDKG 108

RESULT 3
 Q9FR82
 ID Q9FR82 PRELIMINARY; PRT; 446 AA.
 AC Q9FR82;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE Delta 8-sphingolipid desaturase.
 OS Suid.
 OS Borage officinalis (Boraginaceae) (Borage).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Lamiales; Boraginaceae; Borage.
 OC NCBI_TaxID=13363;
 RN [1]
 RP SEQUENCE FROM N.A.
 DR EMBL: X87143; CAA60621.1; -
 DR HSSP: P00171; 1F03.
 DR InterPro: IPR001199; Cyt_B5.

RA Libisch B., Michaelson L.V., Lewis M.J., Shewry P.R., Napier J.A.;
 RT "Chimeras of delta6-fatty acid and delta8-sphingolipid desaturases";
 RL Biochem. Biophys. Res. Commun. 279:779-785 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21260464; PubMed=11368168;
 RA Sperling P., Libisch B., Zaehring U., Napier J.A., Heinz E.;
 RT "Functional identification of a delta 8-sphingolipid desaturase from
 Borage officinalis";
 RL Arch. Biochem. Biophys. 388:293-298 (2001).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AF13728; AAG3277.1; -
 DR HSSP: P00171; 1F03.
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 446 AA; 50926 MW; EBD579F035A3AF0C CRC64;

Query Match 47.7%; Score 282.5; DB 10; Length 446;
 Best Local Similarity 51.9%; Pred. No. 1.6e-21;
 Matches 54; Conservative 16; Mismatches 33; Indels 1; Gaps 1;

QY 12 RMISTKELQAAADLMISGSDVYDTPWLRHNGGVEPLTTAGODATDAFMAVHP 71
 DB 6 KYISVELEKHNDLGWVWISIQGKYVNVWDWKHKGGVPLNNLAGODATDAFVHPG 65

QY 72 SVRPLRRFFVGLTDTYVPPASADFRRLAQLSSAGLPERVG 114
 DB 66 TANKNLNENLFTGYHEDYLVSEISKDYRKLVAFESKAGLPERVG 109

RESULT 4
 Q43469
 ID Q43469 PRELIMINARY; PRT; 458 AA.
 AC Q43469;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE Delta-8 sphingolipid desaturase.
 GN SUD1.
 OS Helianthus annuus (Common sunflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Campanulids; Asterales; Asteraceae; Asteroideae;
 OC Heliantheae; Helianthus.
 OC NCBI_TaxID=4232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN=cv. Inbred line HA89;
 RC TISSUE=Cotyledons of developing sunflower fruits;
 RX MEDLINE=96028121; PubMed=7588718;
 RA Sperling P., Schmidt H., Heinz E.;
 RT "A cytochrome b5-containing fusion protein similar to plant acyl lipid
 desaturases";
 RL Eur. J. Biochem. 232:798-805 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP STRAIN=cv. Inbred line HA89;
 RC TISSUE=Cotyledons of developing sunflower fruits;
 RX MEDLINE=21116801; PubMed=11171153;
 RA Sperling P., Blume A., Zaehring U., Heinz E.;
 RT "Further characterization of delta 8-sphingolipid desaturases from
 higher plants";
 RL Biochem. Soc. Trans. 28:638-641 (2000).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: X87143; CAA60621.1; -
 DR HSSP: P00171; 1F03.
 DR InterPro: IPR001199; Cyt_B5.

[illegible]

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DT 01-OCY-2002 (TREMBLrel. 22, Last annotation update)
DE Delta-6-desaturase.
GN D6DS.
OS Echinium gentianoides.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Acerifidae; Iamidae; Boraginaceae; Echinium.
CX NCBI_TaxID=173991;
RN [1]
RP SEQUENCE FROM N.A.
RA Maroto F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz J.R.;
RT "Cloning and Molecular Characterization of the D6-Desaturase from
RT Echinium: Functional Expression in Yeast and Tobacco."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AY055117; AL23580.1; -.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.
SQ SEQUENCE 448 AA; 51428 MW; CZA937951B87C183 CRC64;
Query Match 44.5%; Score 263.5; DB 10; Length 448;
Best Local Similarity 48.1%; Pred. No. 1.76-19;
Matches 50; Conservative 1%; 20; Mismatches 33; Indels 1; Gaps 1.
Qy 12 RMISTKELQHAADDLWISISGVYDYTPMLRHHPGSEVLLITLGGADATDAFAAYPP 71
Db 7 KYIAEELKHKDKDEGDMWISIQGVYVSDWLKHPGGKPELLSLAGEVDAFAVHSG 66
Qy 72 SVRLLRRPFVG-RLDTYVTPASADPRRLAOLSSAGLPERVG 114
Db 67 STWKFLSPFTGYTLKDYSSEVSKDTRKLVFERNKGLFDPKKG 110

RESULT 7
O9ZTV9 PRELIMINARY; PRT; 446 AA.
ID O9ZTV9
AC O9ZTV9;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCY-2002 (TREMBLrel. 22, Last annotation update)
DE Desaturase/cytochrome b5 protein.
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eumetazoa I; Malpighiales; Euphorbiaceae; Ricinus.
CX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Seed endosperm;
RC MEDLINE=97268723; PubMed=9108131;
RA Savanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,
RA Christie W.W., Shewry P.R., Napier J.A.;
RT "Expression of a borage desaturase cDNA containing an N-terminal
RT cytochrome b5 domain results in the accumulation of high levels of
RT delta6-desaturated fatty acids in transgenic tobacco."
RT Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
RL -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AF005096; AAD01240.1; -.
DR HSP; P00173; 11SU.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR Pfam; PF00173; heme_1; 1.
DR ProDom; PD000612; Cyt_B5; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW Heme.

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SQ SEQUENCE 446 AA; 51418 MW; A1954FDB2DB600F CRC64;
 Query Match 44.3%; Score 262.5; DB 10; Length 446;
 Best Local Similarity 50.9%; Pred. No. 2.1e-19;
 Matches 55; Conservative 15; Mismatches 35; Indels 3; Gaps 3;
 QY 9 ADVRMISTKE-LQNAADLWISISGDVYDTPWLRHHPGGEVPLITLAGODATDAFM 67
 2 AERKYYTKRDLKDEHNNRPGDLWISIGKINVTDMSDHKGVSPLHLAQGVTDADFV 61
 Db
 QY 68 YHPSVRLRRFPVG-RLTDYTPPASADFRRLAQLSSAGLFEFVG 114
 62 YHGTAMQVLDKFTGYHLKDYVSFSSKDYRRLVAFSKLG-PEKKG 108
 Db
 RESULT 8
 Q9SAUS PRELIMINARY; PRT; 448 AA.
 AC Q9SAUS; (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
 DE Delta 6-desaturase.
 OS Borago officinalis (Bourrache) (Borage).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Boraginaceae; Borago.
 NCBI_TaxID=13363;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Seed;
 RA Nunberg A.N., Beremand P.D., Thomas T.L.;
 RT "Engineering of Plant Seed Oils to Produce Gamma Linolenic Acid
 (GLA)."
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AF007561; AAD01410.1; -
 DR InterPro: IPR001199; Cyt B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase_1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PSS0255; CYTOCHROME_B5_2; 1.
 KM Heme.
 SQ SEQUENCE 448 AA; 51626 MW; EAC370B22E0DB00 CRC64;
 Query Match 43.6%; Score 258; DB 10; Length 448;
 Best Local Similarity 46.8%; Pred. No. 6.4e-19;
 Matches 51; Conservative 21; Mismatches 35; Indels 2; Gaps 2;
 QY 8 AADV-RMISTKELOAADAADLWISISGDVYDTPWLRHHPGGEVPLITLAGODATDAFM 66
 2 AAOIKYITTSDELDKNDKDPDLWISIGKAYDVSDWKDPGGSFPLKSLAGQEVTDADFV 61
 Db
 QY 67 AYHPSVRLRRFPVG-RLTDYTPPASADFRRLAQLSSAGLFEFVG 114
 62 AFHPASTWKLDKFTGYHLKDYVSFSSKDYRRLVAFSKLG 110
 Db
 RESULT 9
 Q04353 PRELIMINARY; PRT; 448 AA.
 AC Q04353; (T-EMBLrel. 04, Created)
 DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
 DE Delta 6-desaturase.
 OS Borago officinalis (Bourrache) (Borage).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamids; Boraginaceae; Borago.
 NCBI_TaxID=13363;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97268723; PubMed=9108131;
 RA Savyanova O., Smith M.A., Lapienis P., Stobart A.K., Dobson G.,
 RA Christie W.W., Shewry P.R., Napier J.A.;
 RT "Expression of a borage desaturase cDNA containing an N-terminal
 cytochrome b5 domain results in the accumulation of high levels of
 delta6-desaturated fatty acids in transgenic tobacco."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: U79010; AAC49700.1; -
 DR InterPro: IPR001199; Cyt B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase_1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PSS0255; CYTOCHROME_B5_2; 1.
 KM Heme.
 SQ SEQUENCE 448 AA; 51635 MW; B62EE701680909F CRC64;
 Query Match 43.6%; Score 258; DB 10; Length 448;
 Best Local Similarity 46.8%; Pred. No. 6.4e-19;
 Matches 51; Conservative 21; Mismatches 35; Indels 2; Gaps 2;
 QY 8 AADV-RMISTKELOAADAADLWISISGDVYDTPWLRHHPGGEVPLITLAGODATDAFM 66
 2 AAOIKYITTSDELDKNDKDPDLWISIGKAYDVSDWKDPGGSFPLKSLAGQEVTDADFV 61
 Db
 QY 67 AYHPSVRLRRFPVG-RLTDYTPPASADFRRLAQLSSAGLFEFVG 114
 62 AFHPASTWKLDKFTGYHLKDYVSFSSKDYRRLVAFSKLG 110
 Db
 RESULT 10
 Q9ZRP8 PRELIMINARY; PRT; 449 AA.
 AC Q9ZRP8; (T-EMBLrel. 10, Created)
 DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Delta-8 sphingolipid desaturase.
 RN SLD1.
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosids II; Brassicales; Brassicaceae; Brassica.
 NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SRRAIN=cy. Drakkar; TISSUE=ripening embryos;
 RX MEDLINE=99003197; PubMed=9766850;
 RA Speerling P., Zaehntinger U., Heinz B.;
 RT "A sphingolipid desaturase from Higher Plants Identification of a New
 Cytochrome b5 Fusion Protein."
 RL J. Biol. Chem. 273:28590-28596(1998).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: A0224160; CAA11857.1; -
 DR HSSP: P82291; ICXY.
 DR InterPro: IPR001199; Cyt B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase_1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PSS0255; CYTOCHROME_B5_2; 1.
 KM Heme.
 SQ SEQUENCE 449 AA; 51490 MW; FEF37AF9D390C1 CRC64;
 Query Match 42.3%; Score 250.5; DB 10; Length 449;
 Best Local Similarity 47.1%; Pred. No. 4e-18;
 Matches 49; Conservative 17; Mismatches 37; Indels 1; Gaps 1;

QY 12 RMISTKELOAHAAADDLMWISGVDYDVTWMLRHHGCEVPLITLACODATDAPMAHYRP 71
 DB 8 RFTISDLKKNHNGPGLMISIGKVVDSHWKSHKPGEAALINLAGQDVTAFLIYHFG 67
 QY 72 SVAPLRRFPVGR-RLTDYTPPASPAPRRLLAQLSSAGLPERVG 114
 DB 68 TAWRHLENLHNGYHVDHNSVDVSRDYLRAAEFSKRGJFDKXG 111

RESULT 11

Q8L717 PRELIMINARY; PRT; 448 AA.
 ID Q8L717;
 AC Q8L717;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Delta-6-desaturase.
 OS Argania spinosa.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Sapotaceae; Argania.
 NC NCB1_TaxID=85884;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA B1 Filali A., Anderson M., Abbae K.;
 RT "Characterization and cloning of delta-6-desaturase in Argania spinosa
 RT fruit.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AY131238; AAM94345.1; -
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR005804; PA_desat_fam.
 DR Pfam; PF00487; PA_desaturase_1.
 DR Pfam; PF00173; heme_1.1.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR ProDom; PD001081; PA_desat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 448 AA; 51304 MW; 0B46F81B7DEE29EF CRC64;

Query Match 42.1%; Score 249; DB 10; Length 448;
 Best Local Similarity 45.3%; Pred. No. 5.7e-18;
 Matches 50; Conservative 20; Mismatches 37; Indels 2; Gaps 2;
 QY 8 AADV-RMISTKELOAHAAADDLMWISGVDYDVTWMLRHHGCEVPLITLACODATDAPMA 66
 DB 2 AAGIKYITSDKKNHNDKPGDLWISLIGKAYDVSDWVTHPGSPFLKSLAGQDVTAFLY 61
 QY 67 AYHPSVRPLRRFPVGR-RLTDYTPPASPAPRRLLAQLSSAGLPERVG 114
 DB 62 AFHPASTWKNLDFFTGYIKDYSVEVSKDYSKLVFERSKMGLYDKAG 110

RESULT 12

Q8L896 PRELIMINARY; PRT; 449 AA.
 ID Q8L896;
 AC Q8L896;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Delta-8 sphingolipid desaturase.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
 NC NCB1_TaxID=3702;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation.";
 RL Genome Biol. 0:0-0(2002).

QY 12 RMISTKELOAHAAADDLMWISGVDYDVTWMLRHHGCEVPLITLACODATDAPMAHYRP 71
 DB 8 RFTISDLKKNHNGPGLMISIGKVVDSHWKSHKPGEAALINLAGQDVTAFLIYHFG 67
 QY 72 SVAPLRRFPVGR-RLTDYTPPASPAPRRLLAQLSSAGLPERVG 114
 DB 68 TAWRHLENLHNGYHVDHNSVDVSRDYLRAAEFSKRGJFDKXG 111

RN (2)
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RT "Full-length cDNA from Arabidopsis thaliana.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL; AY087345; AAM64895.1; -
 DR InterPro; IPR001199; Cyt_B5.
 DR InterPro; IPR005804; PA_desat_fam.
 DR Pfam; PF00487; PA_desaturase_1.
 DR Pfam; PF00173; heme_1.1.
 DR ProDom; PD000612; Cyt_B5; 1.
 DR ProDom; PD001081; PA_desat_fam; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 KW Heme.
 SQ SEQUENCE 449 AA; 51744 MW; A1B557B8CE03E18 CRC64;

Query Match 39.9%; Score 236.5; DB 10; Length 449;
 Best Local Similarity 39.4%; Pred. No. 1.2e-16;
 Matches 43; Conservative 24; Mismatches 41; Indels 1; Gaps 1;
 QY 7 DAADV-RMISTKELOAHAAADDLMWISGVDYDVTWMLRHHGCEVPLITLACODATDAPMA 66
 DB 3 BTEKKYITNEDLKKHNSGDLWIAIGKVVNSDMIKTHPGQDVTAFLIYHFG 62
 QY 67 AYHPSVRPLRRFPVGR-RLTDYTPPASPAPRRLLAQLSSAGLPERVG 114
 DB 63 AFHPASTWKNLDFFTGYIKDYSVEVSKDYSKLVFERSKMGLYDKAG 111

RESULT 13

Q9ZRP7 PRELIMINARY; PRT; 449 AA.
 ID Q9ZRP7;
 AC Q9ZRP7;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Delta-8 sphingolipid desaturase (AT3G61580/2A19_180).
 GN SLD1 OR F2A19.180 OR AT3G61580.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
 NC NCB1_TaxID=3702;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA STRAIN=cv. Columbia; TISSUE=flower, MAINLY GREEN PARTS, and Root;
 RX MEDLINE=99003197; PubMed=9786850;
 RA Sperling P., Zaehner U., Heinz B.;
 RT "A sphingolipid desaturase from higher plants. Identification of a new
 RT cytochrome b5 fusion protein.";
 RL J. Biol. Chem. 273:28590-28596(1998).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA De Haan M., Maarse A.C., Grivell L.A., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X., Queclier F., Salanoubat M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN (4)
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Natsuka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Tortum M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;

QY 12 RMISTKELOAHAAADDLMWISGVDYDVTWMLRHHGCEVPLITLACODATDAPMAHYRP 71
 DB 8 RFTISDLKKNHNGPGLMISIGKVVDSHWKSHKPGEAALINLAGQDVTAFLIYHFG 67
 QY 72 SVAPLRRFPVGR-RLTDYTPPASPAPRRLLAQLSSAGLPERVG 114
 DB 68 TAWRHLENLHNGYHVDHNSVDVSRDYLRAAEFSKRGJFDKXG 111

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN SEQUENCE FROM N.A.
 RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
 RA Gernlert P., Chen H., Cheuk R., Chan W.M., Chang C.H., Dale J.M.,
 RA Deng J.M., Hayashitaki Y., Heuan V.W., Lee J.M., Ishida J., Kamiya A.,
 RA Seki M., Kim C.J., Natusaka M., Quach H.L., Sakurai T., Satou M.,
 RA Kawai J., Shin P., Tang C.C., Toriumi M., Wallender B.K., Wong C.,
 RA Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
 RA Theologis A., Davis R.W.,
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AJ224161; CA119858.1; -
 DR EMBL: AL132962; CAB71088.1; -
 DR EMBL: AF428420; AL16189.1; -
 DR EMBL: BT000442; AA117419.1; -
 DR HSSP: P00171; 115U.
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KM Heme.
 SQ SEQUENCE 449 AA; 51675 MW; 1450489FD35964 CRC64;
 Query Match 39.9%; Score 236.5; DB 10; Length 449;
 Best Local Similarity 39.4%; Pred. No. 1,2e-16;
 Matches 43; Conservative 24; Mismatches 41; Indels 1; Gaps 1;
 QY 7 DAADVMTSTKELOAHAAADLWISISGDYDVTPLRHNGEVPPLITLAGODATDAFM 66
 DB 3 ETEKKTITMEDLKGKHSKGLWALQKTYNVSDWKITPGSGTIVLNVGDVTAFI 62
 QY 67 AYHPPSVPLRRFVGR-RLTDYTVPPASADFRLLAQLSSAGLFEFVVG 114
 DB 63 AFHGTAMHLDHFLFTGYHIRDFQVSYSRNDYRMAAFRLGTFENKG 111
 RESULT 14
 Q8RAB0 PRELIMINARY; PRT; 477 AA.
 AC Q8RAB0;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Delta 6 fatty acid desaturase D6.
 GN D6.
 OS Phaeodactylum tricornutum.
 OC Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
 OC Bacillariophycidae; Naviculales; Phaeodactylaceae; Phaeodactylum.
 OX NCBI_TaxID=2850;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=UTEX 646;
 RA Domergue F., Lereh J., Zehring U., Heinz E.,
 RA "Cloning and functional characterization of Phaeodactylum tricornutum
 RA front-end desaturases involved in eicosapentaenoic acid
 RA biosynthesis.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AY082393; AL92563.1; -
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 1.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KM Heme.
 SQ SEQUENCE 477 AA; 53452 MW; 2A48B830F8BD99F CRC64;

Query Match 32.9%; Score 195; DB 10; Length 477;
 Best Local Similarity 39.5%; Pred. No. 3.2e-12;
 Matches 45; Conservative 20; Mismatches 41; Indels 8; Gaps 4;
 QY 4 ASGDADVMTSTKELOAHAAADLWISISGDYDVTPLRHNGEVPPLITLAGODATD 63
 DB 9 ASGSGTAARISQOEKVTASPEDAWIHSNKRYDVSNW-HEHGGAV-IFTLAGDMDT 66
 QY 64 AFMAHPPSVPLRRFVGRRLTDYTV---PPASA---DFRLLAQLSSAGLFE 111
 DB 67 IFPAFAPSGSLMKKFTIGELIPETTGKPEQOIAFEKGYRDLRSKLIMGMNK 120
 RESULT 15
 Q944W4 PRELIMINARY; PRT; 459 AA.
 AC Q944W4;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Delta-6 fatty acid desaturase.
 OS Pythium irregulare.
 OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae; Pythium.
 OX NCBI_TaxID=36331;
 RN
 RP SEQUENCE FROM N.A.
 RA Hong H., Datta N., Mackenzie S.L., Qiu X.,
 RA "A delta-6 fatty acid desaturase from Pythium irregulare."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
 DR EMBL: AF419296; AL113110.1; -
 DR InterPro: IPR001199; Cyt_B5.
 DR InterPro: IPR005804; FA_desat_fam.
 DR InterPro: IPR001199; Cyt_B5.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR Pfam: PF00173; heme_1; 1.
 DR ProDom: PD000612; Cyt_B5; 1.
 DR ProDom: PD001081; FA_desat_fam; 2.
 DR PROSITE: PS50255; CYTOCHROME_B5_2; 1.
 KM Heme.
 SQ SEQUENCE 459 AA; 52498 MW; 286464DA761B055 CRC64;
 Query Match 32.7%; Score 193.5; DB 10; Length 459;
 Best Local Similarity 37.0%; Pred. No. 4.4e-12;
 Matches 44; Conservative 20; Mismatches 34; Indels 21; Gaps 4;
 QY 12 RMISTELOAHAAADLWISISGDYDVTPLRHNGEVPPLITLAGODATDAFMAYHPP 71
 DB 10 RLVSWEKREHATPATAMWIVHHKVVYDISKW-DSHGGSV-MITQAGDADTDAFAVHPS 67
 QY 72 SVRPLLRFPVGRRLTDYTV---PPASA---DFRLLAQLSSAGLFE 111
 DB 68 SALKLLEQFLYGVDETSTKAEIGEPASDEBARRRERINEFLASRYRLKVKVGMGLYD 126

Search completed: January 1, 2004, 06:33:58
 Job time: 12.4316 secs

FILED DATE: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-934-254-5

Query Match 43.6%; Score 258; DB 4; Length 448;
Best Local Similarity 46.8%; Pred. No. 3.8e-23;
Matches 51; Conservative 21; Mismatches 35; Indels 2; Gaps 2;

QY 8 AADV-RMISTKELQAAADLWISISGDVYVTPMLRHHHGGVPLITLAGODATDAM 66
DB 2 AAQIKKYITSDKLNHDKRGDLMISIQKAYDVSDVWVNDHPGSGFPLKSLAGQEVTDATV 61

QY 67 AYHPPSVRLRRFFVG-RLTDYTPPASADPRRLAQLSAGLPERVG 114
DB 62 AFHPASTWKNLKKFTGYLYLKDYSVSESVKVRKLVFEFSKMGLYDKG 110

RESULT 5
US-08-833-610-5
Sequence 5, Application US/08833610
Patent No. 5972664
GENERAL INFORMATION:
APPLICANT: KUTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.123.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-833-610-5

Query Match 42.1%; Score 249; DB 2; Length 446;
Best Local Similarity 45.9%; Pred. No. 4.7e-22;
Matches 50; Conservative 21; Mismatches 36; Indels 2; Gaps 2;

QY 8 AADV-RMISTKELQAAADLWISISGDVYVTPMLRHHHGGVPLITLAGODATDAM 66
DB 2 AAQIKKYITSDKLNHDKRGDLMISIQKAYDVSDVWVNDHPGSGFPLKSLAGQEVTDATV 61

QY 67 AYHPPSVRLRRFFVG-RLTDYTPPASADPRRLAQLSAGLPERVG 114
DB 62 AFHPASTWKNLKKFTGYLYLKDYSVSESVKVRKLVFEFSKMGLYDKG 110

RESULT 6
US-08-834-033A-15
Sequence 15, Application US/08834033A
Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KUTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
NUMBER OF SEQUENCES: 26
CURRENT APPLICATION DATA:
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300.USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-15

Query Match 42.1%; Score 249; DB 3; Length 446;
Best Local Similarity 45.9%; Pred. No. 4.7e-22;
Matches 50; Conservative 21; Mismatches 36; Indels 2; Gaps 2;

QY 8 AADV-RMISTKELQAAADLWISISGDVYVTPMLRHHHGGVPLITLAGODATDAM 66
DB 2 AAQIKKYITSDKLNHDKRGDLMISIQKAYDVSDVWVNDHPGSGFPLKSLAGQEVTDATV 61

QY 67 AYHPPSVRLRRFFVG-RLTDYTPPASADPRRLAQLSAGLPERVG 114
DB 62 AFHPASTWKNLKKFTGYLYLKDYSVSESVKVRKLVFEFSKMGLYDKG 114

DB 62 AFHASTWKLJDKFTGYLKDYSVSEVSKYRKLVEFSKMGJLYDKG 110

RESULT 7

US-08-833-610-2
Sequence 2, Application US/08833610
Patent No. 5972664
GENERAL INFORMATION:
APPLICANT: KUNITZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YONG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVE, P.O. BOX 60039
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,610
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.123.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
TELEFAX: (650)328-4477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-833-610-2

Query Match 25.1%; Score 148.5; DB 2; Length 446;

Best Local Similarity 40.8%; Pred. No. 8e-10; Matches 31; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 17 KELOAHAAADDLMISISGVYDVTPLRHHGGEVPLITLAGDADAFMAVHP-PSVRP 75
DB 12 EELAAHNTKDDLLAIGRVDYTKFLSRHGGVDTLLAGAGDVTFVEMVHAFGAADA 71
QY 76 LRRFFVGRLTDTYVP 91
DB 72 IMKXYVGTIVSNELP 87

RESULT 8

US-08-834-033A-5
Sequence 5, Application US/08834033A
Patent No. 6075183
GENERAL INFORMATION:
APPLICANT: KUNITZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YONG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300.USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-033A-5

Query Match 25.1%; Score 148.5; DB 3; Length 446;
Best Local Similarity 40.8%; Pred. No. 8e-10; Matches 31; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 17 KELOAHAAADDLMISISGVYDVTPLRHHGGEVPLITLAGDADAFMAVHP-PSVRP 75
DB 12 EELAAHNTKDDLLAIGRVDYTKFLSRHGGVDTLLAGAGDVTFVEMVHAFGAADA 71
QY 76 LRRFFVGRLTDTYVP 91
DB 72 IMKXYVGTIVSNELP 87

RESULT 9

US-09-145-828A-23
Sequence 23, Application US/09145828A
Patent No. 6403349
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda B. Y.
APPLICANT: Huang, Yong-Sheng
APPLICANT: Thurmond, Jennifer
APPLICANT: Kitchen, Stephen J.
APPLICANT: Parker-Barnes, Jennifer M.
TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
FILE REFERENCE: 6407 US. 01
CURRENT APPLICATION NUMBER: US/09/145,828A
CURRENT FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 446
TYPE: PRT
ORGANISM: Mortierella alpina
US-09-145-828A-23

Query Match 25.1%; Score 148.5; DB 4; Length 446;

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(without alignments)
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Title: US-09-857-524B-17
Perfect score: 592
Sequence: 1 MPAAKADADVMISTKEIQ.....ADFRLLQLSSAGLFEVVG 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 733937 seqs, 200641211 residues
Total number of hits satisfying chosen parameters: 733937

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
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2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	274.5	46.4	458	US-10-340-779A-11	Sequence 11, Appl
2	266	44.9	452	US-10-029-756-27	Sequence 27, Appl
3	258	43.6	448	US-10-340-779A-13	Sequence 13, Appl
4	193.5	32.7	459	US-09-967-477B-8	Sequence 5, Appl
5	161	27.2	453	US-09-769-863-14	Sequence 8, Appl
6	161	27.2	453	US-10-054-534B-14	Sequence 14, Appl
7	161	27.2	453	US-10-431-952-20	Sequence 14, Appl
8	160.5	27.1	509	US-09-769-863-20	Sequence 37, Appl
9	157.5	26.6	470	US-10-120-637A-37	Sequence 20, Appl
10	157.5	26.6	470	US-10-054-534B-20	Sequence 20, Appl
11	157.5	26.6	470	US-10-431-952-20	Sequence 20, Appl
12	157.5	25.9	456	US-09-967-477B-6	Sequence 6, Appl
13	151.5	25.6	519	US-09-967-477B-2	Sequence 2, Appl
14	151.5	25.5	141	US-10-369-493-5090	Sequence 5090, Ap

16	150.5	25.4	487	15	US-10-168-274-9	Sequence 9, Appl
17	148.5	25.1	446	10	US-09-903-456-30	Sequence 30, Appl
18	148.5	25.1	446	12	US-10-278-391-2	Sequence 2, Appl
19	148.5	25.1	446	12	US-10-156-911-10	Sequence 30, Appl
20	148.5	25.1	446	12	US-10-408-726-27	Sequence 27, Appl
21	148.5	25.1	447	15	US-10-191-513A-10	Sequence 10, Appl
22	146.5	24.7	103	12	US-10-369-493-6503	Sequence 6503, Ap
23	145	24.5	112	12	US-10-369-493-12640	Sequence 12640, A
24	144.5	24.4	446	12	US-10-340-779A-3	Sequence 3, Appl
25	144.5	24.4	446	12	US-10-340-779A-14	Sequence 14, Appl
26	141.5	23.9	129	9	US-09-911-781-5	Sequence 5, Appl
27	141.5	23.9	129	12	US-10-400-902-5	Sequence 5, Appl
28	138	23.3	513	12	US-10-120-637A-16	Sequence 46, Appl
29	136.5	23.1	155	15	US-10-106-698-4650	Sequence 4650, Ap
30	136.5	23.1	169	9	US-09-925-301-902	Sequence 902, Ap
31	135	22.8	360	15	US-10-191-513A-39	Sequence 39, Appl
32	135	22.8	444	15	US-10-262-617-3	Sequence 3, Appl
33	135	22.8	444	15	US-10-191-513A-12	Sequence 12, Appl
34	134	22.6	515	11	US-09-849-199A-18	Sequence 18, Appl
35	134	22.6	515	11	US-09-849-199A-19	Sequence 19, Appl
36	134	22.6	515	11	US-09-849-199A-20	Sequence 20, Appl
37	134	22.6	515	11	US-09-849-199A-21	Sequence 21, Appl
38	134	22.6	515	12	US-10-120-637A-18	Sequence 18, Appl
39	134	22.6	515	12	US-10-120-637A-19	Sequence 19, Appl
40	134	22.6	515	12	US-10-120-637A-20	Sequence 20, Appl
41	134	22.6	515	12	US-10-120-637A-21	Sequence 21, Appl
42	134	22.6	515	12	US-10-120-637A-70	Sequence 70, Appl
43	134	22.6	515	12	US-10-060-793-29	Sequence 29, Appl
44	134	22.6	859	12	US-10-148-907A-31	Sequence 31, Appl
45	131.5	22.2	445	15	US-10-262-617-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-340-779A-11
; Sequence 11, Application US/10340779A
; Publication No. US20030152963A1
; GENERAL INFORMATION:
; APPLICANT: Napier, Johnathan A.
; APPLICANT: Michaelson, Louise
; APPLICANT: Stobart, Keith
; TITLE OF INVENTION: Degatrase
; FILE REFERENCE: 005407, 00004
; CURRENT APPLICATION NUMBER: US/10/340, 779A
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/582, 034
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/GB98/03895
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: UK 9814034.6
; PRIOR FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: UK 9727256.1
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Helianthus annuus
US-10-340-779A-11
Query Match 46.4%; Score 274.5; DB 12; Length 458;
Best Local Similarity 50.0%; Pred. No. 3, 2e-24;
Matches 52; Conservative 19; Mismatches 32; Indels 1; Gaps 1;

QY 12 RMISTEIQAHAAADLWISIGDYVDYPMRHRHGGCVPLITLAGODATAFMAYHP 71
DB 17 KITSKEIKKHNNDLWISIGKYVNTWEMKEHGGAPLNLGQVTDFAIFHPG 76
QY 72 SVRPLRRFFVG-RITDYTVPPASADFRLLQLSSAGLFEVVG 114

Db 77 TAWKHLDTFTGYHLKDQVSDISRDYKRLASEFAKAMEFKG 120

RESULT 2

US-10-029-756-27

Sequence 27, Application US/10029756

Publication No. US20020108147A1

GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.

TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A DELTA 6-DESATURASE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/029,756

FILING DATE: 21-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,254

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Presser, Leopold

REGISTRATION NUMBER: 19,827

REFERENCE/DOCKET NUMBER: 83832YXWVU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 452 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 27:

US-10-029-756-27

Query Match 44.8%; Score 266; DB 14; Length 452;

Best Local Similarity 49.5%; Pred. No. 3,2e-23;

Matches 52; Conservative 18; Mismatches 33; Indels 2; Gaps 1;

QY 12 RMISTKELQAAADLMISISGDVYDVTPLRHHHGGEVPLITLAGODATDAFMAYHP 71

Db 7 KYTAEDELRRHNSGDLWISIQKAYVDSHMAAHPGGEVPLITLAGODVTDFAIVHPG 66

QY 72 SVRPLRRFVG--RLTDYTPPASADFRLLAQLSAGLFEVVG 114

Db 67 TAWRHLDTFTGYHLKDQVSDISRDYKRLASEFAKAMEFKG 111

RESULT 3

US-10-340-779A-13

Sequence 13, Application US/10340779A

Publication No. US20030152983A1

GENERAL INFORMATION:

APPLICANT: Napier, Johnathan A.

APPLICANT: Michaelson, Louise

APPLICANT: Stobart, Keith

TITLE OF INVENTION: Desaturase

FILE REFERENCE: 005407,00004

CURRENT APPLICATION NUMBER: US/10/340,779A

CURRENT FILING DATE: 2003-03-24

PRIOR APPLICATION NUMBER: US 09/582,034

PRIOR FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: PCT/GB98/03895

PRIOR FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: UK 9814034.6

PRIOR FILING DATE: 1998-06-29

PRIOR APPLICATION NUMBER: UK 9727256.1

PRIOR FILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FaesEQ for Windows Version 4.0

SEQ ID NO 13

LENGTH: 448

TYPE: PRT

ORGANISM: Borago officinalis

US-10-340-779A-13

Query Match 43.6%; Score 258; DB 12; Length 448;

Best Local Similarity 46.8%; Pred. No. 2.9e-22;

Matches 51; Conservative 21; Mismatches 35; Indels 2; Gaps 2;

QY 8 AADV-RMISTKELQAAADLMISISGDVYDVTPLRHHHGGEVPLITLAGODATDAFM 66

Db 2 AAQIKRYTSDLEKNHDKRGDLWISIQKAYVDSHMAAHPGGEVPLITLAGODVTDFAV 61

QY 67 AYHPSVRPLRRFVG--RLTDYTPPASADFRLLAQLSAGLFEVVG 114

Db 62 AHPHASTWKNLDTFTGYHLKDQVSDISRDYKRLASEFAKAMEFKG 110

RESULT 4

US-10-029-756-5

Sequence 5, Application US/10029756

Publication No. US20020108147A1

GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.

TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A DELTA 6-DESATURASE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/029,756

FILING DATE: 21-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,254

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Presser, Leopold

REGISTRATION NUMBER: 19,827

REFERENCE/DOCKET NUMBER: 83832YXWVU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 448 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-029-756-5

Query Match	43.6%	Score 258;	DB 14;	Length 448;
Best Local Similarity	46.8%	Pred. NO. 2.9e-22;		
Matches	51;	Conservative	21;	Mismatches 35;
				Indels 2;
				Gaps 2.

Qy	8	AAAV-RNISTKKEIQAHAADLMISISGVYDTPTLYRNHPSGEVLTITAGADATDAM	66
Db	2	AAQIKKITYTDELEKNHKPGDLMISIQKAYVDSDWKHPGGSFPLKSLAGGEVTDARV	61
Qy	67	AHPSPVRLPLRRPFVQ-RLDTYTPPASADEFRLLAQSSAGLFEKRV	114
Db	62	AFHPASWKKLDFKFTFGYIYKDYSSVSASVDYIKLVPFSSKMGILYKKG	110

RESULT 5

```

US-09-967-477B-8
: Sequence 8, Application US/09967477B
: Patent No. US20020156254A1
: GENERAL INFORMATION:
: APPLICANT: Xiao Qiu
: APPLICANT: Haiping Hong
: TITLE OF INVENTION: PAD4, PAD5, PAD5-2, AND PAD6, NOVEL
: TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
: FILE REFERENCE: BNZ-001
: CURRENT APPLICATION NUMBER: US/09/967,477B
: CURRENT FILING DATE: 2002-04-16
: PRIOR APPLICATION NUMBER: 60/236,303
: PRIOR FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: 60/227,562
: PRIOR FILING DATE: 2001-06-12
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8
: LENGTH: 459
: TYPE: PR1
: ORGANISM: Thraustochytrium sp.
US-09-967-477B-8

```

Query Match	32.7%	Score	193.5	DB	10	Length	459
Best Local Similarity	37.0%	Pred. No.	1.6e-14				
Matches	44	Conservative	20	Mismatches	34	Indels	21
						Gaps	4

[illegible]

RESULT 6

```

US-09-769-863-14
; Sequence 14, Application US/09769863
; Publication No. US20030157144A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Dae, Tapas
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DEBRATRAE GENES AND USES THEREOF
; FILE REFERENCE: 6763 US.O1
; CURRENT APPLICATION NUMBER: US/09/769,863
; CURRENT FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: PR1
; ORGANISM: Saprolengia dictyna
US-09-769-863-14

```

Query Match	27.2%	Score 161;	DB 12;	Length 453;
Best Local Similarity	34.8%	Pred. No. 1,2e-10;		
Matches 39;	Conservative 20;	Mismatches 37;	Indels 16;	Gaps 4.

```

QY      14  ISKRELOAHNAADMLTISISGVYVDPYLRHNPGEVLLITLACGADATDAEFAAHPSPV  73
Db      10  ISMATIREHNROQNAIVIHVKYLDISAF-EDHPGS-VVMFPGAGSDATDAFAVHPRSA  67

QY      74  RLLRRRFFGRLDYF-----VPPASDF-----RLLAQSASAFLE  111
Db      68  LKLLREQYVGVDDOSTAANDVTSISDEVKKSQSFSTASYKRLYLEVGRLLYD  119

```

RESULT 7

```

US-10-054-534B-14
Sequence ID: Application US/1,005,453AB
Publication No. US20030167525A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Sheng
APPLICANT: Das, Tapas
APPLICANT: Thurmond, Jennifer M.
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DSSATRASE GENES AND USES THEREOF
FILE REFERENCE: 6763, US, P1
CURRENT APPLICATION NUMBER: US/10/054,534B
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 09/769,863
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 453
TYPE: PRT
ORGANISM: Saprolegnia diclina
US-10-054-534B-14

```

Query Match	27.2%	Score 161;	DB 10;	Length 453;
Best Local Similarity	34.8%	Pred. No. 1.2e-10;		
Matches 39; Conservative	20;	Mismatches 37;	Indels 16;	Gaps 4;

```

QY      14  ISRKELQAAHAADLWISISGDIYDVTPLRHHPGSEVLITLTAOGADATDAEMAHPREV 73
Db      10  ISMATIRENNRQDMATIVIHKKVYDSAF-EDHPGS-VVMFQAQSGADATDAVAVHPSSA 67

QY      74  RPLLRPFPPGRGLDLY-----VPPASADF-----RRLAQSSAGLFE 111
Db      68  LKLLREIVGGDVQSTAAVDTISDEVKKSQSDFLASTYKLLLEVRKGLGYLD 119

```

RESULT 8

```

US-10-431-952-14
Sequence 14, Application US/10411952
Publication No. US20030190733A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Sheng
APPLICANT: Das, Tapas
APPLICANT: Thurmond, Jennifer
APPLICANT: Perleix, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
FILE REFERENCE: 6793 US '01
CURRENT APPLICATION NUMBER: US/10/431,952
CURRENT FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: US/09/769,863
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FaSTSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 453

```

TYPE: PRT
ORGANISM: Saprolegnia diclina
US-10-431-952-14

Query Match 27.2%; Score 161; DB 12; Length 453;
Best Local Similarity 34.8%; Pred. No. 1.2e-10;
Matches 39; Conservative 20; Mismatches 37; Indels 16; Gaps 4;

QY 14 ISRKELOAHAAADLMWISGVDYDTPMLRHHPGGEVPLITLAGODATDAFMAVHPPSV 73
DB 10 ISMTTTEHRQDAMVIHHKVDISAF-EDHPGG-VVMTQAGDATDAFAVHPPSSA 67
QY 74 RPLLRFFVGRLLTDYT-----VPPASADF-----RRLAQLSSAGLFE 111
DB 68 LKLEQYVVDVQSTAAVDTSTISDEVKSGSDPIASRYRLRLVEVRLGLYD 119

RESULT 9

US-10-120-637A-37
Sequence 37, Application US/10120637A
Publication No. US20030134400A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Thurmond, Jennifer M.
APPLICANT: Das, Yung-Sheng
APPLICANT: Leonard, Amanda E.
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DELTA 4-DESATURASE GENES AND USES
FILE REFERENCE: 6804 US. P1
CURRENT APPLICATION NUMBER: US/10/120,637A
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: US 09/849,199
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 509
TYPE: PRT
ORGANISM: Schizochytrium aggregatum
US-10-120-637A-37

Query Match 27.1%; Score 160.5; DB 12; Length 509;
Best Local Similarity 36.0%; Pred. No. 1.6e-10;
Matches 40; Conservative 21; Mismatches 33; Indels 17; Gaps 4;

QY 15 STEKLOAHAAADLMWISGVDYDTPMLRHHPGGEVPLITLAGODATDAFMAVHPPSV 74
DB 10 SMAQVRHNTPTDDAWCAIHGEVYELTKFARTHPGGDITLLA-AKKEATILFETTH---VR 65
QY 75 PL-----LRFFVGRLL-----TDYTVPPASADFRLAQLSSAGLFE 112
DB 66 PISDAVLRKRYRIGKTLAAAGKDEPANDSTYVMSDFYKVLQRVAVRLER 116

RESULT 10
US-09-769-863-20
Sequence 20, Application US/09769863
Publication No. US20030157144A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Sheng
APPLICANT: Das, Tapas
APPLICANT: Thurmond, Jennifer
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
FILE REFERENCE: 6763 US. O1
CURRENT APPLICATION NUMBER: US/09/769,863
CURRENT FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 470
TYPE: PRT
ORGANISM: Saprolegnia diclina
US-09-769-863-20

Query Match 26.6%; Score 157.5; DB 12; Length 470;
Best Local Similarity 39.1%; Pred. No. 3.2e-10;
Matches 34; Conservative 12; Mismatches 34; Indels 7; Gaps 2;

QY 2 PAASKDADVRMISTEKLOAHAAADLMWISGVDYDTPMLRHHPGGEVPLITLAGODA 61
DB 18 PVAGKKA-----FTWQEVAGQHTTAASAWIIRKQYDVTENANKHPGGREMYLLHAGREA 72
QY 62 TDAFMAVHPPS--VRPLLRFFVGRLLT 86
DB 73 TDTFDSYHPPSDKAESILNKYEIGTFT 99

RESULT 11

US-10-054-534B-20
Sequence 20, Application US/10054534B
Publication No. US20030167525A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Sheng
APPLICANT: Das, Tapas
APPLICANT: Thurmond, Jennifer M.
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
FILE REFERENCE: 6763 US. P1
CURRENT APPLICATION NUMBER: US/10/054,534B
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 09/769,863
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 470
TYPE: PRT
ORGANISM: Saprolegnia diclina
US-10-054-534B-20

Query Match 26.6%; Score 157.5; DB 12; Length 470;
Best Local Similarity 39.1%; Pred. No. 3.2e-10;
Matches 34; Conservative 12; Mismatches 34; Indels 7; Gaps 2;

QY 2 PAASKDADVRMISTEKLOAHAAADLMWISGVDYDTPMLRHHPGGEVPLITLAGODA 61
DB 18 PVAGKKA-----FTWQEVAGQHTTAASAWIIRKQYDVTENANKHPGGREMYLLHAGREA 72
QY 62 TDAFMAVHPPS--VRPLLRFFVGRLLT 86
DB 73 TDTFDSYHPPSDKAESILNKYEIGTFT 99

RESULT 12
US-10-431-952-20
Sequence 20, Application US/10431952
Publication No. US20030190733A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Sheng
APPLICANT: Das, Tapas
APPLICANT: Thurmond, Jennifer
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
FILE REFERENCE: 6763 US. O1
CURRENT APPLICATION NUMBER: US/10/431,952
CURRENT FILING DATE: 2003-05-08

PRIOR APPLICATION NUMBER: US/09/769,863
 PRIOR FILING DATE: 2001-01-25
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 20
 LENGTH: 470
 TYPE: PRF
 ORGANISM: *Saprolegnia diclina*
 US-10-431-952-20

Query Match 26.6%; Score 157.5; DB 12; Length 470;
 Best Local Similarity 39.1%; Pred. No. 3.2e-10;
 Matches 34; Conservative 12; Mismatches 34; Indels 7; Gaps 2;

QY 2 PAAKAAVPMISTELQAAADLMISGSDVYDTPWLRHHGGEVPLITLAGODATDAFWAYHPPSV 61
 DB 18 PAAKAA----FTWEEVQAHNTAASAMITIRKGVYDTEWANKHGGEMVLLHAGREA 72
 QY 62 TDAFWAYHPPSV--VRPLRRFFVGRLT 86
 DB 73 TDTFDSYHPPSDKASILNKYEIGTFT 99

RESULT 13
 US-09-967-477B-6
 Sequence 6, Application US/09967477B
 Patent No. US20020156254A1
 GENERAL INFORMATION:
 APPLICANT: Xiao Qiu
 APPLICANT: Haijing Hong
 TITLE OF INVENTION: FAD5, FAD5-2, AND FAD6, NOVEL
 TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
 FILE REFERENCE: BNZ-001
 CURRENT APPLICATION NUMBER: US/09/967,477B
 CURRENT FILING DATE: 2002-04-16
 PRIOR APPLICATION NUMBER: 60/236,303
 PRIOR FILING DATE: 2000-09-28
 PRIOR APPLICATION NUMBER: 60/297,562
 PRIOR FILING DATE: 2001-06-12
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 6
 LENGTH: 456
 TYPE: PRF
 ORGANISM: *Thraustochytrium* sp.
 US-09-967-477B-6

Query Match 25.9%; Score 153.5; DB 10; Length 456;
 Best Local Similarity 37.3%; Pred. No. 9.4e-10;
 Matches 31; Conservative 15; Mismatches 34; Indels 3; Gaps 2;

QY 17 KELQAAHAADLMISGSDVYDTPWLRHHGGEVPLITLAGODATDAFWAYHPPSV-- 74
 DB 12 QEVAKKNTAKSAMVIRGEVYDTEWADKHGSEILVHSGRECTDTFYSYHPPFNRA 71
 QY 75 PLRRFFVGRLT-DYTVPPASAD 96
 DB 72 KILAKYKIKLVGVGEYFPVFKPD 94

RESULT 14
 US-09-967-477B-2
 Sequence 2, Application US/09967477B
 Patent No. US20020156254A1
 GENERAL INFORMATION:
 APPLICANT: Xiao Qiu
 APPLICANT: Haijing Hong
 TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL
 TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
 FILE REFERENCE: BNZ-001
 CURRENT APPLICATION NUMBER: US/09/967,477B
 CURRENT FILING DATE: 2002-04-16
 PRIOR APPLICATION NUMBER: 60/236,303

PRIOR FILING DATE: 2000-09-28
 PRIOR APPLICATION NUMBER: 60/297,562
 PRIOR FILING DATE: 2001-06-12
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 519
 TYPE: PRF
 ORGANISM: *Thraustochytrium* sp.
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: 462
 OTHER INFORMATION: Xaa = Gly
 US-09-967-477B-2

Query Match 25.6%; Score 151.5; DB 10; Length 519;
 Best Local Similarity 37.8%; Pred. No. 1.9e-09;
 Matches 37; Conservative 21; Mismatches 37; Indels 3; Gaps 3;

QY 14 ISTKELQAAHAADLMISGSDVYDTPWLRHHGGEVPLITLAGODATDAFWAYHPPSV 73
 DB 9 IPPEQVRAHKKPDAMCAIHGHVYDTPKASVHPGSDITLLA-AGKATVLTETVARGV 67
 QY 74 R-PLRRFFVGRLTDTYTVPPASADFFRLAQLSSAGLP 110
 DB 68 SDAVLRKRIKLPD-GCGGANEKERTLSGLSSASY 104

RESULT 15
 US-10-369-493-5090
 Sequence 5090, Application US/10369493
 Publication No. US20030233675A1
 GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianfeng
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO 5090
 LENGTH: 141
 TYPE: PRF
 ORGANISM: *Caenorhabditis elegans*
 US-10-369-493-5090

Query Match 25.5%; Score 151; DB 12; Length 141;
 Best Local Similarity 39.1%; Pred. No. 4.2e-10;
 Matches 34; Conservative 14; Mismatches 35; Indels 4; Gaps 2;

QY 9 ADVRMISTKELQAH--AAADLMISGSDVYDTPWLRHHGGEVPLITLAGODATDAF 65
 DB 2 SELRVISLDEVSKEHWEDADQSCWIVISGKYDVTFLNEHGGGEVITQLAGKATVGF 61
 QY 66 M-AHYHPPSVPLRRFFVGRLTDTYTP 91
 DB 62 LDVGHSKAIEMANEYLIQLPESDVP 88

Search completed: January 1, 2004, 06:58:38
 Job time: 22.7174 secs

